

Interlaboratory Comparison on Dioxins in Food 2009



Tenth Round of an International Study

Veronica Horpestad Liane
Georg Becher

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Authors:

Veronica Horpestad Liane
Georg Becher

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P. O. Box 4404 Nydalen
NO-0403
Norway

Tel: +47-21 07 70 00

E-mail: folkehelseinstituttet@fhi.no

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Summary

In 2009, the tenth round of the Interlaboratory Comparison on Dioxins 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 2009 study was performed on sample homogenates of beef, butter oil and herring. In addition, six standard solutions were provided containing known concentrations of a) PCDDs/PCDFs, b) non-ortho PCBs, c) mono-ortho PCBs, d) PBDEs, e) Indicator PCBs and f) α -HBCD. The testing materials were sent to 103 laboratories in January 2009, and results were returned from 92 laboratories in 31 different countries by the deadline in April. Most laboratories analysed all the three food items. A draft report was made available on the web in August and was discussed among the participants at the Waters Users' Meeting during the DIOXIN2009 Symposium in Beijing, China.

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 76-84% of the laboratories. The majority of the laboratories (85-88%) 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 is quite low (7-11%). 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.

For the different food samples, between 53-64 laboratories reported results for the six Indicator PCBs, 30-41 laboratories reported concentrations for the seven tetra- to hepta-BDEs and 20-25 laboratories reported concentrations for BDE-209. The concentrations of the sum of seven PBDEs ranged from 111 pg/g fresh weight in beef to 863 pg/g fresh weight in herring. The RSD for PBDE concentrations on fresh weight basis was on average 13, 14 and 16% for beef, butter oil and herring, respectively. The consensus concentrations for BDE-209 were 26, 28 and 14 pg/g fresh weight in beef, butter oil and herring, respectively. The corresponding RSD on fresh weight basis was 66, 59 and 75%. The consensus concentrations calculated for HBCD are just indicative values as only few laboratories had reported results. The sum of concentrations for six Indicator PCBs ranged from 11.6 ng/g fresh weight in butter oil to 105 ng/g fresh weight in beef. The average RSDs were 11, 13 and 14% for beef, butter oil and herring, 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 tenth round of a world-wide interlaboratory comparison study on dioxin-like compounds in food organised by the Department of Analytical Chemistry, Division of Environmental Medicine, Norwegian Institute of Public Health, Oslo, Norway.

The exercise took place from January 2009, when the samples were shipped to the laboratories for analysis, to the beginning of April 2009, when the last reports on the results were received. A draft report was made available to the participants on the web

(<http://www.fhi.no>) in August and was discussed during the Waters Users' Meeting at the DIOXIN2009 Symposium in Beijing, China.

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 analyse these persistent organic pollutants.

All of the participants from previous rounds of this series of "Interlaboratory Comparisons on Dioxins 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 92 laboratories that submitted results, and thereby contributed to the study results, are presented in Table 1

Table 1. Participants that reported results in the tenth round of Interlaboratory Comparison on POP's in food 2009

Agripapadigma Ravenna, Italy	Department of Environmental and Occupational Health, National Cheng Kung University, College of Medicine Tainan, Taiwan, R.O.C.
Alcontrol AB Linköping, Sweden	Dioxin Analysis Unit, National Measurement Institute Sydney, Australia
ALS Czech Republic, s.r.o. Pardubice, Czech Republic	Environmental Laboratory - Institut Quimic de Sarria Barcelona, Spain
ALS Laboratory Group Edmonton, Alberta, Canada	FDA, Arkansas Regional Laboratory, Dioxin Group Jefferson, USA
Analytical Perspectives Wilmington, USA	Federal Environment Agency Berlin, Germany
AsureQuality Limited Wellington, New Zealand	Food and Environment Research Agency (FERA) York, UK
AXYS Analytical Services Ltd. Sidney, Canada	FOOD GmbH Analytik Jena, Germany
Calgary Laboratory, Canadian Food Inspection Agency Calgary, Alberta, Canada	Food Research Division Ottawa, Canada
CARSO Lyon, France	GfA mbH Hamburg, Germany
CART University of Liège Liège, Belgium	Government Laboratory Hong Kong SAR, China
Central Agricultural Office Food and Feed Safety Directorate Budapest, Hungary	Helmholtz Zentrum München, German Research Center for Environmental Health (GmbH) Neuherberg, Germany
Central Laboratory of Residue Analysis of Pesticides and Heavy Metals In Food Giza, Egypt	Hong Kong Baptist University/Dioxin Analysis Laboratory Kowloon, Hong Kong SAR, China
Chemisches Landes- und Staatliches Veterinäruntersuchungsamt Münster Münster, Germany	Hong Kong Government Laboratory Hong Kong SAR, China
Chemisches und mikrobiologisches Institut UEG GmbH Wetzlar, Germany	Institute of Aquaculture Stirling, UK
Chemisches und Veterinäruntersuchungsamt (CVUA) Freiburg, Germany	Istituto Zooprofilattico Sperimentale Dell'Abruzzo E Del Molise "G. Carporale" Teramo, Italy
Consorzio Interuniversitario Nazionale la Chimica per l'Ambiente Marghera (VE), Italy	Istituto Zooprofilattico Sperimentale delle Regioni Lazio Rome, Italy

Danish Veterinary and Food Administration Ringsted, Denmark	Japan Food Research Laboratories Tokyo, Japan
Kansas City District Lab Lenexa, Kansas, USA	National Food and Veterinary Risk Assessment Institute Vilnius, Lithuania
Korea Food And Drug Administration Seoul , Republic of Korea	National Food Institute Søborg, Denmark
LABERCA Nantes, France	National institute of nutrition and food safety Beijing, China
Laboratoire de Rouen Rouen, France	National Institute for Health and Welfare Kuopio, Finland
Institute of Environmental Assessment and Water Research (IDÆA-CSIC) Barcelona, Spain	NCSR "Demokritos" Athens, Greece
Laboratorio CSMO Magistrato alle Acque di Venezia Padova, Italy	Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit Oldenburg, Germany
Laboratory of Vendee La Roche sur Yon, France	Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit Braunschweig, Germany
Landesamt für Umweltschutz Sachsen-Anhalt, Labor Reilstrasse Halle, Germany	NIFES- National Institute of Nutrition and Seafood Research Bergen, Norway
Landeslabor Brandenburg Frankfurt, Germany	NILU- Norsk Institutt for luftforskning Kjeller, Norway
Landesuntersuchungsamt, Institut für Lebensmittelchemie Speyer, Germany	Nofalab BV Schiedam, The Netherlands
Landwirtschaftliche Untersuchungs- und Forschungsanstalt Speyer Speyer, Germany	Norwegian Institute of Public Health Oslo, Norway
LUFA Rostock Rostock, Germany	Oekometric GmbH Bayreuth, Germany
Marchwood Scientific Services Southampton, UK	Pacific Rim Laboratories Inc. Surrey, Canada
mas münster analytical solutions gmbh Münster, Germany	POP Lab, Shenzhen Center for Disease Control & Prevention Shenzhen, Guangdong, China
Max Rubner-Institut (MRI), Bundesforschungsinstitut für Ernährung und Lebensmittel Kulmbach, Germany	Qlip N.V. Leusden, The Netherlands
Maxxam Analytics Mississauga, Ontario, Canada	R&C LAB SRL Vicenza, Italy

Micropolluants Technologie Thionville, France	Research and Productivity Council (RPC) Fredericton, New Brunswick, Canada
RIKILT Wageningen, The Netherlands	Toxicological Chemistry Unit, Department of the Environment and Primary Prevention Rome, Italy
Scientific Institute of Public Health Brussels, Belgium	U. S. EPA/Environmental Chemistry Laboratory Stennis Space Center, USA
Servizos De Apoio Á Investigación A Coruña, Spain	Umeå University Umeå, Sweden
SGS Belgium NV Antwerpen, Belgium	Umweltbundesamt GmbH Vienna, Austria
SGS Institut Eyeserius GmbH Bayreuth, Germany	Vimta Labs Limited Hyderabad , India
SHIMADZU TECHNO-RESEARCH, INC. Kyoto, Japan	VITO Mol, Belgium
South-China Subcenter of State Environmental dioxins-monitoring Center, SCIES.MEP Guangzhou, P.R.China	Wellington Laboratories Inc Guelph, Ontario, Canada
State Laboratory County Kildare, Ireland	WESSLING Laboratorien GmbH Altenberge, Germany
SunDream Environmental Technology Corp Taichung City, Taiwan, R.O.C.	Western Region Laboratory, Health Canada Burnaby, Canada
Super Micro Mass Research & Technology Center Niaosong Township, Kaohsiung County, Taiwan, R.O.C.	Worthies Engineering Consultants Corp. Taichung, Taiwan
Swedish National Food Administration Uppsala, Sweden	Zavod za zdravstveno varstvo Maribor - Institut za varstvo okolja Maribor, Slovenia

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 a) seventeen 2,3,7,8-substituted PCDDs/PCDFs, b) four non-ortho PCBs, c) eight mono-ortho PCBs, d) eight PBDEs, e) six Indicator PCBs and f) α -HBCD were to be analysed using the laboratory's own quantification standards and methods. The results were reported on separate forms.

The test materials consisted of beef, butter oil and herring. The laboratories could choose to analyse 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 web in August 2009. The draft of the final report was discussed at the Waters users' meeting at DIOXIN2009 in August in Beijing, China.

Collection, preparation, and distribution of samples

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

- Beef: Obtained from Germany (80 g)
- Butter oil: Obtained from The Netherlands (20 g)
- Herring: Obtained from the Swedish part of the Baltic Sea (75g)

The test materials consisted of three natural products not fortified with standards. The contaminated beef was provided by Dr. Rainer Malisch, CVUA, Freiburg, Germany; the butter oil by Dr. Wim Traag, RIKILT – Institute of Food Safety, Wageningen, The Netherlands; and the Baltic herring by Dr. Marie Aune, National Food Administration, Uppsala, Sweden.

Homogenisation of the beef and herring was performed by repeatedly grinding portions of the food item in a grinder and homogenising 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. Butter oil was heated, thoroughly mixed by stirring, filtered through a sieve and subsequently subdivided. Sub-samples of at least 80g of beef (B), 20g of butter oil (O) and 75g of herring (H) were placed into carefully cleaned screw-cap glass bottles or ampoules. All samples were stored at -20°C until shipment. The frozen samples were shipped to the participating laboratories marked as test material B, O and H.

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 2009. The draft was discussed at the Waters Users' Meeting at the DIOXIN2009 Symposium in August in Beijing, China.

A certificate, stating the participant's code, will be sent to each participant contributing to the results at the end of 2009. The final report will be made available to the participants in pdf format.

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:

Veronica Horpestad Liane, Senior Engineer
veronicah.liane@fhi.no

Georg Becher, PhD, Department Director and Professor
georg.becher@fhi.no

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

Ninety-two 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 beef, butter oil and herring in Appendix 2, 3 and 4.

Summarising comments on results

PCDDs/PCDFs

Analyte solution

Concentrations for PCDDs/PCDFs were reported by 83 laboratories. The average RSD for the 17 congeners was 8.4% ranging from 6.9% for 1,2,3,7,8,9-HxCDF to 11% for 2,3,7,8-TCDF. The calculation of Z-scores for the TEQs (target 13.7 pg TEQ/ μ l) of the PCDD/PCDF standard solution showed that 98% 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.

Beef

For the beef sample, PCDD/PCDF results from 70-71 laboratories were received. The consensus TEQ was

0.235 pg TE/g fresh weight and 0.619 pg TE/g lipid weight. The average RSD was 42% ranging from 24-67%. Z-scores within ± 1 were obtained by 70% of the laboratories and 87% of the laboratories had Z-scores within ± 2 . About 80% percent of the PCDD/PCDF TEQ is made up by the three 1,2,3,7,8-PeCDD, 2,3,4,7,8-PeCDF and 1,2,3,4,7,8-HxCDF.

Butter oil

PCDD/PCDF concentrations in the eel sample were reported by 75 laboratories. The consensus TEQ was 2.6 pg TE/g fresh. The average RSD was 27% ranging from 14-57%. Z-scores were within ± 1 for 89% of the laboratories and within ± 2 for 96% of the laboratories. About 77% 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.

Herring

For the herring sample 81 laboratories determined PCDD/PCDF concentrations. The consensus TEQ was 1-3 pg/g fresh weight and 24 pg/g lipid weight. The average RSD was 36% ranging from 21-63%. Z-scores for PCDD/PCDF TEQ within ± 1 were obtained by 73% of the laboratories and 86% had Z-scores within ± 2 . About 88% of the PCDD/PCDF TEQ is made up by the three congeners 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 analysed and reported by 75 to 80 laboratories. The RSDs for the different congeners were 0.86-10% with an average of 6,5%.

Beef

Dioxin-like PCB concentrations were reported from 64 to 65 laboratories. The concentrations of the 12 congeners varied between 0.17 pg/g fresh weight (CB-81) and 3547 pg/g fresh weight (CB-118). The dioxin-like PCBs contribute 78% to the total TEQ in the sample with CB-126 as the main contributor (49%). The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 25% ranging from 18% to 45% (CB-77).

Butter oil

The number of laboratories measured and reported dioxin-like PCB concentrations in butter oil were between 68 and 69. The concentrations ranged from 3.1 pg/g fresh weight for CB-81 to 2.6 ng/g fresh weight for CB-118. The dioxin-like PCBs contribute to about 50% 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 20% ranging from 12% to 32% for CB-77.

Herring

Dioxin-like PCBs were reported by 74 to 77 laboratories. Levels were ranging from 0.54 pg/g fresh weight for CB-81 to 1762 pg/g fresh weight for CB-118. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 24% ranging from 18% to 35% for CB-81. The contribution of the dioxin-like PCBs to the total TEQ was about 56% with CB-126 as the main contributor.

Total TEQ

In Figure 1, the contribution of the three groups of dioxin-like compounds is depicted. For all three sample types, dioxin-like PCBs contributed to 50% or more of the total TEQs, 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 11% for beef, 7% for butter oil and 10% for herring.

Indicator PCBs

Analyte solution

Sixty-three laboratories reported Indicator PCBs in the analyte solution. The average RSD was 10% ranging from 8-11%.

Beef

For the beef sample Indicator PCB results were received from 53 laboratories. The concentrations were varying between 43 pg/g fresh weight (CB-28) and 384 ng/g fresh weight (CB-153). The RSDs were ranging from 16-39% with an average of 27%. The consensus median for the sum of Indicator PCBs was 105 ng/g fresh weight.

Butter oil

Within the deadline, 53 laboratories reported results of Indicator PCBs in the butter oil sample. The concentrations ranged from 52 pg/g fresh weight (CB-52) to 5.2

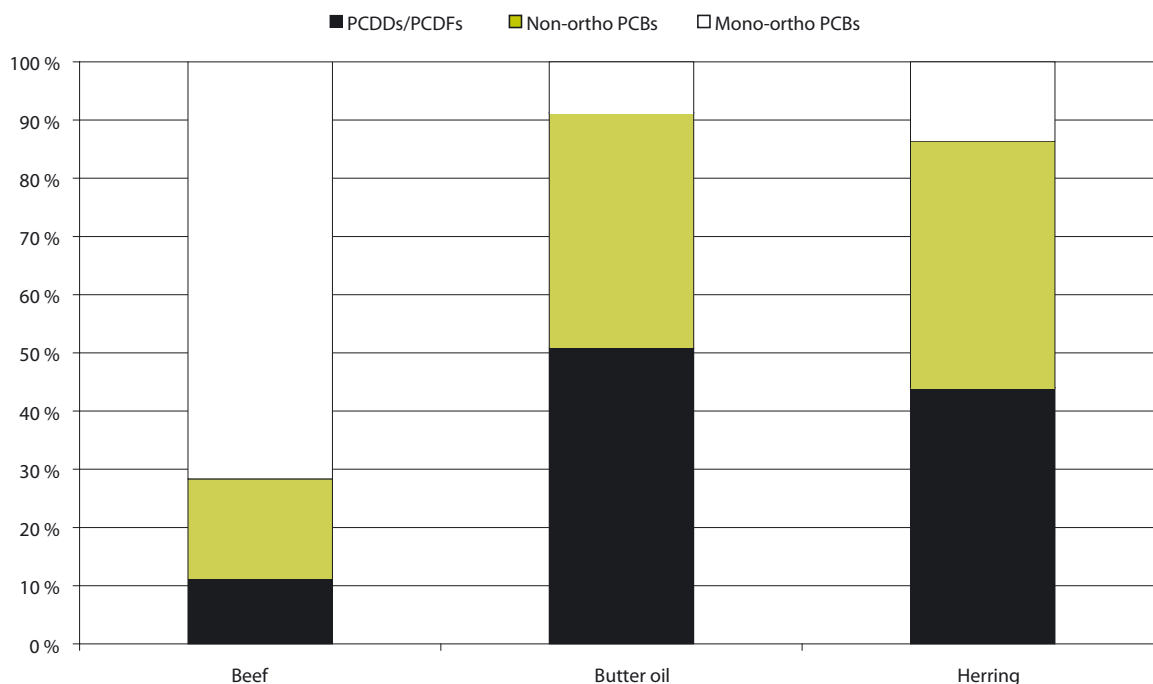


Figure 1. The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using the WHO₁₉₉₈ TEFs, in the three food samples.

ng/g fresh weight (CB-153) with a consensus median for the sum of Indicator PCBs of 11.6 ng/g fresh weight. The average RSD was 27% ranging from 20-40%.

Herring

Results were obtained from 64 laboratories. The concentrations of Indicator PCBs in the herring sample were ranging from 263 pg/g fresh weight (CB-28) to 5.7 ng/g fresh weight (CB-153) and the consensus median for the sum was 14.1 ng/g fresh weight. The average RSD was 29% ranging from 23-32%.

PBDEs

Analyte solution

The PBDE standard solution was analysed by 40 to 41 laboratories (BDE-28 to BDE-183) and 26 laboratories reported values for BDE-209. The RSDs were between 8.0-10% for all congeners except BDE-209 where the RSD was 8.0%.

Beef

PBDE concentrations were reported by 31 to 32 laboratories, except for BDE-209 for which 20 results were received. The consensus concentrations were in the range 0.92 pg/g fresh weight for BDE-28 and 44 pg/g fresh weight for BDE-47. The concentration for BDE-209 was 26 pg/g fresh weight. The sum of tri- to heptaBDEs was 111 pg/g fresh weight. The range of RSDs on fresh weight was 25-53% with an average of 34%, excluding BDE-209 for which the RSD was 77%.

Butter oil

Within the deadline, 34 laboratories had reported results for tri- to hepta BDEs and 21 laboratories reported results for BDE-209. The concentrations varied between 15 pg/g fresh weight (BDE-154) and 258 pg/g fresh weight (BDE-47). The concentration for BDE-209 was 28 pg/g fresh weight. The sum of tri- to heptaBDEs was 587 pg/g fresh weight. The RSD calculated from the concentrations on fresh weight ranged from 17-31% with an average of 22% for the tri- to heptaBDEs. The RSD calculated from the concentrations on fresh weight for BDE-209 was 52%.

Herring

Between 40 and 41 laboratories reported results for tri- to heptaBDEs and 25 reported results for BDE-209. The concentrations varied between 1.8 pg/g fresh weight (BDE-183) and 526 pg/g fresh weight (BDE-47). The concentration for BDE-209 was 14 pg/g fresh weight. The sum of tri- to heptaBDEs was 863 pg/g fresh weight. The RSDs for the individual congeners

were ranging from 20 to 38% with an average of 25%, excluding BDE-209 for which the RSD was 74%.

HBCD

In this round of the interlaboratory study HBCD and the isomers α -, β - and γ -HBCD could voluntarily be determined and reported for the third time. A total of 11 laboratories reported α -HBCD in the standard solution and between 10-12 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 38.2% (8.1%) for beef and 5.3% (20%) for herring.

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 highly appreciate the co-operation with Dr. Rainer Malisch, CVUA, Freiburg, Germany, Dr. Wim Traag, RIKILT – Institute of Food Safety, Wageningen, The Netherlands, Dr. Marie Aune, National Food Administration, Uppsala, Sweden who provided the contaminated food items.

Appendix A:

Participant's affiliations
and addresses

Appendix A: Affiliations and addresses of participants

<p>Agenzia Regionale Protezione Ambiente Del Piemonte - Polo Microinquinanti Giancarlo Cuttica IT-10095 Grugliasco (Torino) Italy g.cuttica@arpa.piemonte.it, c.cappa@arpa.piemonte.it</p>	<p>Agripapadigma Gian Piero Luciani IT-48100 Ravenna Italy agriparadigma@agriparadigma.it</p>
<p>Alcontrol AB Kristofer Warman SE-581 10 Linköping Sweden kristofer.warman@alcontrol.se</p>	<p>ALS Czech Republic, s.r.o. Miloslav Sebránek CZ-530 02 Pardubice Czech Republic miloslav.sebranek@alsglobal.com</p>
<p>ALS Laboratory Group Jill Weatherby, Ewa Przybylo-Komar Edmonton, Alberta T6E 0P5 Canada jill.weatherby@alsenviro.com, ewa.przybylo@alsenviro.com</p>	<p>Analytical Perspectives Bryan Vining Wilmington, NC 28405 USA bv@ultratrace.com</p>
<p>AsureQuality Limited Charlene Gerber Wellington, 5040 New Zealand wgtm-quality@asurequality.com, gerberc@asurequality.com</p>	<p>AXYS Analytical Services Ltd. Dale Hoover Sidney, B.C. V8L 5X2 Canada dhoover@axys.com</p>
<p>Calgary Laboratory David Wotherspoon Calgary, Alberta, T2L 2L1 Canada Dave.Wotherspoon@inspection.gc.ca</p>	<p>CARSO Stephanie Defour FR-69362 Lyon Cedex 07 France sdefour@groupecarso.com</p>
<p>CART University of Liège A.Leroy BE-4000 Liège Belgium A.Leroy@ulg.ac.be</p>	<p>Central Agricultural Office Food and Feed Safety Directorate Lorena Kovacsics, Gábor Domány HU-1095 Budapest Hungary kovacsil@oai.hu, domanyg@oai.hu</p>

<p>Central Lab. of Residue Analysis of Pesticides and Heavy Metals In Food Ashraf Sami Hassanin Giza, 12311 Egypt ashrafsami@link.net</p>	<p>Central Science Laboratory Shaun White York, YO41 1LZ UK s.white@csl.gov.uk</p>
<p>Chelab s.r.l. Vendri Mauro IT-31023 Resana (TV) Italy m.vendri@chelab.it</p>	<p>Chemisches Landes- und Staatliches Veterinäruntersuchungsamt Münster Peter Fürst DE-48147 Münster Germany pfuerst@cvua.nrw.de</p>
<p>Chemisches und mikrobiologisches Institut UEG GmbH Tanja Scharkel, Thomas Trechsler DE-35578, Wetzlar Germany t.schartel@ueg-gmbh.de</p>	<p>Chemisches und Veterinäruntersuchungsamt (CVUA) Freiburg Kerstin Wahl, Alexander Kotz DE-79114 Freiburg Germany kerstin.wahl@cvuafr.bwl.de</p>
<p>Consorzio Interuniversitario Nazionale la Chimica per l'Ambiente Stefano Raccanelli IT-30175 Marghera (VE) Italy s.raccanelli@unive.it, Stefano.Raccanelli@poste.it</p>	<p>Danish Veterinary and Food Administration Søren Sørensen DK-4100 Ringsted Denmark ssn@fvst.dk</p>
<p>Department of Environmental and Occupational Health Pao-Chi Liao Tainan 70428 Taiwan, R.O.C. liaopc@mail.ncku.edu.tw</p>	<p>Dioxin Analysis Unit Alan Yates Sydney, NSW 2073 Australia alan.yates@measurement.gov.au</p>
<p>Institut Quimic de Sarria Environmental Laboratory Jordi Diaz-Ferrero ES-08017 Barcelona Spain jordi.diaz@iqs.edu</p>	<p>FDA, Arkansas Regional Lab., Dioxin Group Paula Barnes, Vincent Litman Jefferson, AR 72079 USA paula.barnes@fda.hhs.gov, vincent.litman@fda.hhs.gov</p>

<p>Federaal Laboratorium voor de Voedselveiligheid Isabelle Defloor BE-3080 Tervuren Belgium isabelle.defloor@favv.be</p>	<p>Federal Environment Agency Peter Lepom DE-14193 Berlin Germany peter.lepom@uba.de</p>
<p>Food and Consumer Products Safety Authority J.A. van Rhijn, A. Waanders NL-7206 AX Zutphen The Netherlands hans.van.rhijn@vwa.nl</p>	<p>FOOD GmbH Analytik, Consulting Jena Uwe Dornberger, Sabine Weissbrodt DE-07743 Jena Germany u.dornberger@food-jena.de</p>
<p>Food Research Division Thea Rawn Ottawa, ON K1A 0K9 Canada thea_rawn@hc-sc.gc.ca</p>	<p>GfA mbH M. Opel DE-21079 Hamburg Germany MatthiasOpel@eurofins.de</p>
<p>Government Laboratory Wing Cheong Sham, Benedict Chen Hong Kong SAR China wcsham@govtlab.gov.hk, benchen@govtlab.gov.hk</p>	<p>South-China Subcenter of State Environmental Dioxins Monitoring Center Sukun Zhang Guangzhou , 510655 China zhangsukun@sciecee.org</p>
<p>Helmholtz Zentrum München Bernhard Henkelmann DE-85764 Neuherberg Germany henkelmann@helmholtz-muenchen.de</p>	<p>Hong Kong Baptist University, Dioxin Analysis Laboratory Zongwei Cai Kowloon Hong Kong SAR, China zwcai@hkbu.edu.hk</p>
<p>Hong Kong Government Laboratory S. Y. Wong Hong Kong SAR, China sywong2@govtlab.gov.hk</p>	<p>Institut Pasteur de Lille Amaury Mathias FR-59019 Lille Cedex France amaury.mathias@pasteur-lille.fr</p>

<p align="center">Institute of Aquaculture Gordon Bell Stirling FK9 4LA Scotland, UK g.j.bell@stir.ac.uk</p>	<p align="center">Instituto Nacional De Engenharia, Tecnologia E Inovação Américo Martins PT-1649-038 - LISBOA Portugal americo.martins@ineti.pt</p>
<p align="center">Istituto Zooprofilattico Sperimentale Dell'Abruzzo E Del Molise "G. Caporale" Scortichini Giampiero IT-64100 Teramo Italy g.scortichini@izs.it</p>	<p align="center">Istituto Zooprofilattico Sperimentale delle regioni Lazio Alessandro Ubaldi, Fabio Busico IT-00178 Rome Italy alessandro.ubaldi@izslt.it, fabio.busico@izslt.it</p>
<p align="center">Japan Food Research Laboratories Yoichi Kono, Toshihiko Yanagi 206-0025 Japan kounoy@jfrl.or.jp, yanagitos@jfrl.or.jp</p>	<p align="center">Kansas City District Lab Ann Rice Lenexa, Kansas 66214 USA annie.rice@fda.hhs.gov</p>
<p align="center">Korea Food And Drug Administration Ock-Jin, Paek Seoul 122-704 Republic of Korea ojpaek@kfda.go.kr</p>	<p align="center">LABERCA Marchand Philippe FR-44300 Nantes France marchand@vet-nantes.fr</p>
<p align="center">Laboratoire de Rouen Francois Blondel FR-76 000 Rouen France francois.blondel@laborouen.fr</p>	<p align="center">Laboratori de Dioxines, Institute of Environmental Assessment and Water Research (IDAEA-CSIC) Josep Rivera, Esteban Abad ES-08034 Barcelona Spain jraeco@iiqab.csic.es, esteban.abad@idaea.csic.es</p>
<p align="center">Laboratorio CSMO Magistrato alle Acque di Venezia Dott. Carrer Claudio IT-35124 Padova Italy claudio.carrer@magisacque.it</p>	<p align="center">Laboratory of SGS Bulgaria Ltd. Veselka Pashova BG-9003 Varna Bulgaria veselka.pashova@sgs.com</p>

<p>Laboratory of Vendee Quetier Emmanuelle, Freneau Michel FR- 85000 La Roche sur Yon France emmanuelle.quetier@vendee.fr, michel.freneau@vendee.fr</p>	<p>Landesamt für Umweltschutz Sachsen-Anhalt Uwe Rauhut DE-06114 Halle Germany rauhut@lau.mlu.sachsen-anhalt.de</p>
<p>Landeslabor Brandenburg Kathrin Brückner, Thomas Wiesmüller DE-15236 Frankfurt Germany Kathrin.brueckner@llb.brandenburg.de</p>	<p>Landesuntersuchungsamt Stefanie Schmitt DE-67346 Speyer Germany poststelle.ilcsp@lua.rlp.de</p>
<p>Landwirtschaftliche Untersuchungs- und Forschungsanstalt Speyer Harald Schäfer DE-67346 Speyer Germany schaefer@lufa-speyer.de</p>	<p>LUFA Rostock Ralf Ludwigs DE-18059 Rostock Germany rludwigs@lms-lufa.de</p>
<p>Marchwood Scientific Services Karl Pettit Southampton, SO40 4BJ United Kingdom karl.pettit@marchwood-scientific.co.uk</p>	<p>mas münster analytical solutions gmbh Armin Maulshagen, Stephan Hamm DE-48149 Münster Germany A.Maulshagen@mas-tp.com</p>
<p>Max Rubner-Institut (MRI) Karl-Heinz Schwind DE-95326 Kulmbach Germany karl-heinz.schwind@mri.bund.de</p>	<p>Maxxam Analytics Ewa Konieczna Mississauga, Ontario, L5N 2L8 Canada ewa.konieczna@maxxamalytics.com</p>
<p>Micropolluants Technologie P.E Lafargue FR-57100 Thionville France pelafargue@mp-tech.net</p>	<p>Ministry Of Agriculture And Rural Affairs Yunus Ucar, Gul Celik Cakirogullari, Devrim Kilic TR-06170 Ankara Turkey yunuseucar@yahoo.com, gcakirogullari@yahoo.com devrimkilic@yahoo.com</p>

<p>MTM Research Centre Jessika Hagberg SE-701 82 Örebro Sweden Jessika.hagberg@oru.se</p>	<p>National Food and Veterinary Risk Assessment Institute Inga Jarmalaite LT-08409 Vilnius Lithuania ijarmalaite@vet.lt</p>
<p>National Food Institute, Technical University of Denmark Tommy Licht Cederberg DK-2860 Søborg Denmark tlce@food.dtu.dk</p>	<p>National institute of nutrition and food safety Jingguang Li, Yongning Wu Beijing, 100050 China lichrom@yahoo.com.cn</p>
<p>National Public Health Institute Hannu Kiviranta FI-70210 Kuopio Finland hannu.kiviranta@ktl.fi</p>	<p>National Tsing Hua University, GMLab Department of Chemistry Yong-Chien Ling Hsinchu 30013 Taiwan ycling@mx.nthu.edu.tw</p>
<p>NCSR "Demokritos" Leondios Leondiadis GR-153 10 Athens, Greece leondi@rrp.demokritos.gr</p>	<p>Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit Elke Bruns-Weller, Annette Knoll DE-26133 Oldenburg Germany elke.brun-weller@laves.niedersachsen.de, annette.knoll@laves.niedersachsen.de</p>
<p>Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit Ines Thiem, Gabriele Böhmler DE-38134 Braunschweig Germany ines.thiem@laves.niedersachsen.de</p>	<p>NIFES- National Institute of Nutrition and Seafood Research Annette Bjordal NO-5005 Bergen Norway abj@nifes.no</p>
<p>NILU Martin Schlabach, Hans Gundersen NO-2027 Kjeller Norway Msc@nilu.no, Hg@nilu.no</p>	<p>Nofalab BV Jeroen Markesteijn NL-3115 JG Schiedam The Netherlands jeroen.markesteijn@nofalab.nl</p>

<p>Norwegian Institute of Public Health May Frøshaug NO-0456 Oslo Norway mafr@fhi.no</p>	<p>Oekometric GmbH Horst Rottler DE-95448 Bayreuth Germany rottler@oekometric.de</p>
<p>Pacific Rim Laboratories Inc. Dave Hope Surrey, BC V3S 8P8 Canada dave@pacificrimlabs.com</p>	<p>POP Lab,Shenzhen Center for Disease Control & Prevention Jianqing Zhang Shenzhen, Guangdong, 518020 China zhjianqing95@gmail.com</p>
<p>Qlip N.V. Philip Steketeer, Ahmed Loukili NL-3833 AN Leusden The Netherlands steketeer@Qlip.nl, loukili@Qlip.nl</p>	<p>R&C LAB SRL Claudio Carraro IT-36077 Vicenza Italy claudio.carraro@rclabsrl.it</p>
<p>Research and productivity Council (RPC) John Macaulay Fredericton, New Brunswick E3B 6Z9 Canada john.macaulay@rpc.ca</p>	<p>RIKILT Wim Traag NL-6708 PD Wageningen The Netherlands wim.traag@wur.nl</p>
<p>Scientific Analysis Laboratories Ltd Lindsay Collins Manchester M16 9FE UK lcollins@salltd.co.uk</p>	<p>Scientific Institute of Public Health Séverine Gosciny BE-1050 Brussels Belgium Severine.Gosciny@iph.fgov.be</p>
<p>Servizos De Apoio Á Investigación Gerardo Fernández Martínez ES-15071 A Coruña Spain sxaipa@udc.es</p>	<p>SGS Belgium NV Marc Van Ryckeghem, Geert De Smet BE-2030 Antwerpen Belgium geert.desmet@sgs.com, marc.vanryckeghem@sgs.com</p>

<p>SGS Institut Eyeserius GmbH Michael Gunzelmann DE-95448 Bayreuth Germany Michael.Gunzelmann@sgs.com</p>	<p>Shimadzu Techno-Research, INC. Takumi Takasuga, Takuji Suzuki Kyoto 604-8435 Japan t_suzuki00@shimadzu-techno.co.jp</p>
<p>State Laboratory John McBride County Kildare Ireland John.McBride@statelab.ie</p>	<p>SunDream Environmental Technology Corp Hsu-chih Hsiao Taichung City 40768 Taiwan , ROC sundream@sudream.com.tw</p>
<p>Super Micro Mass Research & Technology Center, Cheng Shiu University Guo-Ping Chang-Chien Niaosong Township, Kaohsiung County, 833 Taiwan, ROC guoping@csu.edu.tw</p>	<p>Swedish National Food Administration Marie Aune SE-753 23 Uppsala Sweden marie.aune@slv.se</p>
<p>TLR international laboratories Mrs L. van Schie, Mr G. Turkenburg NL-3077 MB Rotterdam The Netherlands QC@TLR.NL</p>	<p>TNO Built Environment and Geosciences Henk de Weerd NL-3584 CC Utrecht The Netherlands henk.deweerd@tno.nl</p>
<p>Toxicological Chemistry Unit Alessandro di Domenico, Anna Laura Iamiceli IT-00178 Rome Italy addeke@iss.it, annalaura.iamiceli@iss.it</p>	<p>U. S. EPA/ Environmental Chemistry Laboratory Joseph B. Ferrario Stennis Space Center, MS 39529 USA ferrario.joseph@epa.gov, pierce.gerry@epa.gov</p>
<p>Umeå University Sture Bergek SE-901 87 Umeå Sweden sture.bergek@chem.umu.se</p>	<p>Umweltbundesamt GmbH Wolfgang Moche AT-1090 Vienna Austria wolfgang.moche@umweltbundesamt.at</p>

<p style="text-align: center;">Vimta Labs Limited Ashutosh Kumar Mittal Hyderabad - 500 078 (A.P) India Ashutosh.mittal@vimta.com</p>	<p style="text-align: center;">VITO Rudy Van Cleuvenbergen, Kelly Servaes BE-2400 Mol Belgium rudy.vancleuvenbergen@vito.be, kelly.servaes@vito.be</p>
<p style="text-align: center;">Wellington Laboratories Inc Colleen Tashiro Guelph, Ontario, N1G 3M5 Canada colleen@well-labs.com</p>	<p style="text-align: center;">WESSLING Laboratorien GmbH Sabina König DE-48341 Altenberge Germany sabina.koenig@wessling.de, frank.leifhelm@wessling.de</p>
<p style="text-align: center;">Western Region Laboratory, Health Canada Victor Verigin, Kenneth Breakell Burnaby, BC. V5G 4P2 Canada victor_verigin@hc-sc.gc.ca, kenneth_breakell@hc-sc.gc.ca</p>	<p style="text-align: center;">Worthies Engineering Consultants Corp. David Fang Taichung 40850 Taiwan ROC DavidF@mail.worthies.com.tw</p>
<p style="text-align: center;">Zavod za zdravstveno varstvo Maribor - Institut za varstvo okolja Snezana Lobnik SI-2000 Maribor Slovenia snezana.lobnik@zzv-mb.si</p>	

Appendix B:

Study announcement and
instructions for participants

Announcement for Interlaboratory Comparison on POPs in Food 2009

Introduction

We hereby announce the tenth round of 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 2008. A draft report will be available prior to the evaluation meeting which will take place at the Dioxin 2009 Symposium in August, Beijing, China. The final report will be prepared and sent to participants by December 2009 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, Beef meat (labelled B) ~80 g, Butteroil (labelled O) ~20 g, and Herring (labelled H) ~75 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 2008
Return of registration form	December 12, 2008
Shipment of test material	January 12, 2009
Confirmation of receipt of test material by participant	Within 7 days
Reporting of test results ^{a)}	April 17, 2009
Publication of draft report on web-site	July/August 2009
Evaluation meeting at Dioxin 2009 in Beijing, China	August 2009
Final report sent to all participants	November 2009

- 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

Thomas Bjellaas

thomas.bjellaas@fhi.no

Phone: +47-21 07 62 54

Veronica H. Liane

veronicah.liane@fhi.no

Georg Becher

georg.becher@fhi.no

Phone: +47-21 07 62 42

Postal Address:

Norwegian Institute of Public Health

P.O.Box 4404 Nydalen

N-0403 Oslo, Norway

Interlaboratory Comparison on Dioxins in Food 2009

Instructions for participants

January 2009

1. Introduction

This is the tenth 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 beef (B), butteroil (O), and herring (H). 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. 98 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. 80 g beef, lipid content about 35-40%
- ca. 20 g butter oil, lipid content about 100%
- ca. 75 g herring, lipid content about 2-10%

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

Beef samples	B
Butteroil samples	O
Herring samples	H

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 24, 2009 to enable us to prepare the draft report for the Dioxin 2009 Symposium in Beijing, China. 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 24. 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 August at the Dioxin 2009 Symposium in Beijing, China.

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 2009 Symposium in Beijing, China. The final report will be printed by November 2009 and thereafter distributed to the participating laboratories. The report will also be partly 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 2008
Return of registration form	December 12, 2008
Shipment of test material	January 19, 2009
Confirmation of receipt of test material by participant	Within 7 days
Reporting of test results ^{a)}	April 24, 2009
Publication of draft report on web-site	July/August 2009
Evaluation meeting at Dioxin 2009 in Beijing, China	August 2009
Final report sent to all participants	November 2009

- 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

Dr. Thomas Bjellaas
thbj@fhi.no
phone: +47- 21 07 62 54

Veronica Horpestad Liane
veli@fhi.no
phone: +47-21 07 62 54

Prof. Georg Becher
georg.becher@fhi.no
phone: +47-21 07 62 42

Postal Address:
Norwegian Institute of Public Health
P.O. Box 4403 Nydalen
NO-0403 Oslo, Norway

Interlaboratory Comparison on Dioxins in Food 2009

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

	Beef		Butteroil		Herring	
	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	0.012	0.032	0.34	0.34	0.090	1.7
1,2,3,7,8-PeCDD	0.030	0.079	1.0	1.0	0.23	4.3
1,2,3,4,7,8-HxCDD	0.024	0.062	0.50	0.50	0.032	0.59
1,2,3,6,7,8-HxCDD	0.10	0.27	1.4	1.4	0.13	2.5
1,2,3,7,8,9-HxCDD	0.021	0.056	0.39	0.39	0.021	0.38
1,2,3,4,6,7,8-HpCDD	0.26	0.69	1.1	1.1	0.050	0.92
1,2,3,4,6,7,8,9-OCDD	0.36	0.95	2.8	2.8	0.10	1.9
2,3,7,8-TCDF	0.014	0.037	0.080	0.080	1.8	33
1,2,3,7,8-PeCDF	0.010	0.026	0.074	0.074	0.31	5.8
2,3,4,7,8-PeCDF	0.44	1.2	2.2	2.2	1.5	27
1,2,3,4,7,8-HxCDF	0.28	0.75	1.0	1.0	0.069	1.3
1,2,3,6,7,8-HxCDF	0.048	0.13	1.1	1.1	0.093	1.7
2,3,4,6,7,8-HxCDF	0.067	0.18	1.2	1.2	0.097	1.8
1,2,3,7,8,9-HxCDF	0.010	0.026	0.030	0.030	0.0062	0.12
1,2,3,4,6,7,8-HpCDF	0.057	0.15	0.52	0.52	0.030	0.56
1,2,3,4,7,8,9-HpCDF	0.019	0.049	0.050	0.050	0.010	0.19
1,2,3,4,6,7,8,9-OCDF	0.041	0.11	0.090	0.090	0.020	0.37
PCB 77	1.1	3.0	4.8	4.8	25	469
PCB 126	5.2	14	24	24	12	224
PCB 169	1.3	3.4	4.7	4.7	3.4	63
PCB 81	0.17	0.45	3.1	3.1	0.54	10
PCB 105	108	284	505	505	542	10056
PCB 114	26	70	52	52	30	564
PCB 118	3547	9335	2560	2560	1762	32693
PCB 123	9.3	24	33	33	18	335
PCB 156	3280	8632	360	360	257	4759
PCB 157	230	606	64	64	58	1076
PCB 167	1000	2632	171	171	158	2931
PCB 189	803	2113	37	37	26	487

Consensus of Congener Concentrations

	Beef		Butteroil		Herring	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
CB 28	43	113	115	115	263	4874
CB 52	37	97	52	52	630	11688
CB 101	60	159	95	95	2324	43117
CB 138	28580	75211	4090	4090	3907	72485
CB 153	38376	100989	5201	5201	5675	105288
CB 180	37960	99895	2067	2067	1320	24490
BDE 28	0.92	2.4	16	16	17	308
BDE 47	44	116	258	258	526	9759
BDE 99	41	107	127	127	122	2254
BDE 100	7.9	21	26	26	119	2208
BDE 153	11	30	110	110	22	409
BDE 154	4.5	12	15	15	56	1040
BDE 183	1.9	5.1	35	35	1.8	34
BDE 209	26	69	28	28	14	260
α-HBCD	16	42	49	49	980	18185
β-HBCD	0.94	2.5			8.6	159
γ-HBCD	13	35	13	13	65	1212
Tot HBCD	31	81	79	79	1069	19841
Sum PCB	105056	276463	11619	11619	14119	261941
Sum BDE without 209	111	293	587	587	863	16012
Sum BDE	137	362	615	615	877	16272

Consensus of TEQs

TEF₁₉₉₈

	Beef		Butteroil		Herring	
	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	0.012	0.032	0.34	0.34	0.090	1.7
1,2,3,7,8-PeCDD	0.030	0.079	1.0	1.0	0.23	4.3
1,2,3,4,7,8-HxCDD	0.0024	0.0062	0.050	0.050	0.0032	0.059
1,2,3,6,7,8-HxCDD	0.010	0.027	0.14	0.14	0.013	0.25
1,2,3,7,8,9-HxCDD	0.0021	0.0056	0.039	0.039	0.0021	0.038
1,2,3,4,6,7,8-HpCDD	0.0026	0.0069	0.011	0.011	0.00050	0.0092
1,2,3,4,6,7,8,9-OCDD	0.000036	0.000095	0.00028	0.00028	0.000010	0.00019
2,3,7,8-TCDF	0.0014	0.0037	0.0080	0.0080	0.18	3.3
1,2,3,7,8-PeCDF	0.00050	0.0013	0.0037	0.0037	0.016	0.29
2,3,4,7,8-PeCDF	0.22	0.58	1.1	1.1	0.74	14
1,2,3,4,7,8-HxCDF	0.028	0.075	0.10	0.10	0.0069	0.13
1,2,3,6,7,8-HxCDF	0.0048	0.013	0.11	0.11	0.0093	0.17
2,3,4,6,7,8-HxCDF	0.0067	0.018	0.12	0.12	0.0097	0.18
1,2,3,7,8,9-HxCDF	0.0010	0.0026	0.0030	0.0030	0.0062	0.12
1,2,3,4,6,7,8-HpCDF	0.00057	0.0015	0.0052	0.0052	0.00030	0.0056
1,2,3,4,7,8,9-HpCDF	0.00019	0.00049	0.00050	0.00050	0.00010	0.0019
1,2,3,4,6,7,8,9-OCDF	0.0000041	0.000011	0.0000090	0.0000090	0.0000020	0.000037
PCB 77	0.00011	0.00030	0.00048	0.00048	0.0025	0.047
PCB 126	0.52	1.4	2.4	2.4	1.2	22
PCB 169	0.013	0.034	0.047	0.047	0.034	0.63
PCB 81	0.000017	0.000045	0.00031	0.00031	0.000054	0.0010
PCB 105	0.011	0.028	0.051	0.051	0.054	1.0
PCB 114	0.013	0.035	0.026	0.026	0.015	0.28
PCB 118	0.35	0.93	0.26	0.26	0.18	3.3
PCB 123	0.00093	0.0024	0.0033	0.0033	0.0018	0.034
PCB 156	1.6	4.3	0.18	0.18	0.13	2.4
PCB 157	0.12	0.30	0.032	0.032	0.029	0.54
PCB 167	0.010	0.026	0.0017	0.0017	0.0016	0.029
PCB 189	0.080	0.21	0.0037	0.0037	0.0026	0.049
PCDDs/PCDFs	0.32	0.85	3.1	3.1	1.3	24
Non-ortho PCBs	0.53	1.4	2.4	2.4	1.2	23
Mono-ortho PCBs	2.2	5.9	0.55	0.55	0.41	7.6
Total TEQ	3.1	8.1	6.1	6.1	3.0	55

Consensus of TEQs

TEF₂₀₀₆

	Beef		Butteroil		Herring	
	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	0.012	0.032	0.34	0.34	0.090	1.7
1,2,3,7,8-PeCDD	0.030	0.079	1.0	1.0	0.23	4.3
1,2,3,4,7,8-HxCDD	0.0024	0.0062	0.050	0.050	0.0032	0.059
1,2,3,6,7,8-HxCDD	0.010	0.027	0.14	0.14	0.013	0.25
1,2,3,7,8,9-HxCDD	0.0021	0.0056	0.039	0.039	0.0021	0.038
1,2,3,4,6,7,8-HpCDD	0.0026	0.0069	0.011	0.011	0.00050	0.0092
1,2,3,4,6,7,8,9-OCDD	0.00011	0.00029	0.00084	0.00084	0.000030	0.00056
2,3,7,8-TCDF	0.0014	0.0037	0.0080	0.0080	0.18	3.3
1,2,3,7,8-PeCDF	0.00030	0.00079	0.0022	0.0022	0.0093	0.17
2,3,4,7,8-PeCDF	0.13	0.35	0.67	0.67	0.44	8.2
1,2,3,4,7,8-HxCDF	0.028	0.075	0.10	0.10	0.0069	0.13
1,2,3,6,7,8-HxCDF	0.0048	0.013	0.11	0.11	0.0093	0.17
2,3,4,6,7,8-HxCDF	0.0067	0.018	0.12	0.12	0.0097	0.18
1,2,3,7,8,9-HxCDF	0.0010	0.0026	0.0030	0.0030	0.0062	0.12
1,2,3,4,6,7,8-HpCDF	0.00057	0.0015	0.0052	0.0052	0.00030	0.0056
1,2,3,4,7,8,9-HpCDF	0.00019	0.00049	0.00050	0.00050	0.00010	0.0019
1,2,3,4,6,7,8,9-OCDF	0.000012	0.000032	0.000027	0.000027	0.0000060	0.00011
PCB 77	0.00011	0.00030	0.00048	0.00048	0.0025	0.047
PCB 126	0.52	1.4	2.4	2.4	1.2	22
PCB 169	0.039	0.10	0.14	0.14	0.10	1.9
PCB 81	0.000051	0.00014	0.00094	0.00094	0.00016	0.0030
PCB 105	0.0032	0.0085	0.015	0.015	0.016	0.30
PCB 114	0.00079	0.0021	0.0016	0.0016	0.00091	0.017
PCB 118	0.11	0.28	0.077	0.077	0.053	0.98
PCB 123	0.00028	0.00073	0.0010	0.0010	0.00054	0.010
PCB 156	0.10	0.26	0.011	0.011	0.0077	0.14
PCB 157	0.0069	0.018	0.0019	0.0019	0.0017	0.032
PCB 167	0.030	0.079	0.0051	0.0051	0.0047	0.088
PCB 189	0.024	0.063	0.0011	0.0011	0.00079	0.015
PCDDs/PCDFs	0.24	0.62	2.6	2.6	1.0	18
Non-ortho PCBs	0.55	1.5	2.5	2.5	1.3	24
Mono-ortho PCBs	0.27	0.71	0.11	0.11	0.086	1.6
Total TEQ	1.1	2.8	5.3	5.3	2.4	44

Consensus statistics

Analyte solution

	Target value pg/µl	Consensus median, pg/µl	Median all values pg/µl	Consensus mean, pg/µl	Standard deviation, pg/µl	Relative standard deviation, %	No. of values reported	No. of values removed
2,3,7,8-TCDD	2.0	2.0	2.0	2.0	0.14	6.9	83	2
1,2,3,7,8-PeCDD	5.0	4.9	4.9	4.9	0.35	7.1	83	2
1,2,3,4,7,8-HxCDD	5.0	4.9	4.9	4.9	0.42	8.4	83	2
1,2,3,6,7,8-HxCDD	5.0	4.8	4.8	4.8	0.37	7.7	83	2
1,2,3,7,8,9-HxCDD	5.0	5.1	5.1	5.1	0.45	8.8	83	1
1,2,3,4,6,7,8-HpCDD	5.0	4.9	4.9	4.9	0.39	8.0	83	3
1,2,3,4,6,7,8,9-OCDD	10	9.7	9.7	9.7	0.65	6.7	83	2
2,3,7,8-TCDF	2.0	1.9	1.9	1.9	0.20	11	83	2
1,2,3,7,8-PeCDF	5.0	5.0	5.0	5.0	0.35	7.1	83	2
2,3,4,7,8-PeCDF	5.0	4.8	4.8	4.8	0.44	9.2	83	1
1,2,3,4,7,8-HxCDF	5.0	4.9	4.9	4.9	0.33	6.7	83	3
1,2,3,6,7,8-HxCDF	5.0	5.0	5.0	4.9	0.50	10	83	1
2,3,4,6,7,8-HxCDF	5.0	4.9	4.9	4.8	0.42	8.8	83	1
1,2,3,7,8,9-HxCDF	5.0	4.9	4.9	4.9	0.30	6.2	83	2
1,2,3,4,6,7,8-HpCDF	5.0	4.9	4.9	4.9	0.38	7.8	83	2
1,2,3,4,7,8,9-HpCDF	5.0	5.0	5.0	5.0	0.42	8.3	83	2
1,2,3,4,6,7,8,9-OCDF	10	9.8	9.8	9.7	0.77	7.9	83	2
PCB 77	10	10	10	10	0.86	8.4	80	2
PCB 126	10	10	10	10	0.91	9.0	80	2
PCB 169	10	10	10	10	0.91	8.9	80	2
PCB 81	10	10	10	10	0.93	8.9	78	1
PCB 105	100	102	102	102	9.0	8.9	76	1
PCB 114	100	102	103	102	10	10	76	1
PCB 118	100	102	102	101	9.4	9.3	76	1
PCB 123	100	103	103	102	10	10	75	1
PCB 156	100	103	103	103	8.3	8.1	76	2
PCB 157	100	104	104	104	8.9	8.6	75	1
PCB 167	100	103	103	103	8.9	8.6	75	1
PCB 189	100	102	102	102	9.4	9.2	75	1

Consensus statistics

Beef, 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-defects
2,3,7,8-TCDD	0.012	0.014	0.013	0.0059	45	71	13	30
1,2,3,7,8-PeCDD	0.030	0.031	0.032	0.014	44	71	6	23
1,2,3,4,7,8-HxCDD	0.024	0.026	0.026	0.0095	36	70	13	16
1,2,3,6,7,8-HxCDD	0.10	0.11	0.10	0.032	31	71	2	4
1,2,3,7,8,9-HxCDD	0.021	0.024	0.023	0.0094	41	70	12	22
1,2,3,4,6,7,8-HpCDD	0.26	0.26	0.27	0.073	27	71	4	2
1,2,3,4,6,7,8,9-OCDD	0.36	0.38	0.37	0.14	36	71	9	6
2,3,7,8-TCDF	0.014	0.020	0.017	0.0099	60	71	18	21
1,2,3,7,8-PeCDF	0.010	0.014	0.012	0.0068	58	70	17	36
2,3,4,7,8-PeCDF	0.44	0.44	0.43	0.11	25	71	1	3
1,2,3,4,7,8-HxCDF	0.28	0.29	0.29	0.068	24	71	2	1
1,2,3,6,7,8-HxCDF	0.048	0.053	0.052	0.017	33	71	8	4
2,3,4,6,7,8-HxCDF	0.067	0.068	0.065	0.020	31	71	6	5
1,2,3,7,8,9-HxCDF	0.010	0.016	0.012	0.0081	67	70	17	47
1,2,3,4,6,7,8-HpCDF	0.057	0.060	0.061	0.020	33	71	9	4
1,2,3,4,7,8,9-HpCDF	0.019	0.020	0.018	0.010	58	70	13	40
1,2,3,4,6,7,8,9-OCDF	0.041	0.050	0.045	0.029	65	71	12	35
PCB 77	1.1	1.5	1.3	0.61	45	64	13	8
PCB 126	5.2	5.2	5.2	1.2	23	64	1	1
PCB 169	1.3	1.4	1.4	0.37	26	65	13	6
PCB 81	0.17	0.20	0.19	0.066	36	64	16	14
PCB 105	108	108	110	19	18	65	0	0
PCB 114	26	26	26	6.1	23	65	0	1
PCB 118	3547	3547	3500	675	19	65	0	0
PCB 123	9.3	9.3	9.3	2.9	31	65	2	4
PCB 156	3280	3280	3237	628	19	65	0	0
PCB 157	230	230	236	41	18	64	0	0
PCB 167	1000	1000	1016	183	18	65	0	0
PCB 189	803	803	806	142	18	65	0	0

Consensus statistics

Butteroil, 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-defects
2,3,7,8-TCDD	0.34	0.35	0.34	0.074	22	75	3	3
1,2,3,7,8-PeCDD	1.0	1.0	1.0	0.16	16	75	4	1
1,2,3,4,7,8-HxCDD	0.50	0.50	0.51	0.10	20	75	6	2
1,2,3,6,7,8-HxCDD	1.4	1.4	1.4	0.24	16	75	2	0
1,2,3,7,8,9-HxCDD	0.39	0.39	0.39	0.10	27	75	5	6
1,2,3,4,6,7,8-HpCDD	1.1	1.1	1.1	0.20	18	75	3	0
1,2,3,4,6,7,8,9-OCDD	2.8	2.8	2.8	0.62	22	75	2	2
2,3,7,8-TCDF	0.080	0.084	0.082	0.026	32	75	13	9
1,2,3,7,8-PeCDF	0.074	0.076	0.076	0.022	29	75	8	13
2,3,4,7,8-PeCDF	2.2	2.3	2.2	0.48	21	75	1	1
1,2,3,4,7,8-HxCDF	1.0	1.0	1.0	0.18	17	75	3	1
1,2,3,6,7,8-HxCDF	1.1	1.1	1.1	0.16	14	75	3	0
2,3,4,6,7,8-HxCDF	1.2	1.3	1.2	0.30	25	75	3	2
1,2,3,7,8,9-HxCDF	0.030	0.040	0.033	0.019	57	75	19	54
1,2,3,4,6,7,8-HpCDF	0.52	0.53	0.53	0.14	26	75	7	2
1,2,3,4,7,8,9-HpCDF	0.050	0.057	0.055	0.020	36	75	16	26
1,2,3,4,6,7,8,9-OCDF	0.090	0.12	0.11	0.057	54	75	18	29
PCB 77	4.8	5.0	5.2	1.7	32	68	6	2
PCB 126	24	24	23	2.8	12	69	1	0
PCB 169	4.7	4.7	4.9	1.1	23	69	1	4
PCB 81	3.1	3.1	3.1	0.75	24	68	4	2
PCB 105	505	505	499	100	20	69	0	0
PCB 114	52	52	51	9.5	19	69	0	2
PCB 118	2560	2560	2533	378	15	69	0	0
PCB 123	33	33	33	8.9	27	69	0	0
PCB 156	360	360	359	66	18	69	0	0
PCB 157	64	64	64	8.8	14	68	0	0
PCB 167	171	171	171	26	15	69	1	0
PCB 189	37	37	38	5.8	15	69	0	1

Consensus statistics

Herring, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-defects
2,3,7,8-TCDD	0.090	0.095	0.093	0.026	28	81	6	4
1,2,3,7,8-PeCDD	0.23	0.24	0.23	0.061	26	81	6	5
1,2,3,4,7,8-HxCDD	0.032	0.034	0.032	0.010	32	81	15	15
1,2,3,6,7,8-HxCDD	0.13	0.14	0.13	0.030	22	81	8	5
1,2,3,7,8,9-HxCDD	0.021	0.022	0.021	0.0076	36	81	17	22
1,2,3,4,6,7,8-HpCDD	0.050	0.057	0.056	0.027	47	81	12	9
1,2,3,4,6,7,8,9-OCDD	0.10	0.12	0.11	0.060	55	81	14	18
2,3,7,8-TCDF	1.8	1.8	1.8	0.36	21	81	1	0
1,2,3,7,8-PeCDF	0.31	0.31	0.31	0.066	22	81	7	2
2,3,4,7,8-PeCDF	1.5	1.5	1.4	0.30	21	81	2	1
1,2,3,4,7,8-HxCDF	0.069	0.070	0.073	0.022	29	81	8	4
1,2,3,6,7,8-HxCDF	0.093	0.094	0.096	0.025	26	81	9	5
2,3,4,6,7,8-HxCDF	0.097	0.10	0.095	0.029	30	80	11	6
1,2,3,7,8,9-HxCDF	0.0062	0.010	0.0087	0.0055	63	80	25	54
1,2,3,4,6,7,8-HpCDF	0.030	0.034	0.031	0.014	45	81	17	12
1,2,3,4,7,8,9-HpCDF	0.010	0.010	0.010	0.0055	55	81	24	54
1,2,3,4,6,7,8,9-OCDF	0.020	0.030	0.023	0.014	61	81	25	34
PCB 77	25	25	26	5.4	21	76	1	0
PCB 126	12	12	12	2.5	21	77	1	0
PCB 169	3.4	3.4	3.3	0.71	21	77	2	2
PCB 81	0.54	0.57	0.51	0.18	35	74	14	13
PCB 105	542	543	529	115	22	76	1	0
PCB 114	30	30	31	8.7	28	76	3	1
PCB 118	1762	1763	1712	348	20	75	1	0
PCB 123	18	20	18	6.8	38	74	14	2
PCB 156	257	257	250	45	18	76	1	0
PCB 157	58	58	57	11	19	75	1	0
PCB 167	158	158	156	37	24	75	2	0
PCB 189	26	26	26	5.4	21	75	2	0

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	1791	104
CB 52	100	105	104	2127	105
CB 101	100	101	101	1945	101
CB 138	100	106	106	1982	107
CB 153	100	106	106	1223	106
CB 180	100	106	106	1701	106
BDE 28	25	24	24	25	25
BDE 47	25	24	24	24	24
BDE 99	25	24	24	25	25
BDE 100	25	25	25	25	25
BDE 153	25	25	25	26	26
BDE 154	25	25	25	25	25
BDE 183	25	25	25	24	24
BDE 209	100	86	86	88	86
α-HBCD *	500	496	496	466	512

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Number of reported values	Number of reported outliers
CB 28	724	10	63	4
CB 52	734	11	63	3
CB 101	731	8.6	63	3
CB 138	730	9.2	63	3
CB 153	690	9.4	63	3
CB 180	713	8.4	63	3
BDE 28	12	9.8	41	1
BDE 47	12	8.6	41	1
BDE 99	14	9.5	41	1
BDE 100	13	9.2	41	1
BDE 153	8.9	8.9	41	0
BDE 154	8.4	8.4	41	0
BDE 183	9.9	9.9	40	0
BDE 209	15	8.3	26	1
α-HBCD *	35	10	11	1

NDS: Non-detects

* : Indicative value due to few reported values

Consensus statistics

Beef, 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	52	43	43	97	47	47
CB 52	42	37	37	100	40	40
CB 101	63	60	60	101	66	66
CB 138	28580	28580	28580	28349	28349	28349
CB 153	38376	38376	38376	37912	37912	37912
CB 180	37960	37960	37960	37836	37836	37836
BDE 28	1.5	1.2	0.92	2.7	1.3	1.1
BDE 47	45	44	44	55	44	45
BDE 99	41	41	41	46	42	42
BDE 100	8.8	8.2	7.9	12	8.6	8.5
BDE 153	11	11	11	13	12	12
BDE 154	4.6	4.5	4.5	6.2	4.6	4.4
BDE 183	2.5	2.0	1.9	5.5	2.4	2.3
BDE 209	57	32	26	82	43	38
α-HBCD *	83	69	16	195	53	37
β-HBCD *	75	20	0.94	186	41	0.94
γ-HBCD *	75	16	13	152	42	13
Tot HBCD *	60	31	31	532	43	43

	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	169	39	39	53	8	2
CB 52	200	39	35	53	9	3
CB 101	119	32	32	53	5	2
CB 138	17	17	17	53	0	0
CB 153	16	16	16	53	0	0
CB 180	21	21	21	53	0	0
BDE 28	147	50	54	32	7	9
BDE 47	59	31	26	32	4	1
BDE 99	41	26	26	32	2	0
BDE 100	88	24	25	32	4	2
BDE 153	37	27	27	32	2	2
BDE 154	83	33	28	32	5	4
BDE 183	145	53	53	31	8	10
BDE 209	87	66	77	20	6	6
α-HBCD *	170	74	115	10	3	6
β-HBCD *	153	100		10	3	8
γ-HBCD *	161	92	25	10	3	7
Tot HBCD *	202	67	67	6	2	1

Consensus statistics
Butteroil, 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	117	115	115	186	122	122
CB 52	54	53	52	116	54	53
CB 101	100	95	95	155	95	95
CB 138	4090	4090	4090	4185	4185	4185
CB 153	5201	5201	5201	5064	5064	5064
CB 180	2067	2067	2067	2065	2065	2065
BDE 28	16	16	16	18	18	17
BDE 47	258	258	258	270	270	270
BDE 99	129	127	127	149	136	136
BDE 100	26	26	26	30	27	27
BDE 153	110	110	110	113	113	113
BDE 154	15	15	15	20	16	16
BDE 183	35	35	35	36	36	36
BDE 209	46	26	28	317	30	27
α-HBCD *	150	109	49	227	119	53
β-HBCD *	150	93		226	89	
γ-HBCD *	150	88	13	208	88	15
Tot HBCD *	93	79	79	260	77	77

	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	166	29	29	53	4	1
CB 52	238	31	29	53	8	3
CB 101	177	40	40	53	6	3
CB 138	23	23	23	53	0	0
CB 153	21	21	21	53	0	0
CB 180	20	20	20	53	0	0
BDE 28	26	22	17	34	1	3
BDE 47	24	24	24	34	0	0
BDE 99	42	22	22	34	2	0
BDE 100	52	24	24	34	2	1
BDE 153	18	18	18	34	0	0
BDE 154	81	31	31	34	3	2
BDE 183	24	24	20	34	0	1
BDE 209	209	59	52	21	9	11
α-HBCD *	109	68	25	10	2	7
β-HBCD *	133	91		10	2	10
γ-HBCD *	129	93	70	10	2	7
Tot HBCD *	117	29	29	6	2	2

Consensus statistics
Herring, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
CB 28	268	263	263	351	274	278
CB 52	634	630	630	715	647	647
CB 101	2327	2317	2324	2422	2285	2290
CB 138	3957	3907	3907	4414	4017	4017
CB 153	5826	5675	5675	5927	5550	5550
CB 180	1360	1338	1320	1346	1293	1282
BDE 28	17	17	17	21	17	17
BDE 47	527	526	526	525	511	511
BDE 99	122	122	122	129	126	126
BDE 100	119	119	119	122	122	122
BDE 153	22	22	22	23	23	23
BDE 154	56	56	56	57	57	57
BDE 183	2.1	1.9	1.8	4.9	1.9	2.0
BDE 209	30	15	14	200	22	19
α-HBCD *	980	980	980	926	926	926
β-HBCD *	52	21	8.6	110	33	8.6
γ-HBCD *	89	58	65	136	83	85
Tot HBCD *	1069	1069	1069	994	994	994

	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	95	34	32	64	5	2
CB 52	52	31	31	64	3	1
CB 101	41	23	23	64	2	1
CB 138	45	30	30	64	4	0
CB 153	38	27	27	64	3	0
CB 180	36	30	29	64	2	1
BDE 28	110	23	23	41	2	0
BDE 47	27	21	21	41	1	0
BDE 99	28	22	22	41	1	0
BDE 100	26	26	26	41	0	0
BDE 153	26	20	20	41	1	0
BDE 154	27	27	27	41	0	0
BDE 183	161	44	38	40	12	12
BDE 209	254	75	74	25	8	7
α-HBCD *	18	18	18	12	0	0
β-HBCD *	130	99	29	12	4	6
γ-HBCD *	97	62	62	12	2	4
Tot HBCD *	21	21	21	13	0	0

NDs: Non-detects

* : Indicative value due to few reported values

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

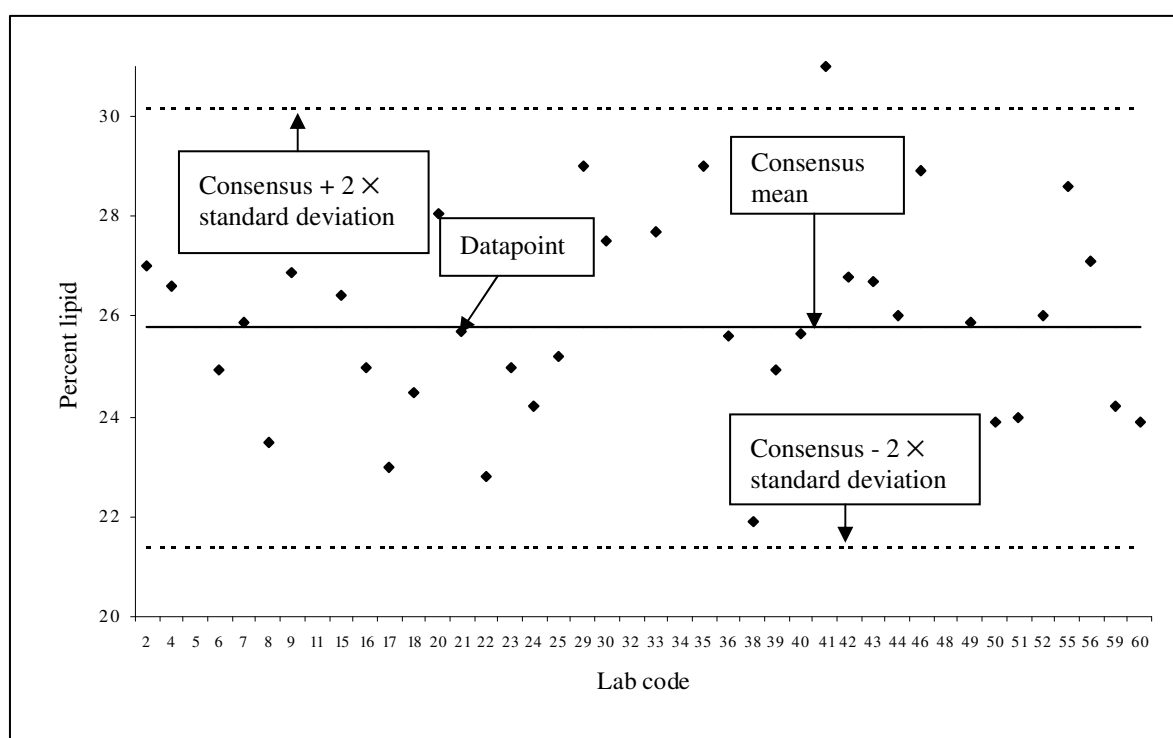
TEF ₁₉₉₈	Median pg/g	Mean pg/g	SD pg/g	RSD %	Min pg/g	Max pg/g	Reporting laboratories
Beef fresh weight							
PCDD/PCDF TEQ	0,34	0,40	0,29	71	0,12	2,1	71
Non-ortho PCB TEQ	0,56	0,61	0,47	76	0,012	4,1	65
Mono-ortho PCB TEQ	2,2	2,2	0,40	18	0,27	3,2	65
Total TEQ	3,0	2,9	1,0	36	0,13	5,9	74
Sum indicator PCB	103909	104396	16729	16	73291	144890	53
Sum BDE without BDE 209	119	139	63	45	82	384	32
Butteroil fresh weight							
PCDD/PCDF TEQ	3,1	4,4	10	234	1,8	92	75
Non-ortho PCB TEQ	2,4	2,9	4,0	139	1,6	36	69
Mono-ortho PCB TEQ	0,55	0,55	0,077	14	0,17	0,74	69
Total TEQ	6,0	7,5	11	141	2,8	92	77
Sum indicator PCB	11640	11770	2383	20	3925	19149	53
Sum BDE without BDE 209	585	637	165	26	466	1217	34
Herring fresh weight							
PCDD/PCDF TEQ	1,3	2,8	12	422	0,69	108	81
Non-ortho PCB TEQ	1,2	1,3	0,44	34	0,53	4,4	77
Mono-ortho PCB TEQ	0,41	0,41	0,13	31	0,18	1,3	76
Total TEQ	3,0	4,3	12	270	1,2	108	83
Sum indicator PCB	14453	15175	5695	38	2690	37375	64
Sum BDE without BDE 209	866	883	190	22	510	1759	41

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 Beef

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
2	40.2		63	40.2				
3	37.8		64	36.9				
4	39.6		65	33.6				
5	32.8		66	38.3				
6	38.6		67	37.3				
7	44.3		68	40.4				
8	37.0		69	37.5				
9	37.6		70	38.3				
12	34.6		71	39.9				
13	35.0		72	38.0				
14	34.2		74	36.8				
16	40.7		75	37.4				
17	46.8		76	38.4				
19	37.8		77	40.0				
20	31.6		81	0.2	outlier			
22	38.2		82	39.5				
24	38.0		85	48.9				
25	45.0		87	35.7				
26	37.8		88	38.1				
27	40.4		89	35.5				
28	53.3	outlier	90	33.5				
30	36.4		91	33.9				
32	35.7		92	38.0				
34	37.0		94	40.1				
35	37.2		96	36.4				
36	34.4		99	38.5				
37	38.6		100	38.2				
38	37.9		101	0.6	outlier			
40	38.1		102	38.2				
42	36.4							
43	31.1							
44	40.1							
45	44.0							
46	39.3							
48	42.5							
49	39.5							
52	39.6							
53	37.3							
54	39.5							
55	40.9							
56	37.0							
57	37.8							
59	37.6							
60	37.6							
61	42.6							
62	38.0							

Mean	Standard deviation	Relative standard deviation	Median
38.2	3.10	8.1	38.0

Lipid determination for Butteroil

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
3	99.4		63	98.8				
4	100.0		64	100.0				
5	99.6		65	99.6				
6	100.0		66	100.0				
7	100.0		67	100.0				
8	100.0		68	99.0				
9	99.6		69	100.0				
11	100.0		70	100.0				
12	100.0		71	100.0				
13	99.5		72	98.2				
14	100.0		74	96.2				
16	80.3		76	100.0				
17	100.0		77	100.0				
18	94.2		79	99.9				
19	100.0		81	1.0	outlier			
22	98.8		82	100.0				
24	100.0		87	98.0				
25	100.0		88	100.0				
26	94.6		89	100.0				
27	100.0		90	100.0				
28	71.3		91	99.1				
30	99.3		94	100.0				
32	100.0		96	100.0				
34	99.7		98	103.0				
35	99.0		99	100.0				
36	100.0		100	100.0				
37	100.0		101	1.0	outlier			
38	100.0		102	100.0				
39	99.9							
40	100.0							
42	93.9							
43	100.0							
44	99.7							
45	100.0							
46	99.5							
48	100.0							
49	100.0							
51	100.0							
52	99.9							
53	100.0							
55	100.0							
57	98.2							
59	100.0							
60	100.0							
61	100.0							
62	100.0							

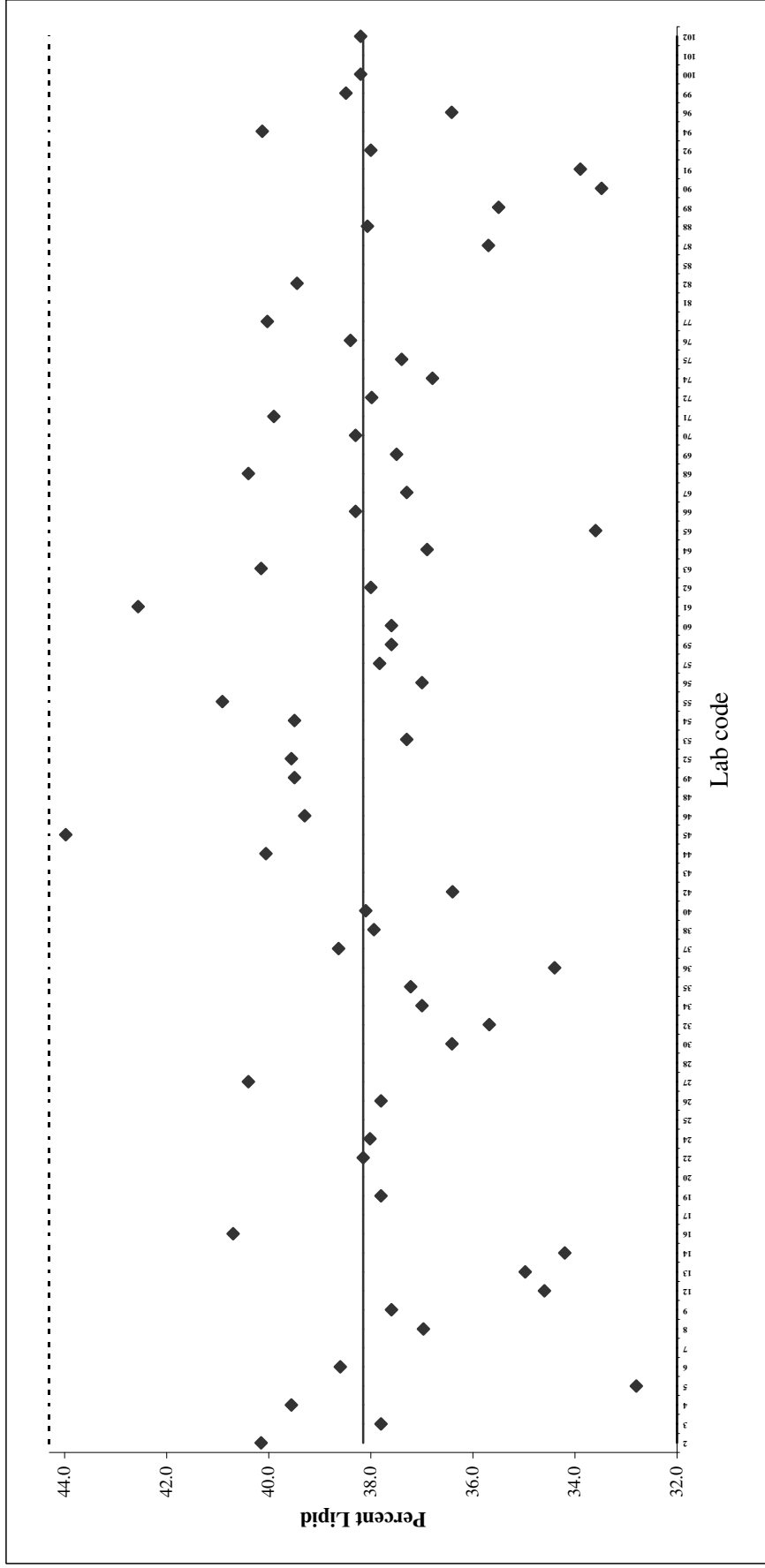
Mean	Standard deviation	Relative standard deviation	Median
98.9	4.21	4.3	100.0

Lipid determination for Herring

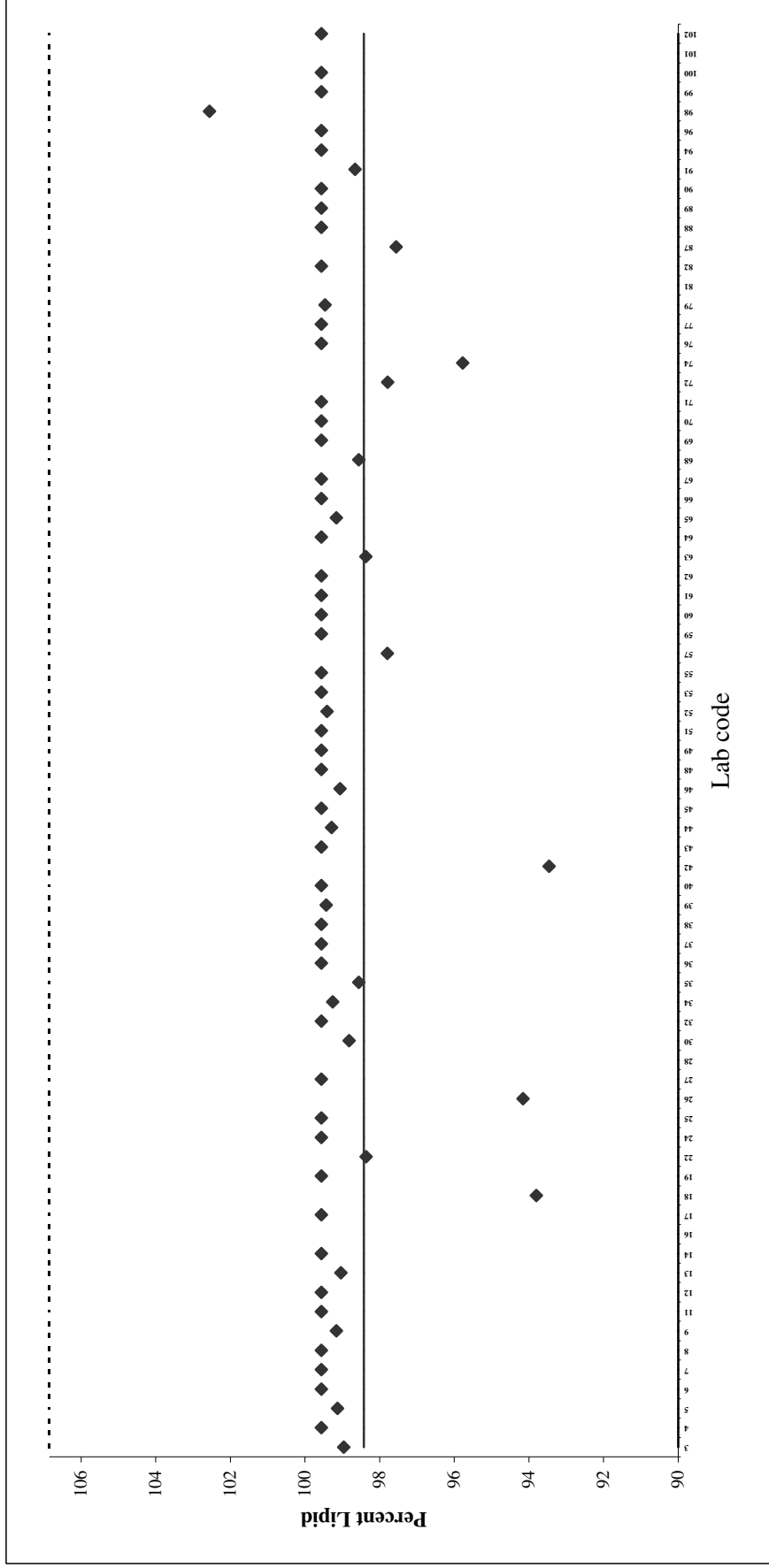
Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
3	4.9		59	5.5				
4	5.6		60	4.3				
5	5.0		61	7.3				
6	6.5		62	5.3				
7	6.0		64	6.6				
8	5.1		66	5.5				
9	5.0		67	5.3				
11	3.0		68	5.9				
12	5.1		69	7.3				
13	5.0		70	6.0				
14	8.3		71	5.9				
16	5.4		72	5.2				
17	6.6		74	5.5				
18	2.4		75	5.4				
19	5.1		76	5.7				
20	2.3		77	5.8				
22	5.2		79	5.9				
23	5.4		80	6.8				
24	5.8		81	2.6				
25	17.4	outlier	82	5.2				
26	5.3		83	5.7				
27	5.8		87	3.9				
28	1.9		88	5.1				
30	5.2		89	6.8				
31	5.5		91	5.3				
32	5.3		92	3.5				
34	5.3		93	6.1				
35	5.0		94	5.4				
36	4.7		95	5.4				
37	4.2		96	4.4				
38	5.4		97	5.6				
40	5.3		98	5.8				
42	5.6		99	5.3				
43	1.4	outlier	100	4.9				
45	7.3		101	0.1	outlier			
46	5.3		102	5.4				
47	5.7							
49	5.0							
50	5.5							
51	6.3							
52	5.5							
53	5.2							
54	6.3							
55	6.1							
56	5.1							
57	5.5							

Mean	Standard deviation	Relative standard deviation	Median
5.3	1.07	19.9	5.4

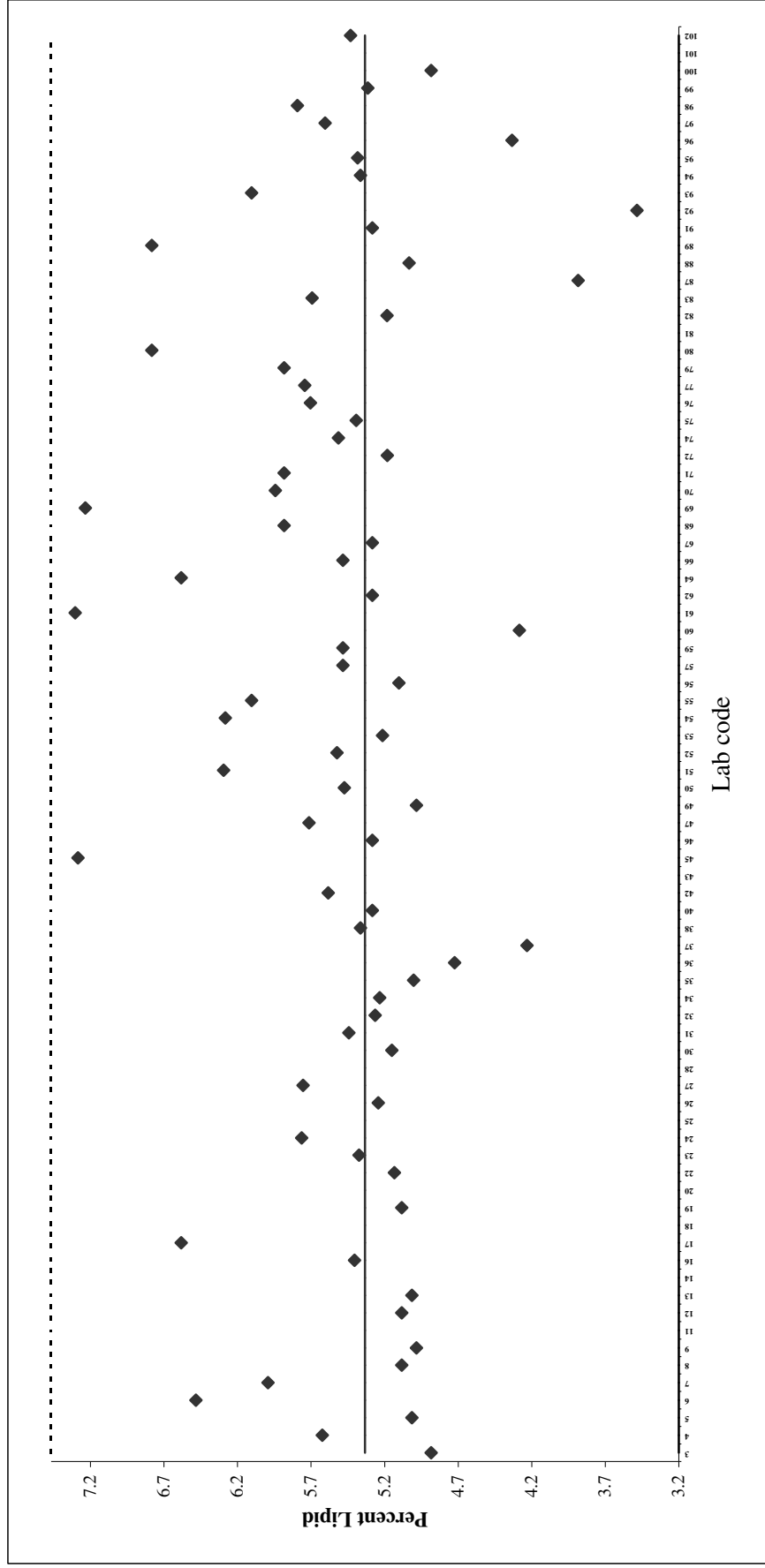
Lipid determination; Beef



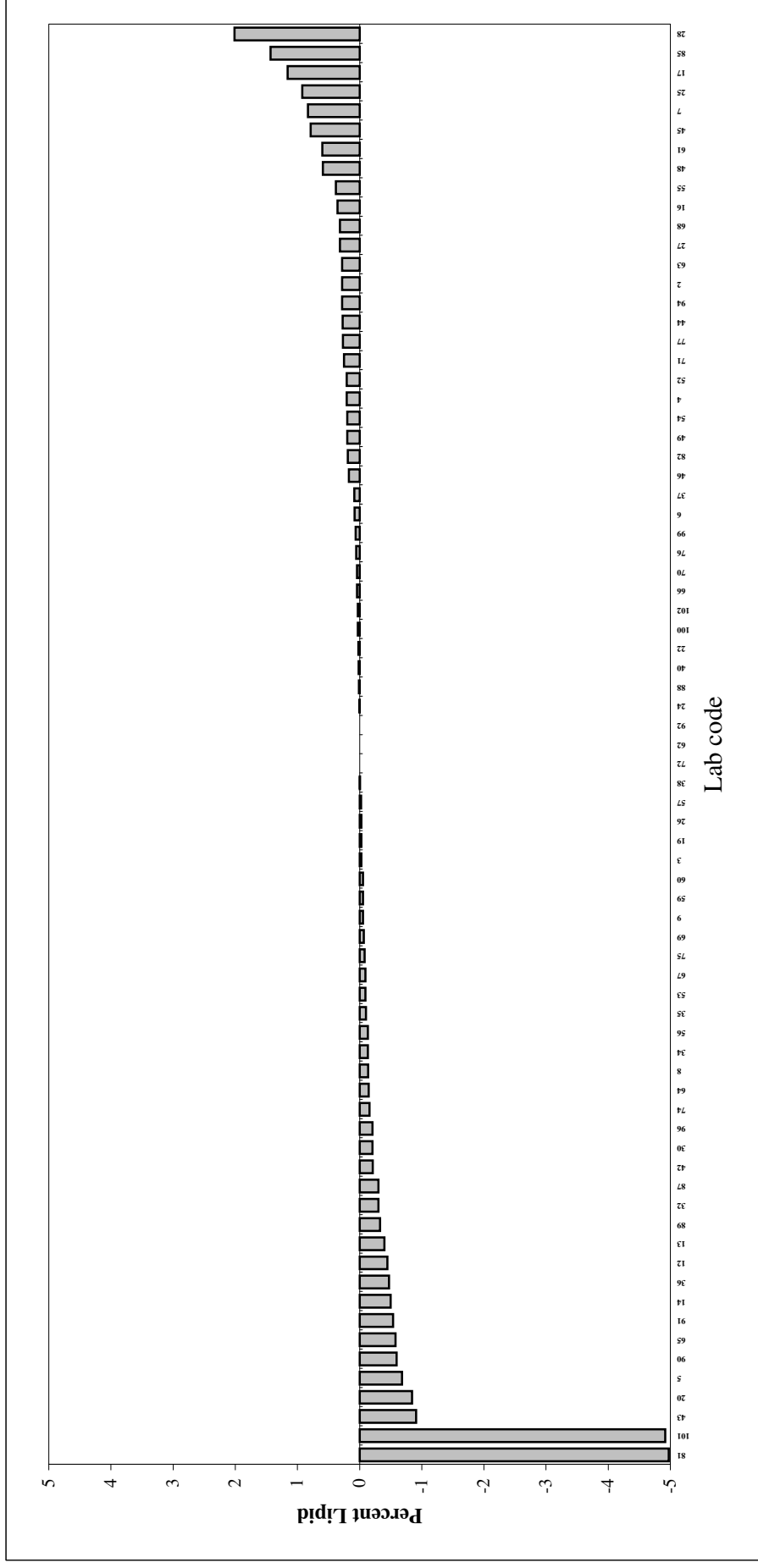
Lipid determination; Butteroil



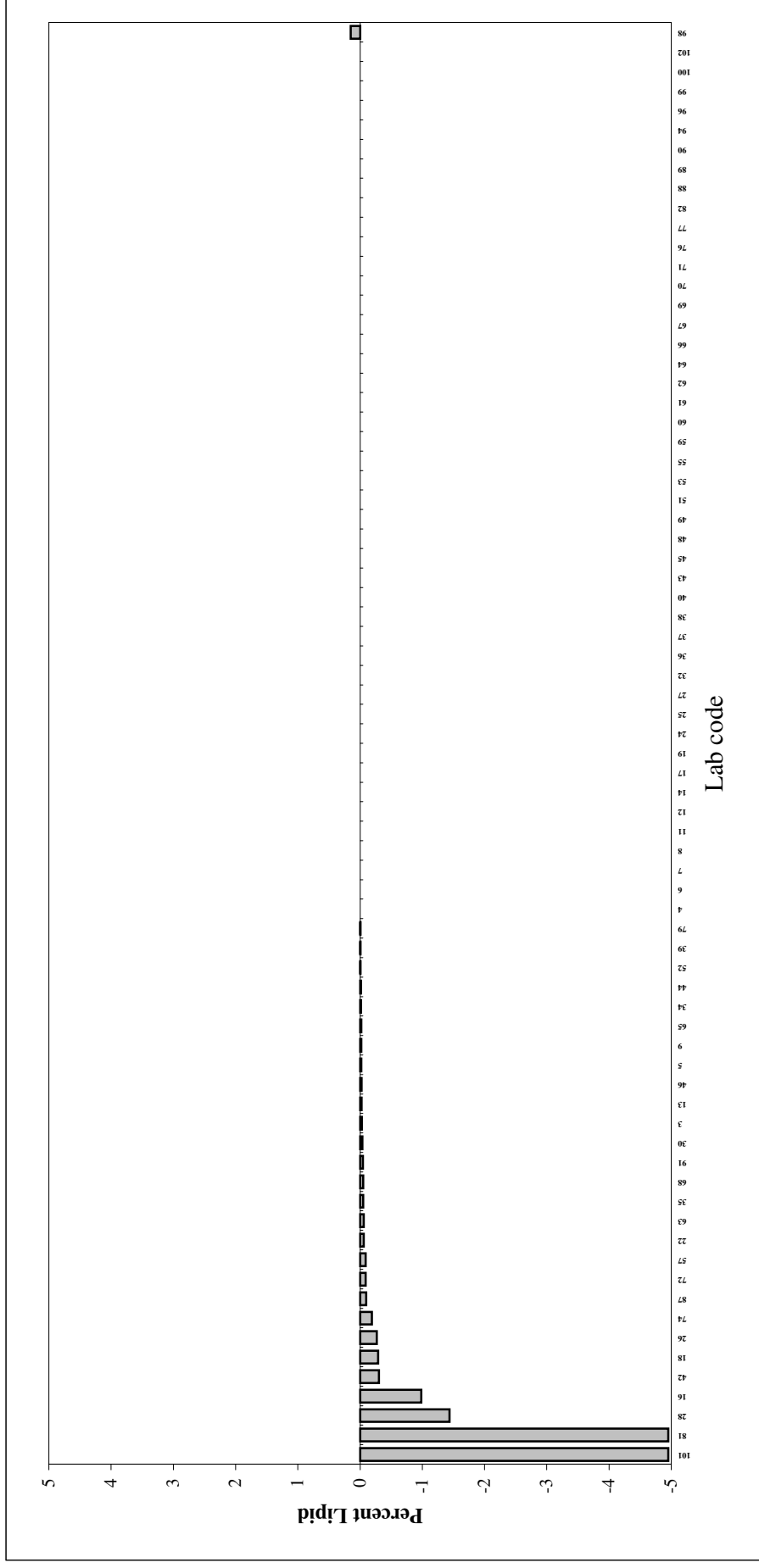
Lipid determination; Herring



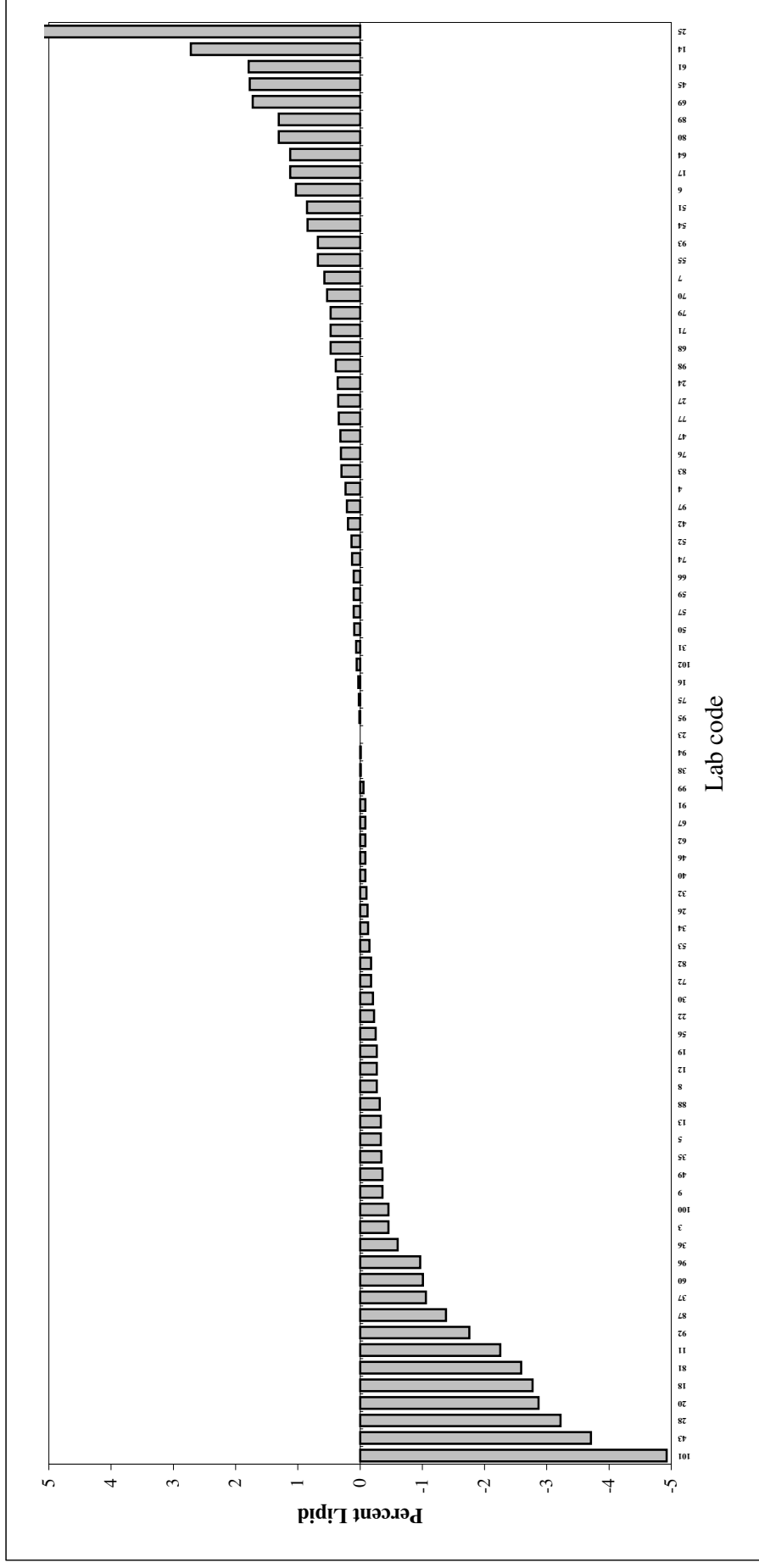
Z-score lipid determination; Beef



Z-score lipid determination; Butteroil



Z-score lipid determination; Herring



Laboratories Z-Scores: Analyte Solution

TEF1998

LAB CODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono- orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209
3	0.22	-0.60	0.24	0.16	0.09	1.2
4	-0.05	0.03	0.18	-0.04		0.02
5	-0.30	-0.27	0.03	-0.30	0.30	
6	-0.64	-1.0	-1.6	-0.68	0.00	-0.20
7	-0.05	0.06	0.09	-0.04		
8	-0.04	0.67	0.11	0.01	0.18	
9	-0.05	-0.23	0.25	-0.06	-0.22	
11	-0.46	0.44	-0.15	-0.39		-0.37
12	-0.54	0.12	-0.09	-0.49	-0.15	
13	0.34	1.7	-0.27	0.44	-0.72	1.5
14	-0.15			-0,57*		
16	240	0.09	0.04	219		
17	-0.81	0.59	0.42	-0.70		
19	0.51	0.74	0.00	0.52	-0.06	
22	-0.07	0.47	0.14	-0.02	0.34	0.26
23	0.09	0.98	0.31	0.16	0.00	0.13
24	0.31	1.2	0.85	0.39	1.4	
25	0.20	0.08	0.62	0.20	-4.6	
26	-0.10	0.16	-0.06	-0.08	0.00	0.06
27	-0.37	0.65	0.20	-0.29	0.00	
28	0.06	-0.26	0.40	0.04		-0.22
30	0.03	0.17	0.28	0.04	-0.02	-0.06
31					0.01	
32	0.00	-0.26	0.05	-0.02	-0.14	0.00
34	0.07	-0.12	-0.02	0.06	-0.20	-0.02
35	-0.16	0.39	0.71	-0.11	0.06	0.39
36	0.11	0.00	0.12	0.10	0.11	
37	-0.19	0.22	0.18	-0.16		
38	0.16	-0.24	-0.19	0.13	-1.3	0.17
39	-0.13	0.27	0.61	-0.09	-1.0	
40	-0.27	-0.17	-0.86	-0.27		
42	-0.09	1.2	0.72	0.01	0.01	-0.32
43	-0.48	0.16	0.16	-0.43	172	
44	0.01			-0,42*		
45	-0.19	0.09	0.36	-0.16	-0.06	-0.07
46	-0.13	-0.03	-0.02	-0.12	-0.25	
47	-0.18	0.00		-0,23*	0.27	0.61
48	-0.66			-0,62*		
49	-0.25	0.01	-0.040	-0.23	-0.13	0.03
50	-0.10	0.02	0.070	-0.09		
51	-0.32	-0.25	-0.85	-0.32		
52	-0.09	-0.41	0.46	-0.10	0.31	-0.34
53	0.10	0.13	0.38	0.11		
54		5081	4495	429*	4929	
55	-0.06	-0.08	-0.66	-0.07	0.25	
56	0.17	0.30	0.03	0.17	0.05	
57	0.02	-0.21	-0.37	0.00	0.46	-0.30
59		0.06	0.19	-4,6*	0.02	0.06
60	-0.10	-0.06		-0,16*		
61	-0.02	0.14	0.15	0.00	-0.06	
62	0.20	0.49	0.83	0.23	0.88	
63	0.08	-0.11	-0.21	0.06		
64	0.09	-0.01	0.24	0.08	0.07	
65	-0.13	0.05	0.12	-0.12		
66	-0.05	-0.05	0.51	-0.04	0.03	
67	-0.52	0.67	0.23	-0.42		
68	-0.02	0.50	0.36	0.02	0.07	0.01
69	-0.06	0.33	-0.02	-0.04	-0.30	0.09
70	-0.18	0.05	0.16	-0.16	0.12	-0.26
71	-0.04	0.20	0.18	-0.02	-0.27	-0.01
72	-0.80	-0.32	0.53	-0.75	0.46	0.12

LAB CODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono- orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209
73		-5,0*		-5,0*		
74	-0.01	0.79	0.58	0.06	0.20	0.27
75					0.06	-0.13
76	-0.21	-0.15	0.35	-0.20	0.16	0.02
77	-0.17	0.37	0.48	-0.12	0.03	0.25
79	-0.23	0.00	0.07	-0.21	-0.20	0.47
80	-0.80	-0,29*	-1,0*	-0,77*	0.12	0,09*
81	-2.6	-0.79	-0,68*	-2,4*	0.33	
82	-0.10			-0,52*		
83	-0.71	0.06	-0.32	-0.64	-0.25	
85	0.00			-0,43*		
87	0.22	0.22	-0.14	0.21		
88	-0.29	0.01	0.46	-0.26	0.73	0.82
89	-0.27	0.01	0.08	-0.25	-0.44	0.18
90	-0.49	-0.43		-0,54*		
91	-0.17	0.32	0.66	-0.13	-0.03	
92	-0.45	-0.25	-0.40	-0.43	-0.39	
93	0.57			0,09*	1.3	
94	-0.27	0.01	0.39	-0.24		-0.02
95	-0.02	0.70	0.62	0.04		-0.12
96	-0.15	-0.07	0.52	-0.13	0.06	
97	0.03	-0.20	0.16	0.01	0.03	0.12
98	-0.25	-0.08	-0.18	-0.24	-0.27	-0.16
99	-0.14	-0.03	0.22	-0.13	-0.06	-0.76
100	0.18	0.14	0.67	0.19	0.16	-0.48
101	-0.13			-0,55*		
102	-0.53	-0.57	0.00	-0.53	-0.15	0.11
103	0.01	-0.11	-0.25	0.00	-0.49	

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

Laboratories Z-Scores: Beef

TEF1998

LAB CODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono- orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209
2	-0.80	1.9	-0.59	-0.19		
3	1.6	-0.37	0.66	0.58	1.2	1.9
4	0.08	0.55	0.63	0.56		-0.25
5	0.16	-0.86	0.11	-0.05	0.10	
6	0.00	0.48	-0.68	-0.41	0.48	-0.22*
7	2.8	-2.2	1.5	1.0		
8	0.00	0.41	-0.12	-0.02	1.0	
9	0.09	1.0	1.4	1.2	1.9	
12	0.56	-0.38	-0.44	-0.33	-1.2	
13	1.1		-0.01	-0.75*	-1.0	3.3
14	0.58			-4.4*		
16	19	34	-4.4	4.6		
17	3.0	1.0	1.2	1.4		
19	0.50*	0.26	-0.28	-0.11*	0.35	
20	27	-0.83	-0.62	2.2	-0.81	1.5
22	-0.30	-0.11	0.07	0.00	0.52	
24	1.0	0.33	0.49	0.52	0.43	
25	-0.17	-0.92	-1.1	-0.95	-1.0	
26	0.10	-0.27	-0.13	-0.13	-0.05	12
27	-0.07	1.5	0.06	0.30	-0.06	
28	14			-3.0*		
30	-0.66	3.4	-0.41	0.22	-0.26	0.61
32	0.33	-0.27	0.19	0.13	0.19	5.5
34	1.2	2.4	-1.9	-0.82	0.53	2.1
35	-0.75	0.62	-0.15	-0.08	-0.33	3.2
36	0.43	0.48	-0.27	-0.07	0.44	
37	-0.29	0.08	0.22	0.14		
38	1.2	0.54	0.00	0.22	-1.2	1.7
40	0.31	0.71	1.2	1.0		
42	1.3	-0.86	-0.13	-0.11	0.20	-1.3
43	0.86	0.80	0.55	0.63	-0.41	
44	0.20			-4.5*		
45	0.13	-0.67	0.18	0.03	-0.55	0.92
46	-0.65	-0.19	0.23	0.07	0.12	
48				-4.8		
49	-0.38	0.40	-0.12	-0.06	1.6	0.74
52	0.66	4.1	-1.5	-0.32	1.2	0.00
53	-0.07	3.2	0.17	0.67		
54		1.9	-0.35	-0.45*	-1.5	
55	-0.82	-1.8	-0.17	-0.52	0.57	
56	0.58	0.45	-0.36	-0.12	0.40	
57	0.42	0.65	-0.39	-0.13	0.02	-0.27
59		0.33	0.06	-0.42	-0.94	1.9
60	0.43	-4.9		-4.4*		
61	1.7	0.97	-0.57	-0.07	-0.26	
62	-0.40	-0.33	0.63	0.36	0.82	
63	0.24	0.77	0.35	0.41		
64	-0.19	-0.48	0.23	0.06	0.08	
65	-0.03	-0.31	0.08	0.00		
66	1.4	1.3	0.22	0.53	-0.78	
67	-0.26	-0.21	0.04	-0.032		
68	-0.24	-0.47	-0.32	-0.34	-0.65	-0.59
69	-0.32	-0.73	-0.98	-0.86	-0.89	-0.43
70	0.44	-0.60	2.2	1.6	0.73	-0.53
71	-0.31	-0.74	-0.41	-0.46	0.33	-0.50
72	-0.48	2.2	1.1	1.1	0.74	7.8
74	-3.2	0.08	0.41	-0.02	-0.35	-0.31
75					-0.16	-0.82
76	-1.0	-0.07	0.07	-0.07	0.10	-0.66
77	0.61	0.58	-1.5	-0.89	-0.43	0.60

LAB CODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono- ortho PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209
81	11	2.9	-0,95*	1,0*	-0.22	
82	1.4			-4,3*		
83						
85	-2.5			-4,7*		
87	1.1	0.71	0.14	0.34		
88	0.10	-0.31	1.0	0.68	1.9	0.70
89	0.19	1.9	-0.07	0.29	-1.3	-0.68
90	-0.73			-4,6*		
91	1.5	0.56	0.20	0.40	-0.81	
92	-0.50	-1.1	-0.65	-0.71	-0.85	
94	-0.41	-0.21	-0.28	-0.28		-0.59
96	0.64	-0.59	0.73	0.49	0.04	
99	0.02	-0.51	-0.38	-0.36	-0.37	-0.63
100	-0.18	-0.26	0.37	0.20	-0.34	0.09
101	3.2			-4,1*		
102	0.44	-0.36	-0.28	-0.22	-0.82	2.9

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

Laboratories Z-Scores: Butteoil
TEF1998

LAB CODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono- orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209
1	-0.08	-0.59	-0.73	-0.34		
3	0.61	-0.17	0.51	0.29	0.28	1.6
4	0.15	0.08	0.26	0.13		-0.27
5	-0.27	-1.6	0.03	-0.79	0.17	
6	-0.09	-0.25	-0.79	-0.21	0.72	-0.60
7	-0.54	-1.3	1.6	-0.67		
8	0.29	0.73	0.18	0.46	0.00	
9	2.0	1.7	1.7	1.8	0.54	
11	-0.16	0.02	-0.49	-0.12		0.49
12	-0.29	-0.50	-0.35	-0.38	0.11	
13	0.42		-0.02	-1.8*	-0.80	-0.61
14	-0.47			-2.7*		
16	0.78	68	-3.5	27		
17	-0.48	0.39	0.51	-0.04		
18	-0.92	0.44	0.07	-0.28		
19	0.73	0.55	-0.19	0.58	-0.24	
22	0.16	0.20	0.01	0.16	0.60	0.37
24	0.73	0.64	0.52	0.68	0.35	
25	0.13	-0.66	-0.08	-0.21	0.23	
26	0.17	-0.30	-0.03	-0.04	0.12	3.9
27	-0.12	0.56	0.11	0.18	0.13	
28	145			71*		
30	-0.28	0.77	0.05	0.17	-0.38	-0.17
32	0.09	-0.29	-0.08	-0.08	-0.61	0.23
34	0.90	0.03	0.33	0.49	0.38	3.0
35	-0.81	-0.07	-0.07	-0.44	-0.11	0.45
36	0.39	-0.38	-0.40	0.01	0.41	
37	0.06	0.10	0.18	0.08		
38	0.25	-0.07	-0.47	0.06	-1.4	0.24
39	1.1	0.71	-0.71	0.77	-0.81	
40	-0.01	0.29	0.18	0.13		
42	-0.17	-0.49	-0.09	-0.29	-0.16	-1.0
43	0.21	0.03	0.25	0.14	-0.22	
44	0.49			-2.2*		
45	0.56	-0.51	0.06	0.08	-0.13	0.55
46	-0.32	-0.52	0.06	-0.37	-0.52	
48				2.9		
49	0.12	-0.70	-2.1	-0.41	-0.28	0.02
51	-0.14	0.02	-0.36	-0.10		
52	-0.10	0.28	0.69	0.13	0.63	1.0
53	0.14	0.32	0.35	0.23		
55	-1.5	-1.8	-0.21	-1.5	2.2	
56	0.31	0.03	-0.33	0.14	0.37	
57	0.57	0.04	-0.26	0.28	0.19	-0.16
59		0.05	-0.09	-2.5*	-1.5	0.30
60	0.41	0.16		-0.18*		
61	0.58	0.88	-0.45	0.61	-1.8	
62	0.28	-0.39	1.1	0.09	0.61	
63	-0.22	0.19	0.22	-0.02		
64	-0.13	-0.25	-0.01	-0.17	0.59	
65	-0.07	-0.10	-0.06	-0.08		
66	-0.08	-0.57	-0.39	-0.31	0.53	
67	-0.37	0.02	0.16	-0.16		
68	-0.23	-0.23	-0.52	-0.26	-0.64	-0.24
69	0.24	-0.12	-0.48	0.03	-0.24	-0.61
70	-0.10	-0.89	0.11	-0.40	0.28	-1.0
71	-0.45	-0.18	-0.37	-0.33	-0.08	-0.51
72	0.07	-0.30	0.81	-0.01	2.2	5.4
74	-2.0	0.08	0.45	-0.93	0.37	-0.25
76	-0.24	0.48	0.35	0.10	0.24	-0.06

LAB CODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono- orto PCB	Sum TE total	Sum Indicator PCB	Sum u/209
77	-0.04	0.45	0.07	0.17	0.01	0.20
79	-0.39	0.23	0.19	-0.09	-0.16	-0.13
81	10	0.14	-1,2*	5,2*	0.55	
82	0.53			-2,2*		
87	0.33	-0.18	-0.28	0.07		
88	-0.07	0.24	1.0	0.16	3.2	0.51
89	0.54	-0.93	0.21	-0.08	-3.3	-0.60
90	0.10			-2,4*		
91	1.0	0.04	0.20	0.56	-0.43	
94	-0.39	-0.68	-0.54	-0.52		-0.29
96	-0.11	-0.29	0.63	-0.11	2.9	
98	0.50	0.23	-0.18	0.33	-0.11	-0.36
99	-0.12	-0.49	-0.33	-0.29	-0.15	-0.24
100	0.03	-0.86	-0.15	-0.34	-0.40	0.44
101	4.3			-0,27*		
102	-0.10	-0.46	0.09	-0.22	-0.27	3.0
103	-0.24	0.30	-0.10	-0.01	-0.87	

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

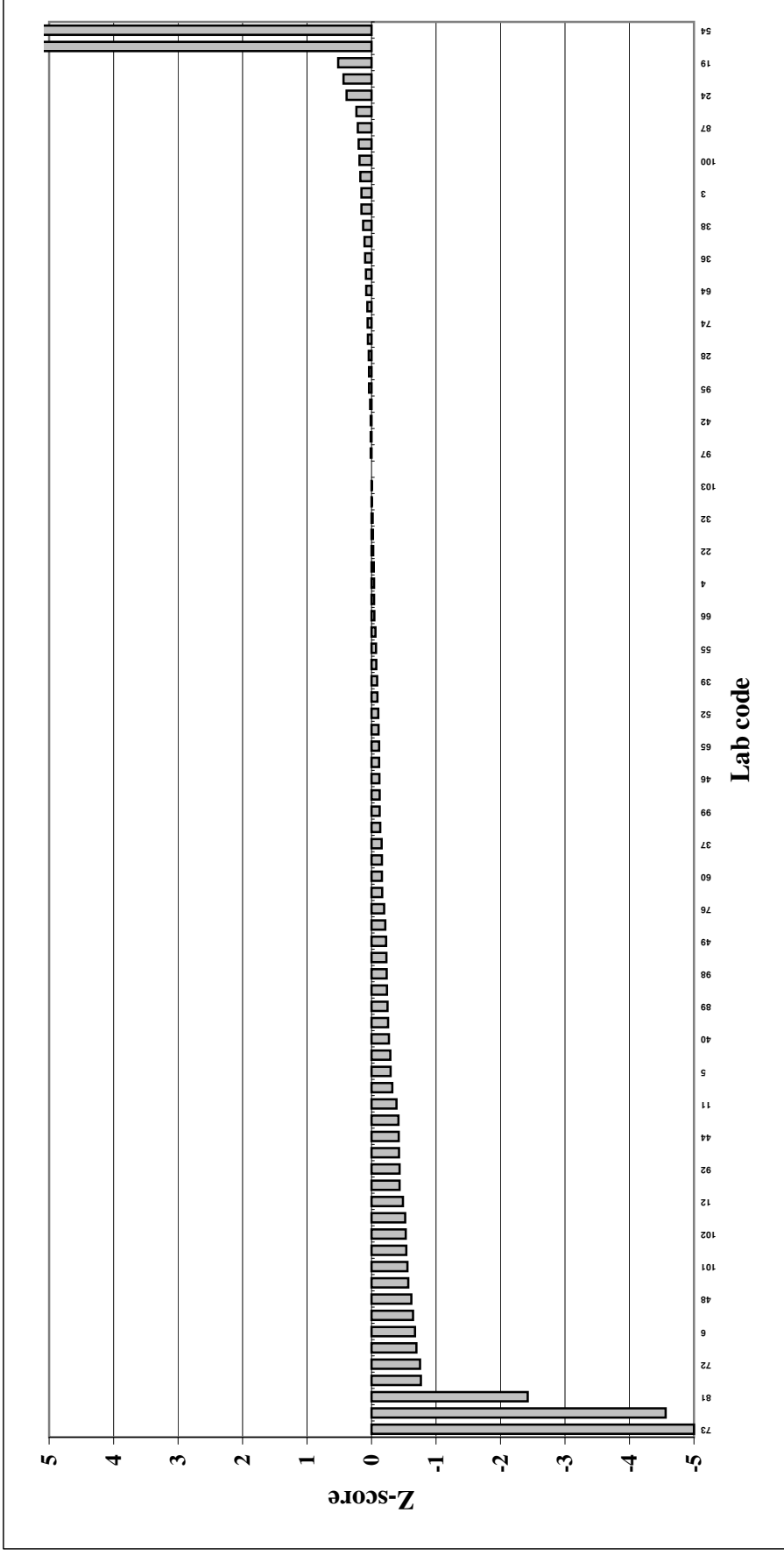
Laboratories Z-Scores: Herring
TEF1998

LAB CODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono- orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209
3	0.14	-0.16	0.56	0.071	0.065	2.0
4	0.26	0.62	0.72	0.47		-0.52
5	-0.48	-0.65	0.18	-0.46	-0.04	
6	-0.74	-0.07	-1.2	-0.52	-0.90	5.2
7	0.23	-1.3	1.9	-0.17		
8	0.25	0.78	0.30	0.48	0.70	
9	0.89	4.2	1.2	2.4	1.1	
11	-2.3	-2.2	-2.4	-2.3		-2.0
12	-0.35	-0.28	-0.31	-0.31	-0.15	
13	0.67		0.19	-1.8*	-0.71	0.55
14	-0.41			-3.0*		
16	4.4	-2.9	-2.8	0.34		
17	0.60	1.2	1.1	0.92		
18	-2.3	-2.5	-2.5	-2.4		
19	0.89	0.58	0.01	0.63	0.04	
20	4.6	-1.7	-2.2	1.0	-2.3	-2.0
22	-0.06	-0.07	-0.18	-0.084	0.71	-0.02
23	0.45	0.48	0.71	0.50	7.5	0.74
24	0.48	0.76	0.49	0.60	0.41	
25	0.16	0.15	0.42	0.20	6.8	
26	-0.15	-0.46	-0.28	-0.30	0.03	0.43
27	0.18	0.19	-0.18	0.13	-0.14	
28	413			179*		
30	-0.52	0.15	-0.54	-0.24	-0.85	-0.45
31	-0.07	0.91	0.62	0.44	-1.8	
32	-0.17	0.00	0.14	-0.054	-0.42	0.15
34	0.87	1.4	0.41	1.0	1.3	0.70
35	-1.1	0.20	-0.28	-0.42	-0.18	0.27
36	0.48	0.85	-0.40	0.51	1.1	
37	-1.1	-1.1	-1.2	-1.1		
38	0.10	-0.09	-0.27	-0.031	-0.98	0.32
40	-0.33	0.76	0.89	0.30		
42	0.09	-0.45	-0.05	-0.16	0.47	-0.17
43	0.31	0.50	0.60	0.43	0.12	
45	0.27	-0.20	-0.16	0.0094	-0.38	0.55
46	-0.58	-0.21	0.15	-0.32	-0.32	
47	1.1	0.22	0.90	0.70	1.2	0.79
49	0.79	-0.69	-0.10	0.044	1.2	-0.40
50	44	-0.58	0.36	19		
51	0.03	0.07	-0.37	-0.0091		
52	0.37	0.41	-0.22	0.31	1.5	0.60
53	0.20	0.64	-0.06	0.35		
54		13	11	4,6*	8.2	
55	-0.10	-1.0	0.07	-0.47	0.77	
56	0.23	0.37	-0.29	0.22	0.95	
57	0.82	0.20	-0.34	0.40	-0.10	-0.33
59		0.00	-0.19	-2,2*	-1.2	0.44
60	0.49	0.75		-0,16*		
61	0.45	0.37	-0.16	0.33	-0.65	
62	0.03	-0.06	-0.01	-0.013	0.94	
64	0.16	0.11	0.36	0.17	0.87	
66	-1.4	-0.83	-0.27	-1.0	-0.52	
67	-0.46	-0.03	-0.02	-0.22		
68	-0.22	-0.53	-0.30	-0.36	-0.67	-0.82
69	0.64	0.49	-0.12	0.47	0.01	-0.38
70	-0.74	-0.35	0.67	-0.38	0.47	-0.48
71	-0.04	0.62	0.11	0.26	0.63	-0.05
72	0.13	1.0	0.67	0.59	0.89	0.89
73	1,9*	0,05*		0,16*		
74	-1.2	0.52	0.59	-0.22	0.62	0.24

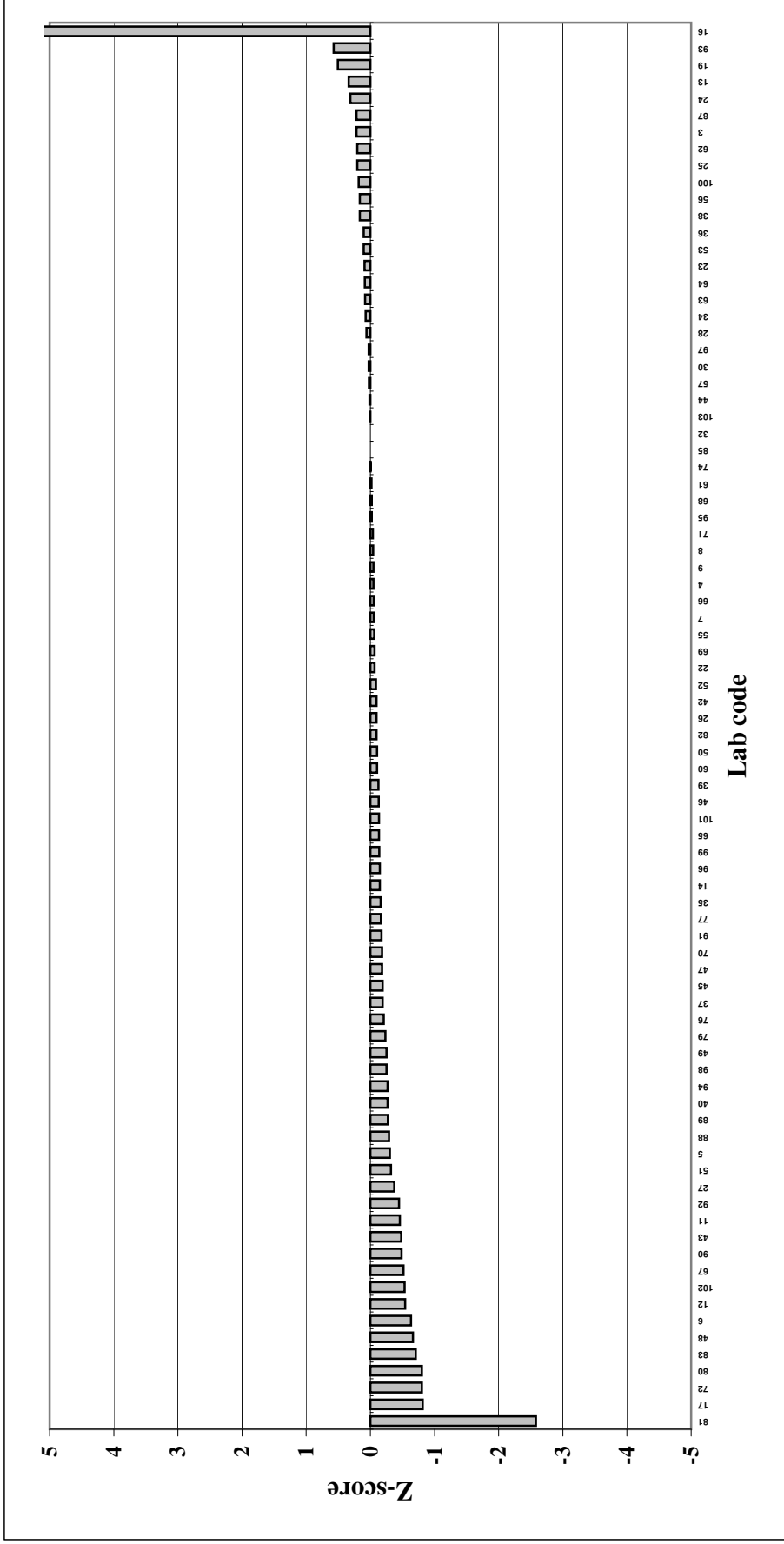
LAB CODE:	Sum TE PCDD/PCDF	Sum TE non- ortho PCB	Sum TE mono- orto PCB	Sum TE totalt	Sum Indicator PCB	Sum u/209
75					0.64	-0.15
76	-0.55	0.64	0.16	0.050	0.36	-0.24
77	0.10	0.73	-0.06	0.35	0.08	0.30
79	-0.24	0.36	0.43	0.11	0.12	-0.09
80	1.3	0,76*	-0,017*	0,87*	0.54	0,87*
81	3.4	-0.71	-0,84*	1,1*	1.5	
82	1.0			-2,4*		
83	-0.30	0.43	-0.17	0.029	-2.6	
87	3.6	-1.6	-1.4	0.72		
88	-0.01	0.32	0.99	0.27	3.8	0.35
89	0.35	-0.29	0.10	0.045	0.20	0.01
91	-1.7	-2.8	-2.5	-2.3	-3.3	
92	-1.1	-1.8	-1.8	-1.5	-1.7	
93	2.5			-1,7*	2.1	
94	-0.48	-0.22	-0.63	-0.39		0.42
95	-0.35	-0.34	0.63	-0.21	-0.77	-0.27
96	-0.05	-0.05	-1,8*	-0,29*	1.9	
97	0.30	-0.16	0.05	0.071	0.28	0.17
98	2.7	0.55	0.22	1.5	0.26	-0.10
99	0.17	-0.40	-0.51	-0.17	0.07	-0.36
100	-0.05	-1.1	-0.42	-0.53	-0.62	-0.97
101	3.9			-1,1*		
102	-0.20	-0.30	-0.08	-0.23	-4.0	-1.3
103	-1.1	-1.1	0.98	-0.80	-1.0	

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

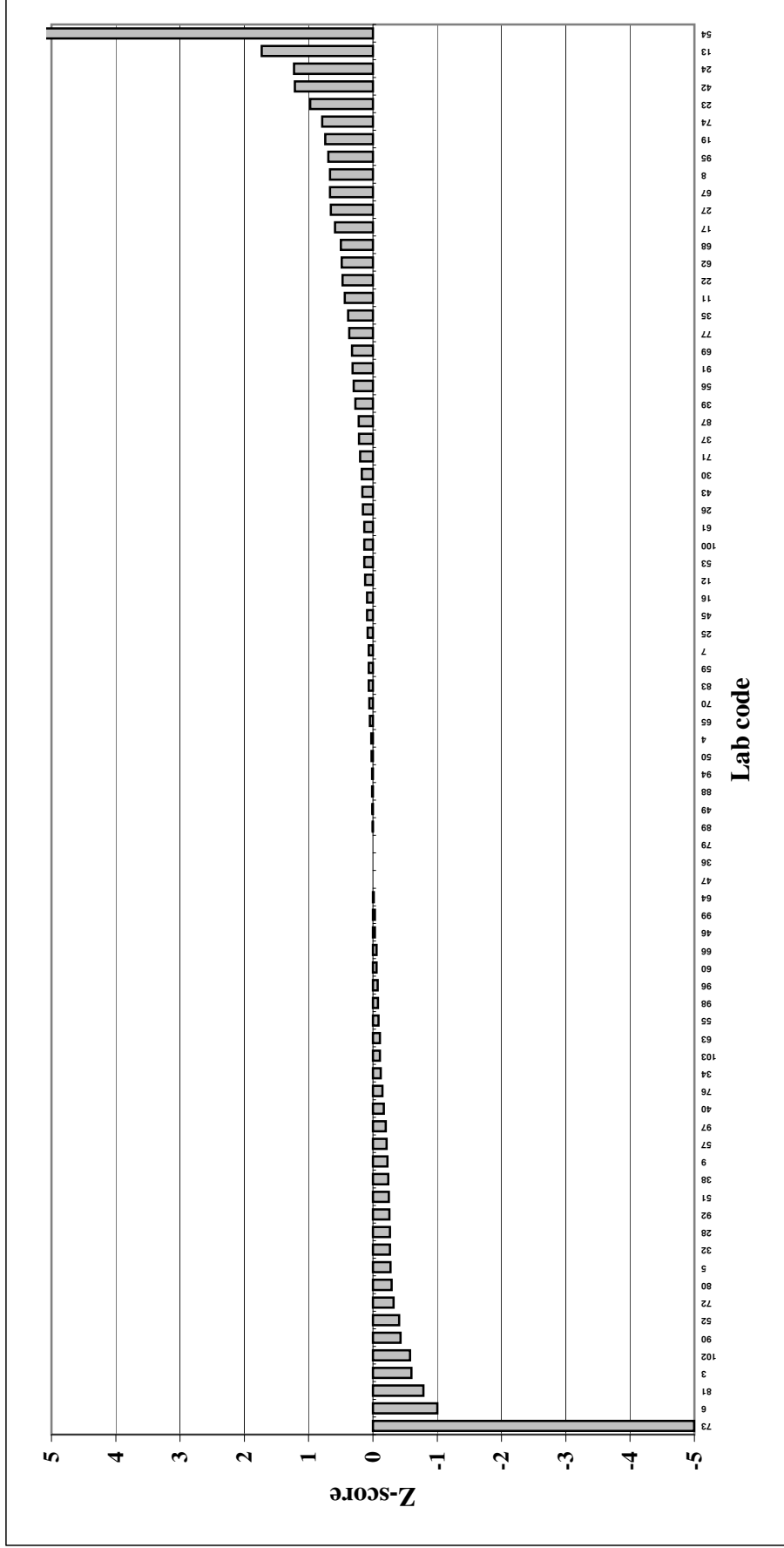
Z-score analyte solution; total TEQ



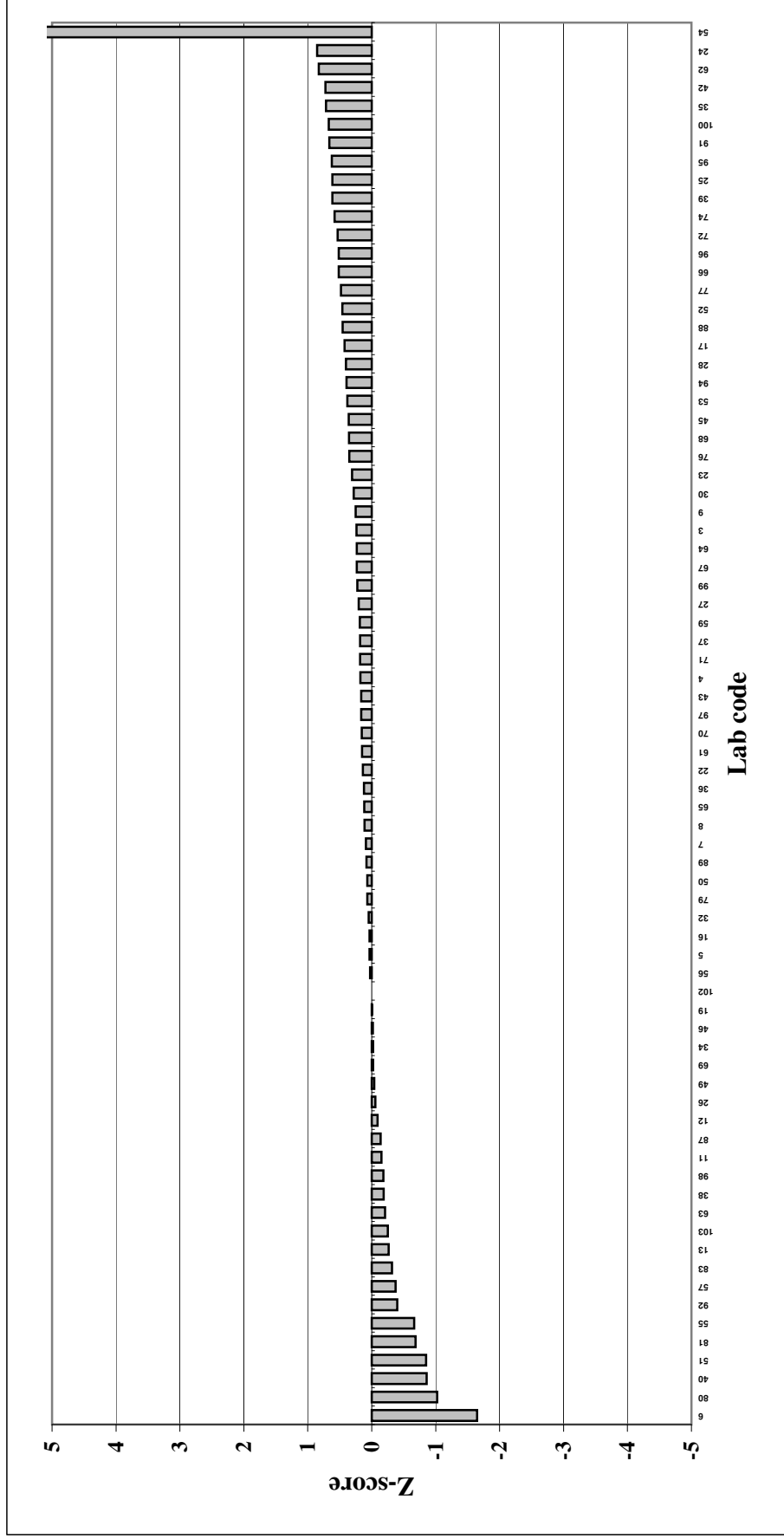
Z-score analyte solution; PCDD/PCDF TEQ



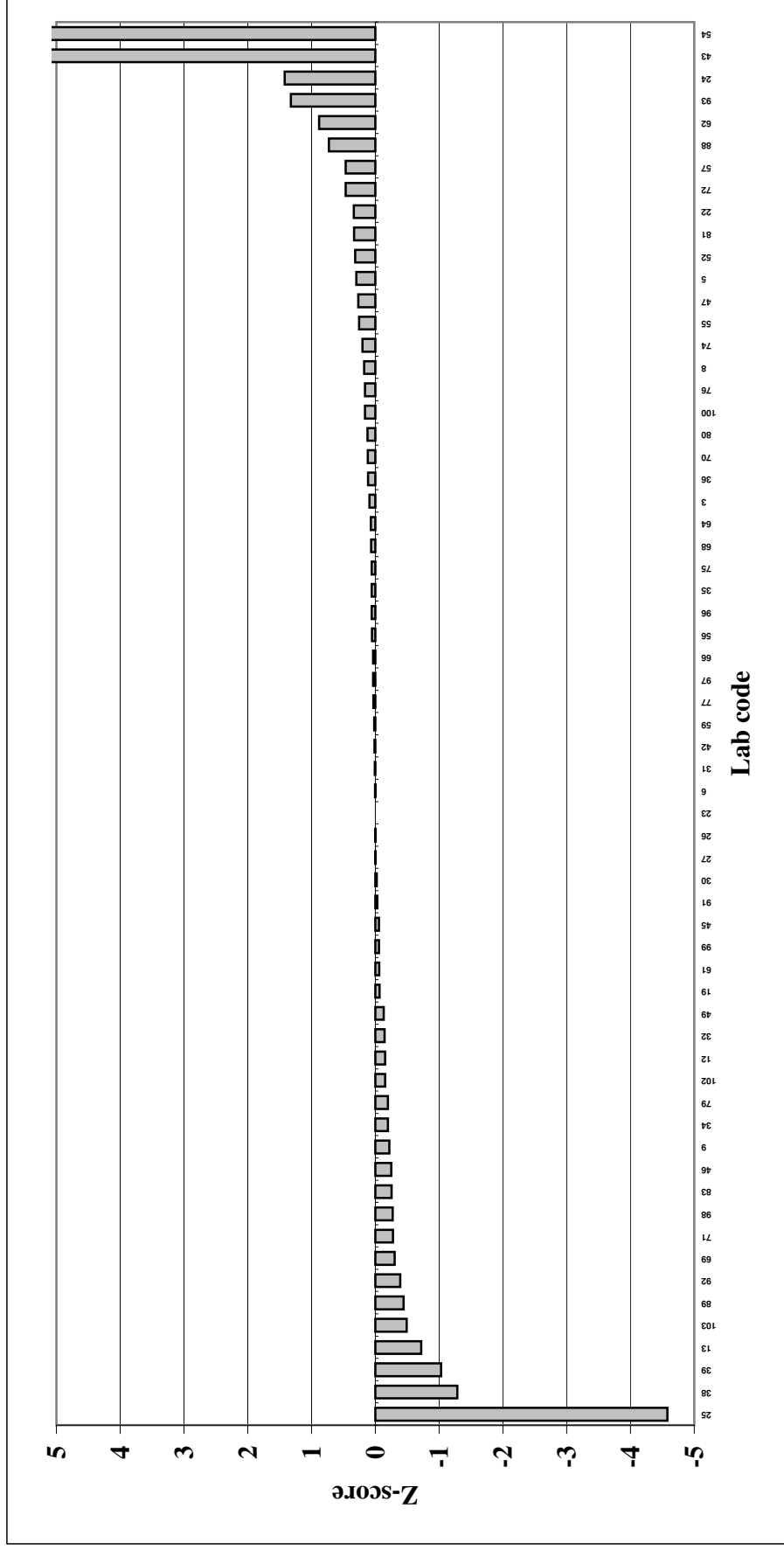
Z-score analyte solution; non-ortho PCB TEQ



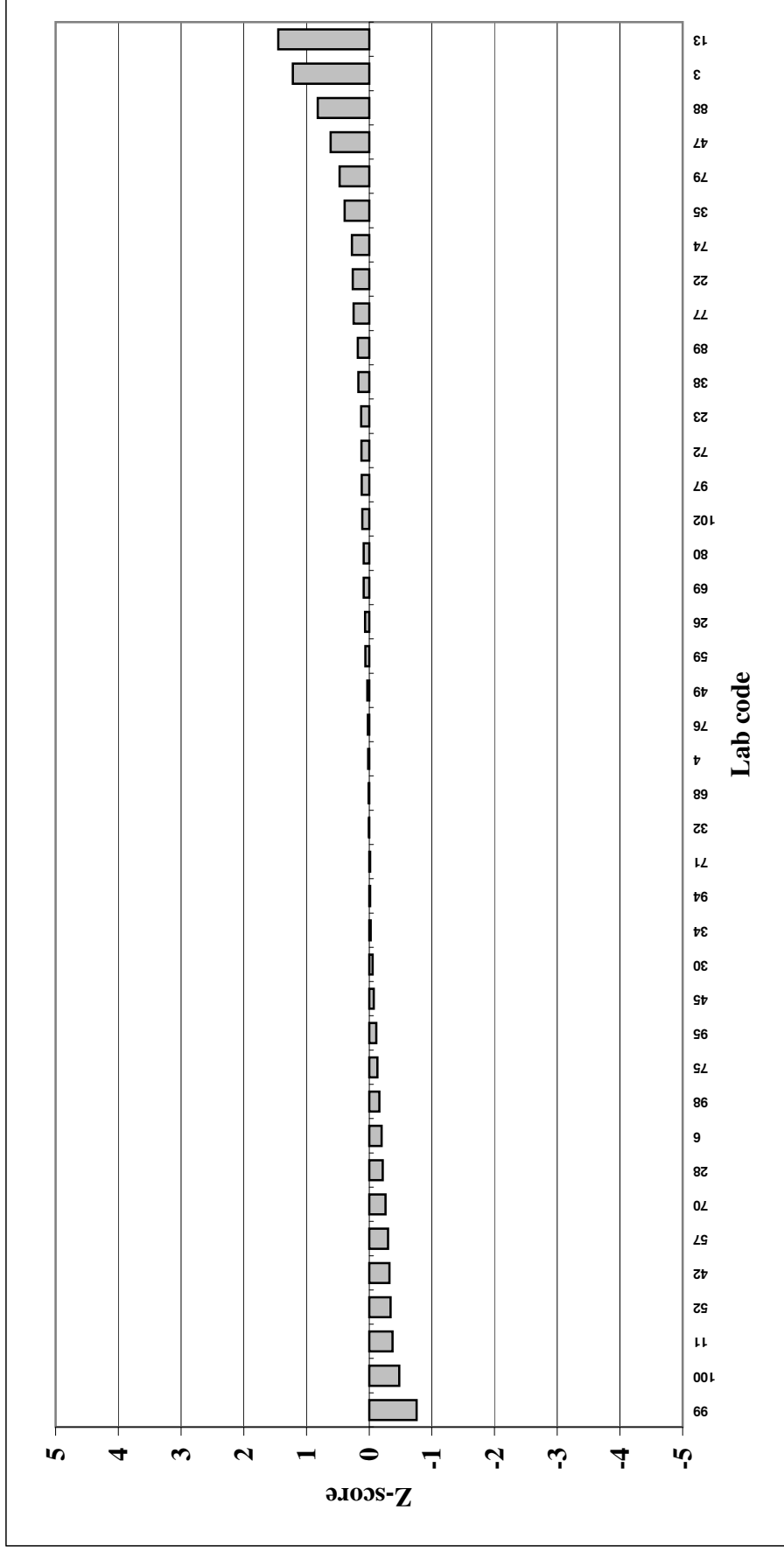
Z-score analyte solution; mono-ortho PCB TEQ



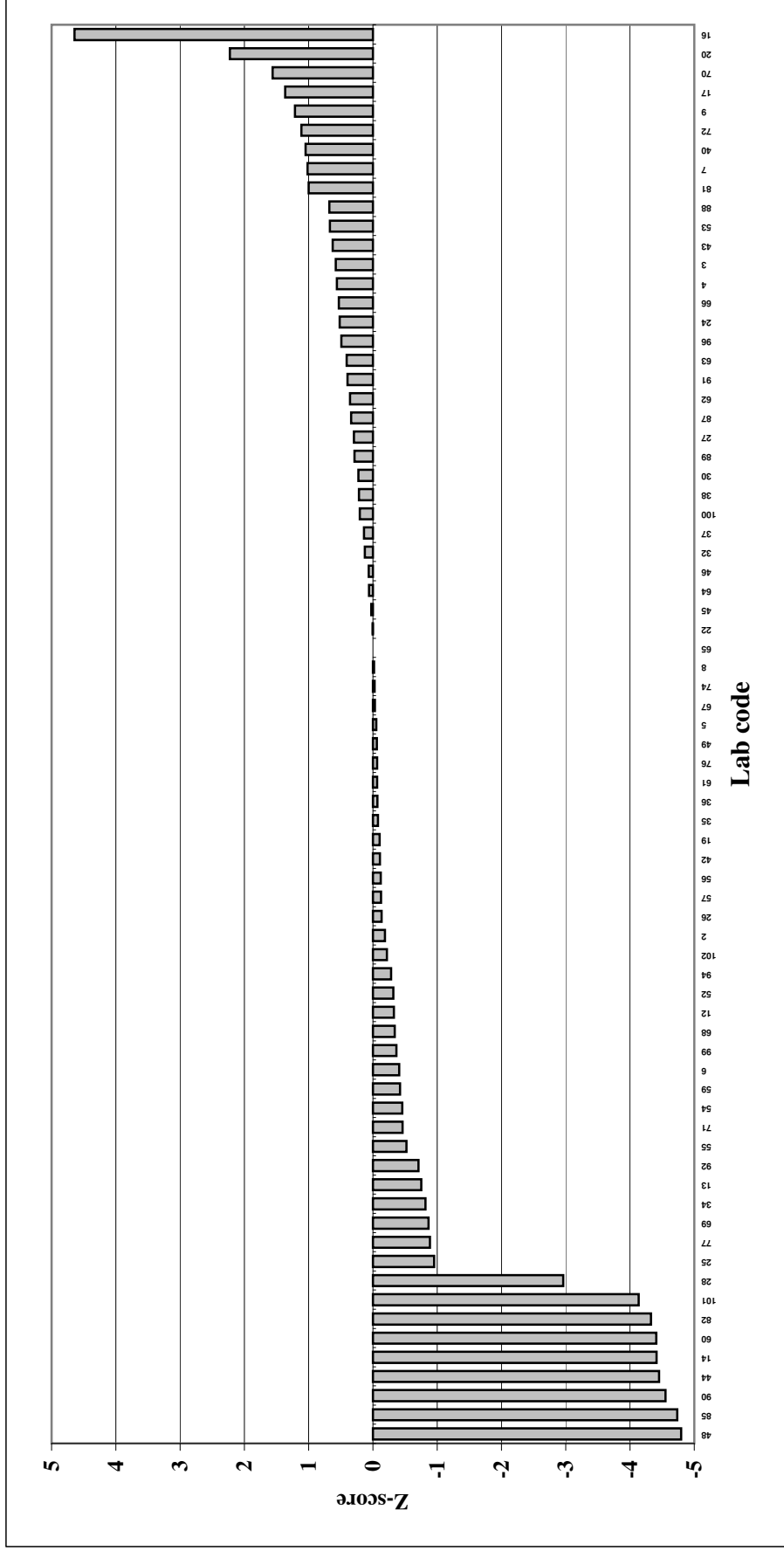
Z-score analyte solution; sum indicator PCB



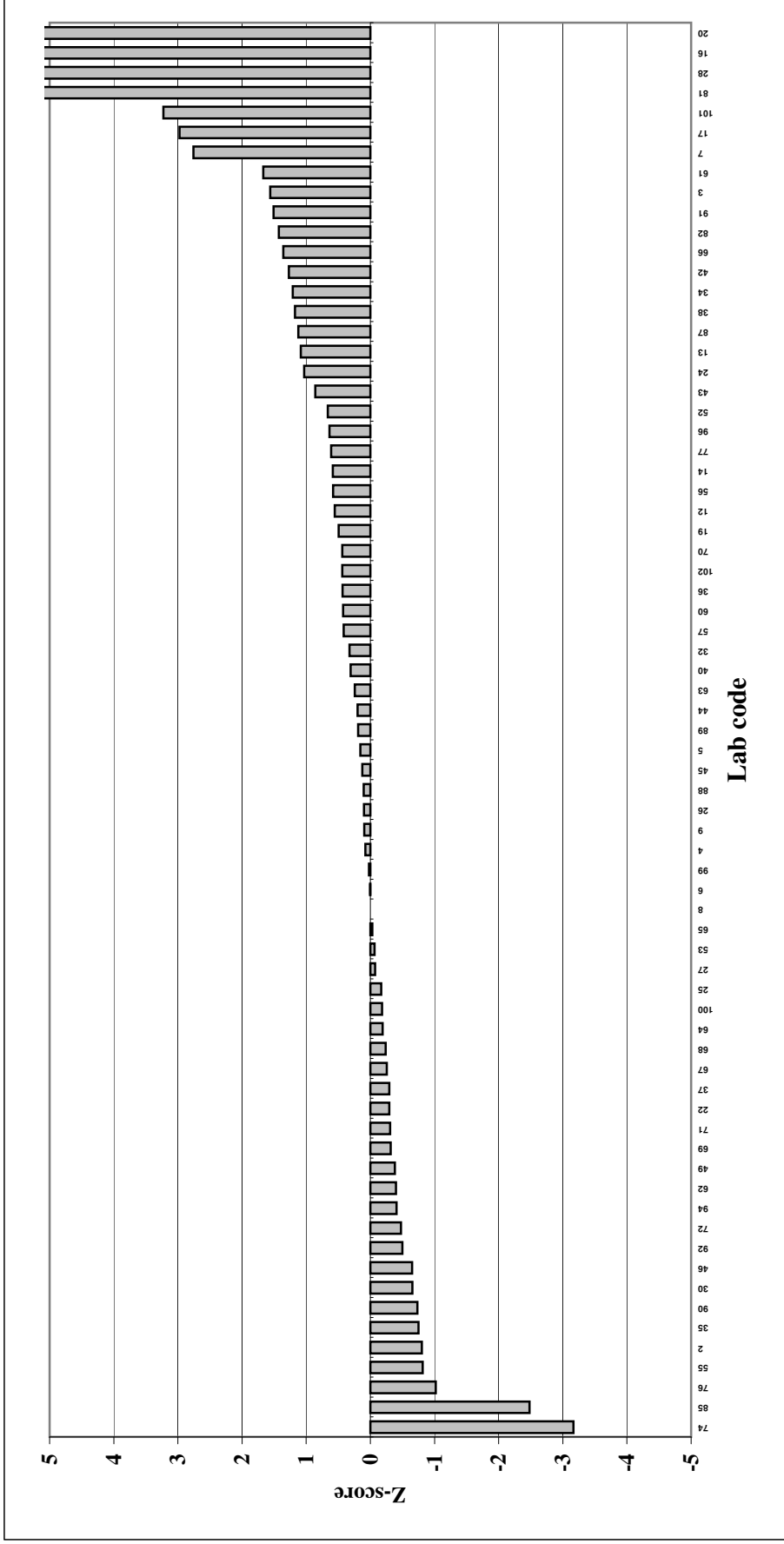
Z-score analyte solution; sum PBDE without BDE-209



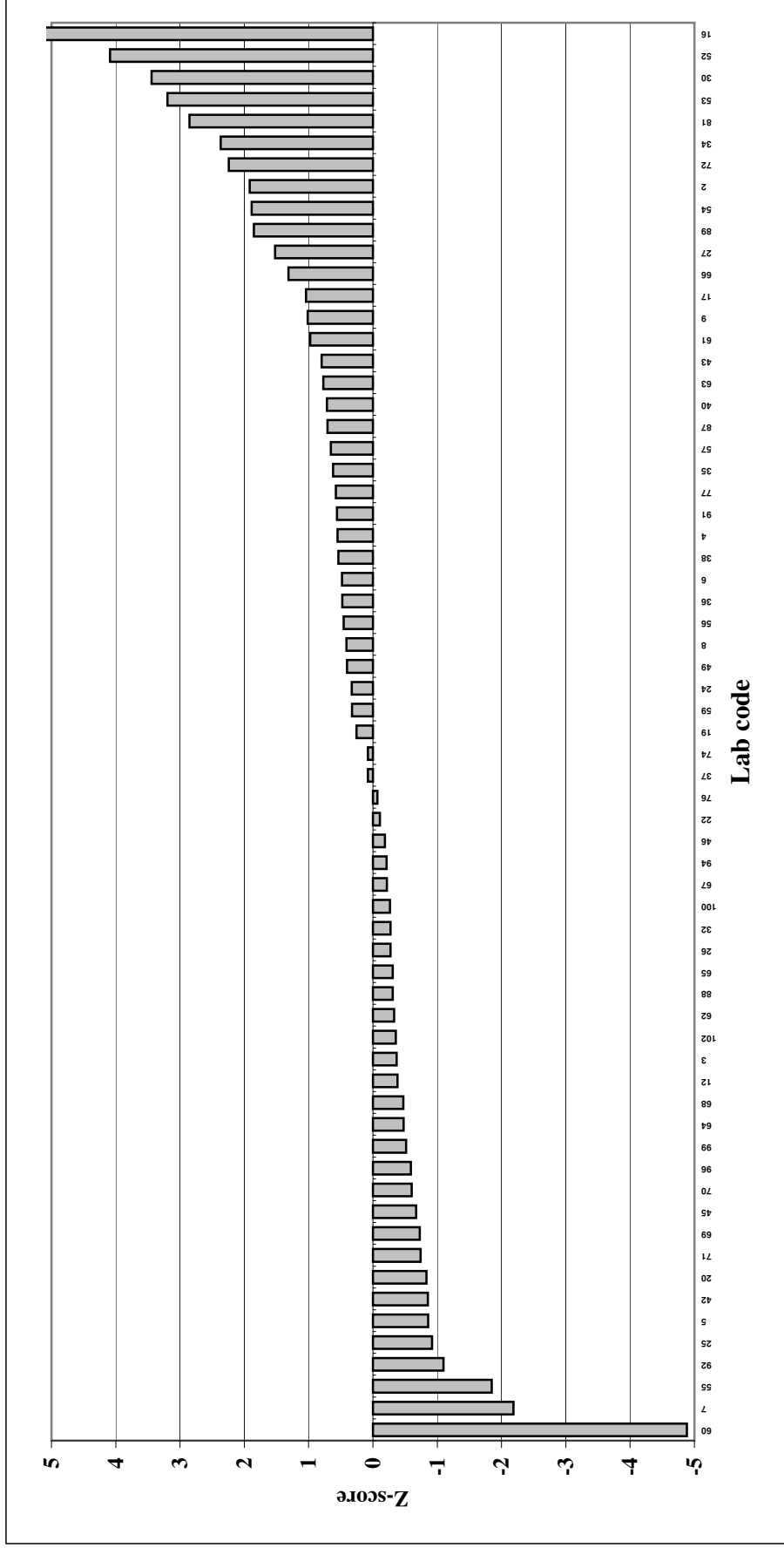
Z-score Beef; total TEQ



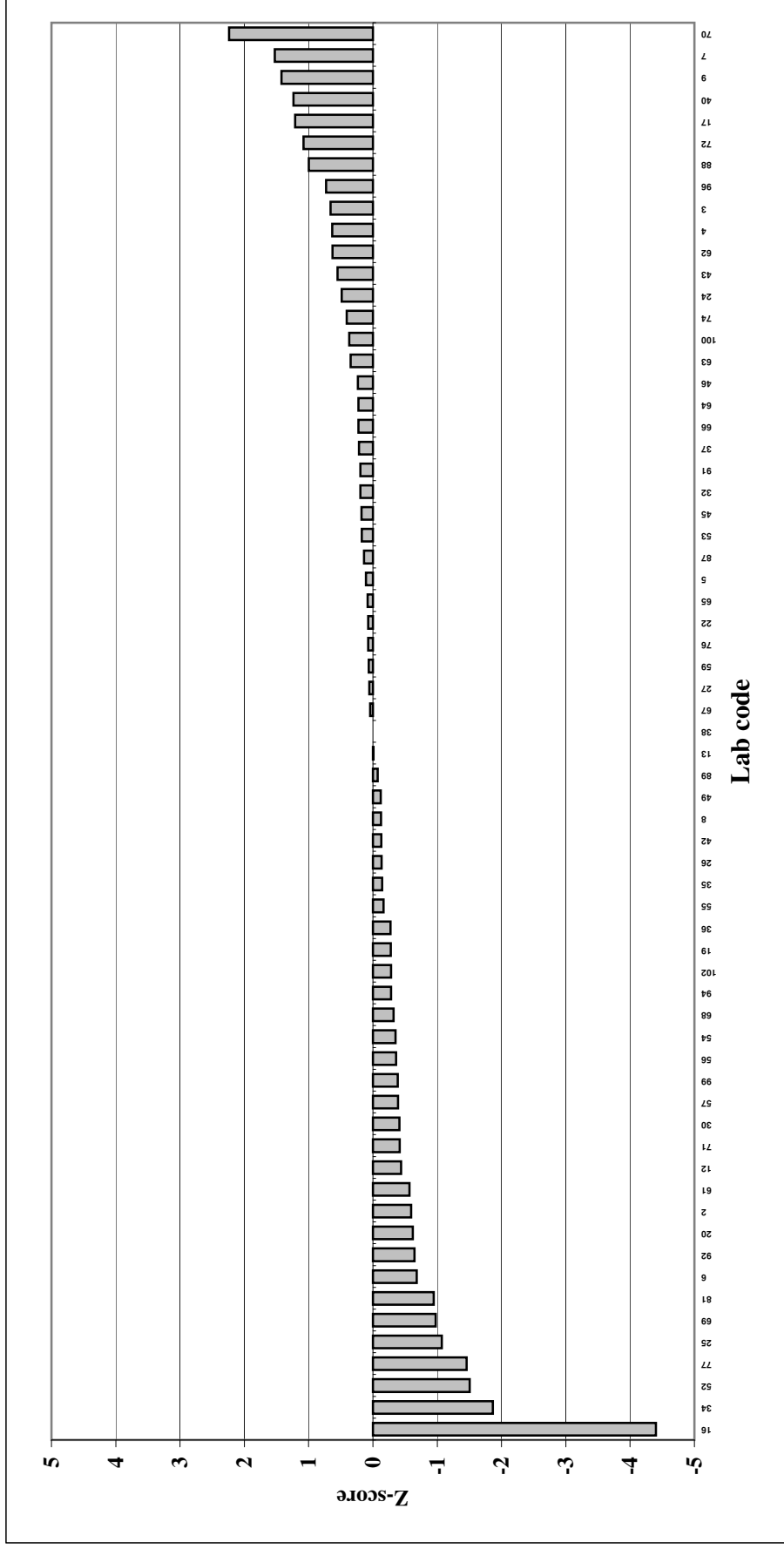
Z-score Beef; PCDD/PCDF TEQ



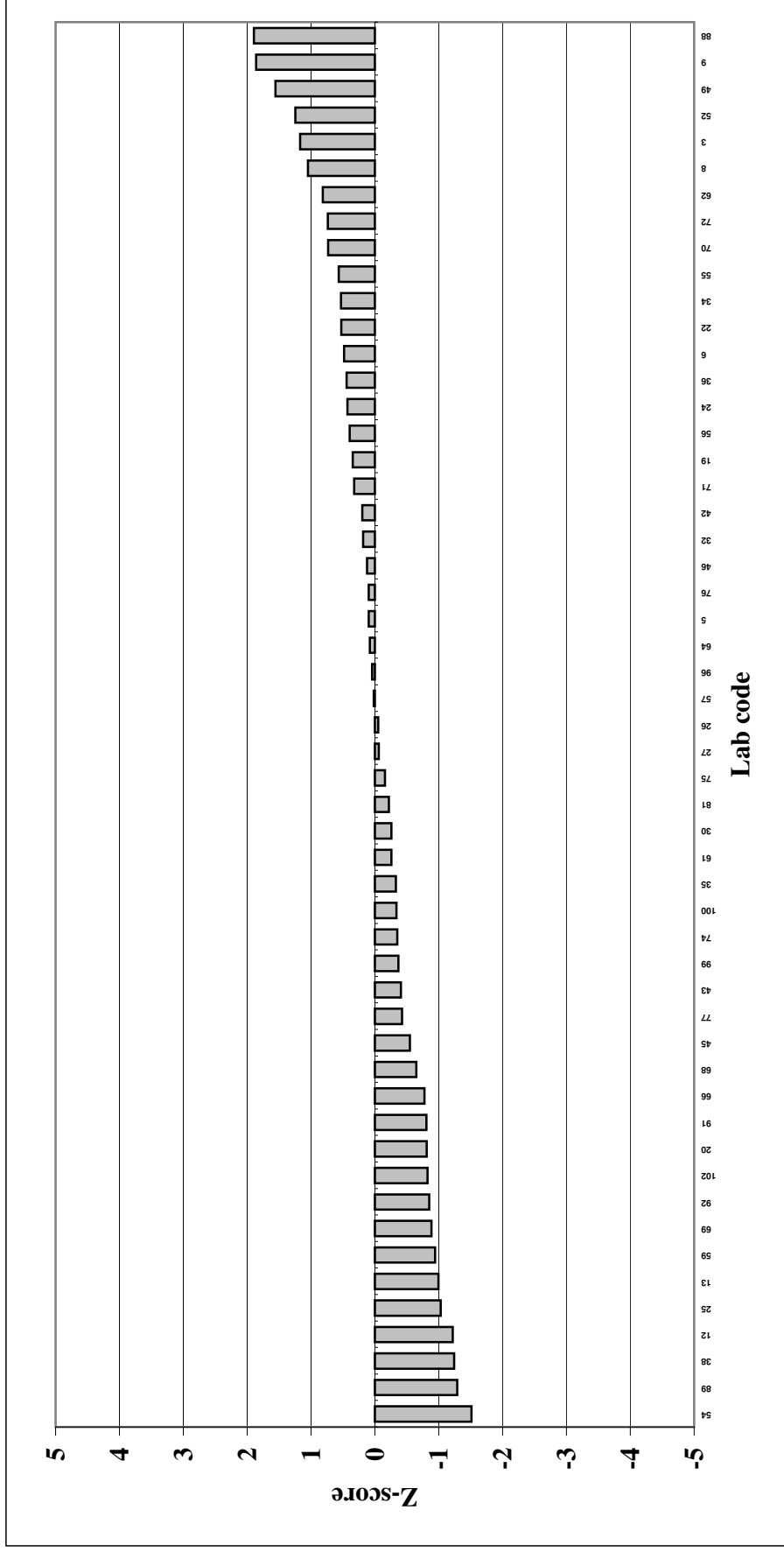
Z-score Beef; non-ortho PCB TEQ



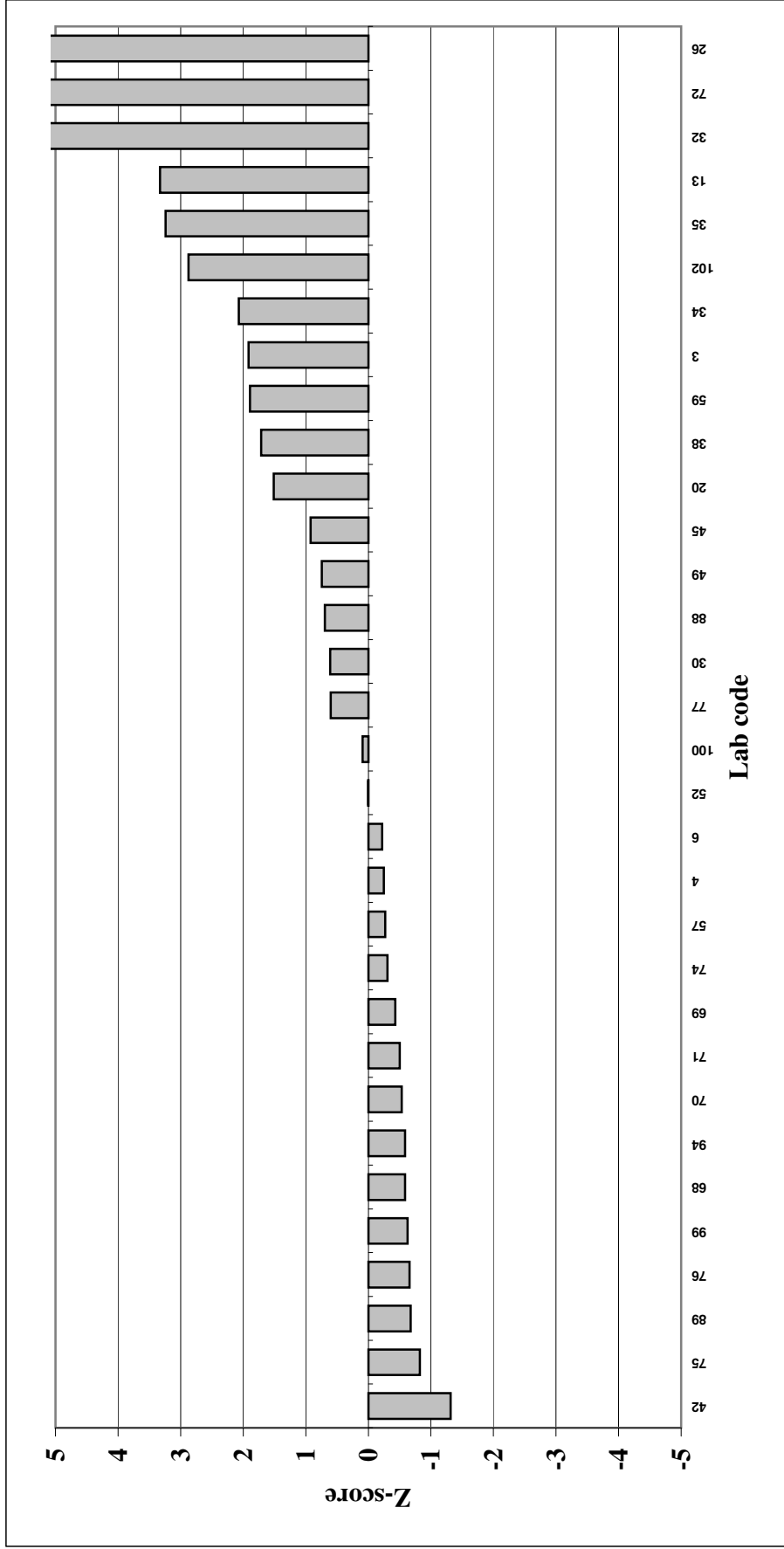
Z-score Beef; mono-ortho PCB TEQ



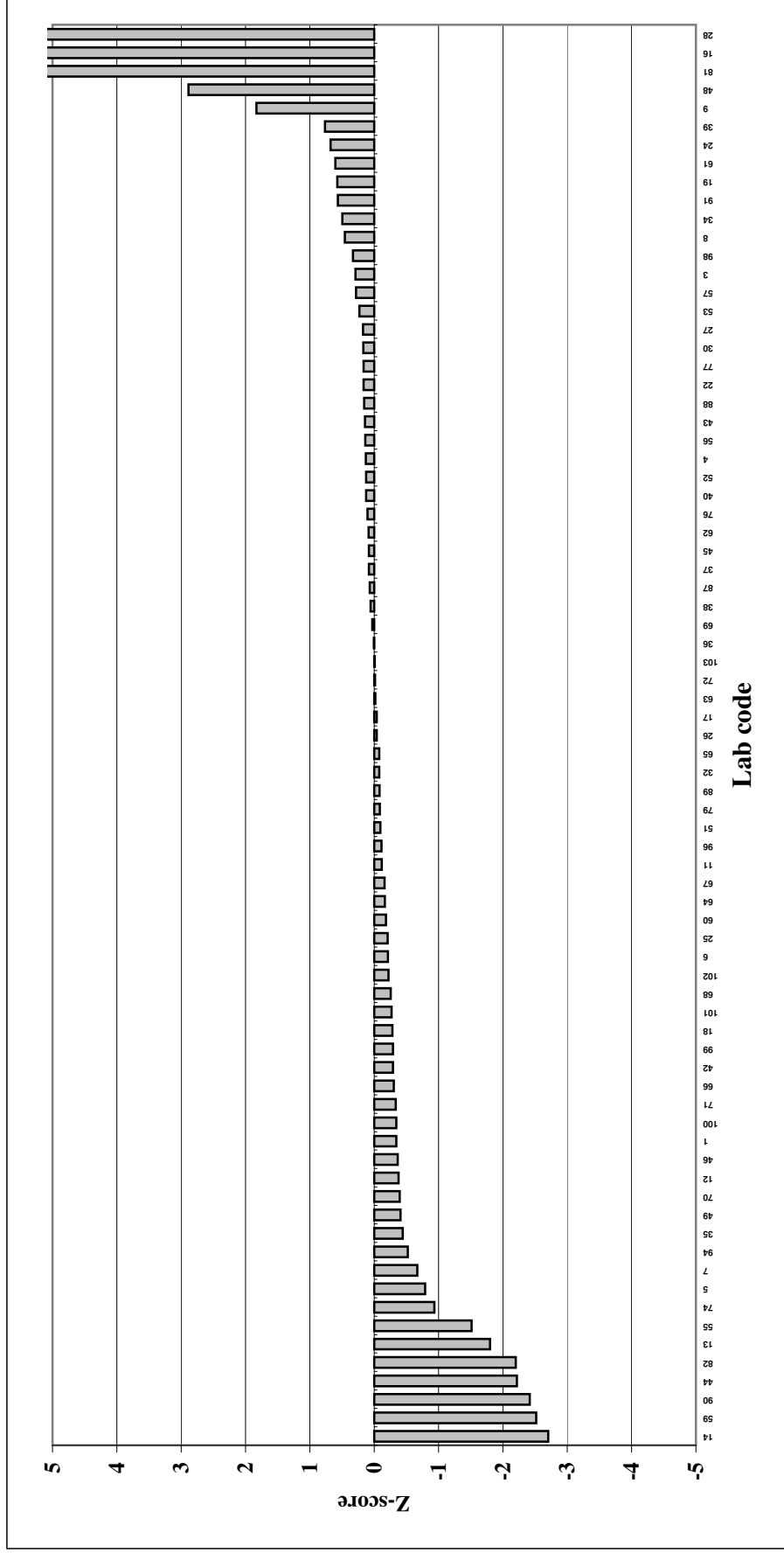
Z-score Beef; sum indicator PCB



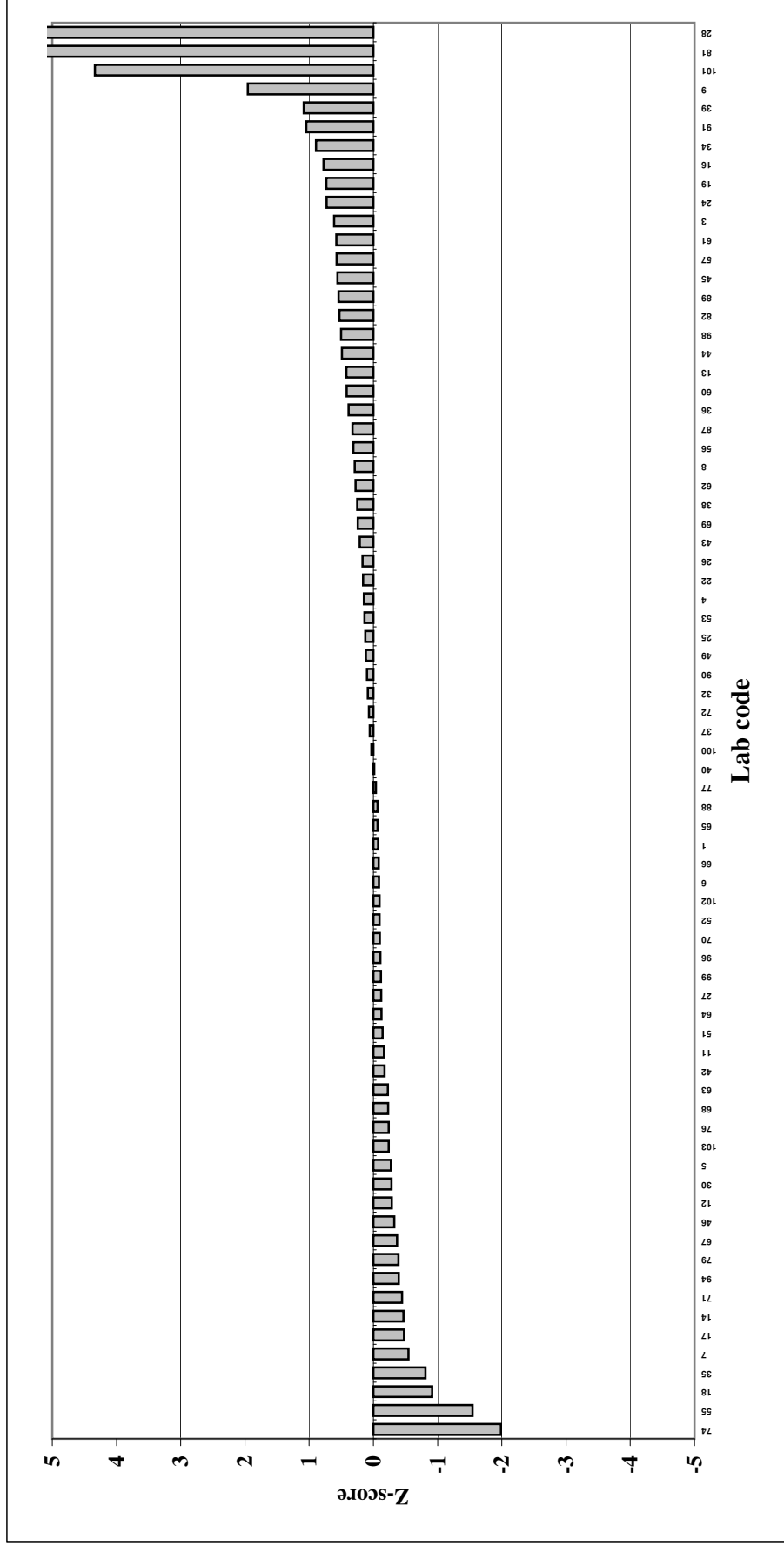
Z-score Beef; sum PBDE without BDE-209



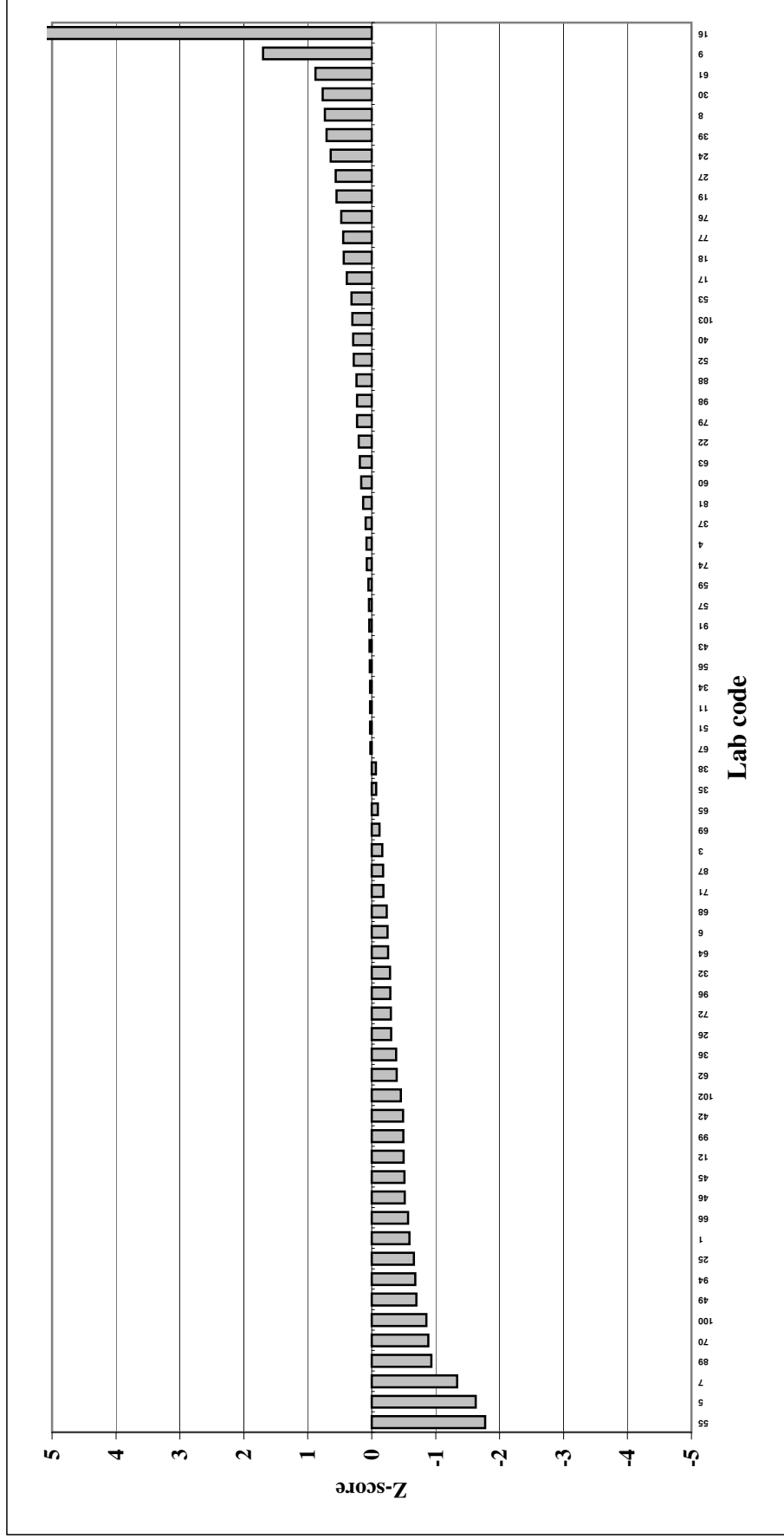
Z-score Butteroil; total TEQ



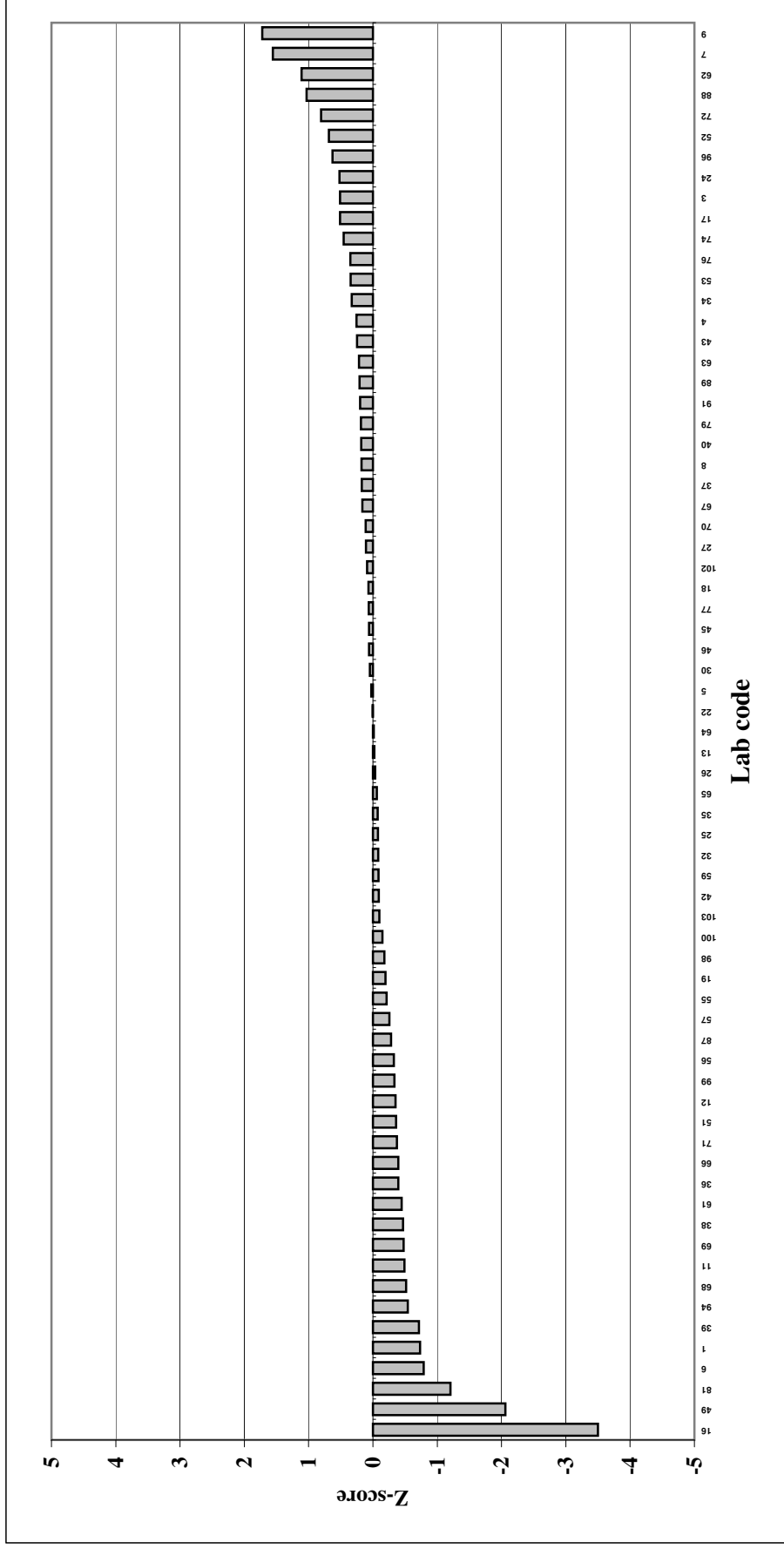
Z-score Butteiroil; PCDD/PCDF TEQ



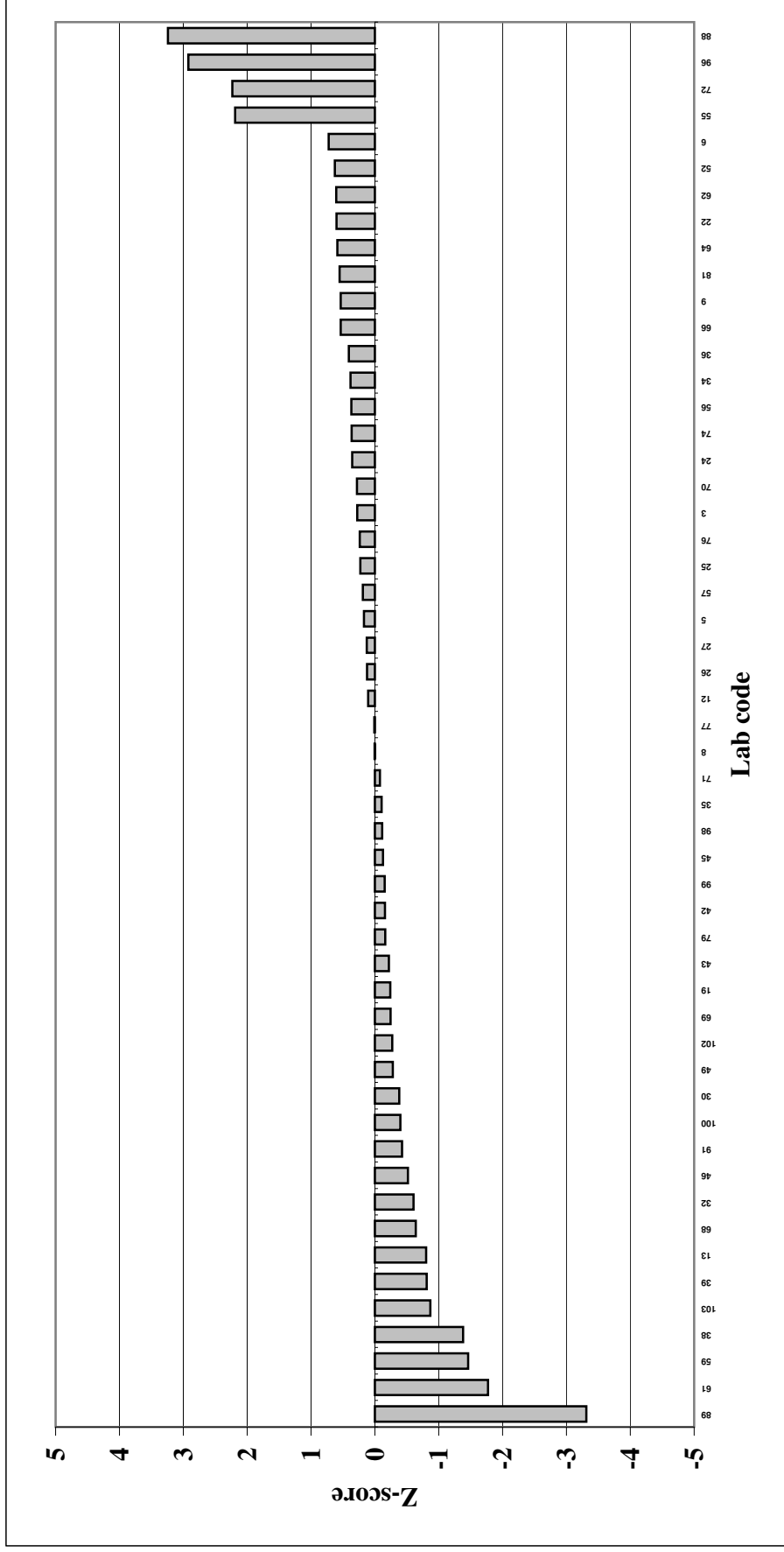
Z-score Butteroil; non-ortho PCB TEQ



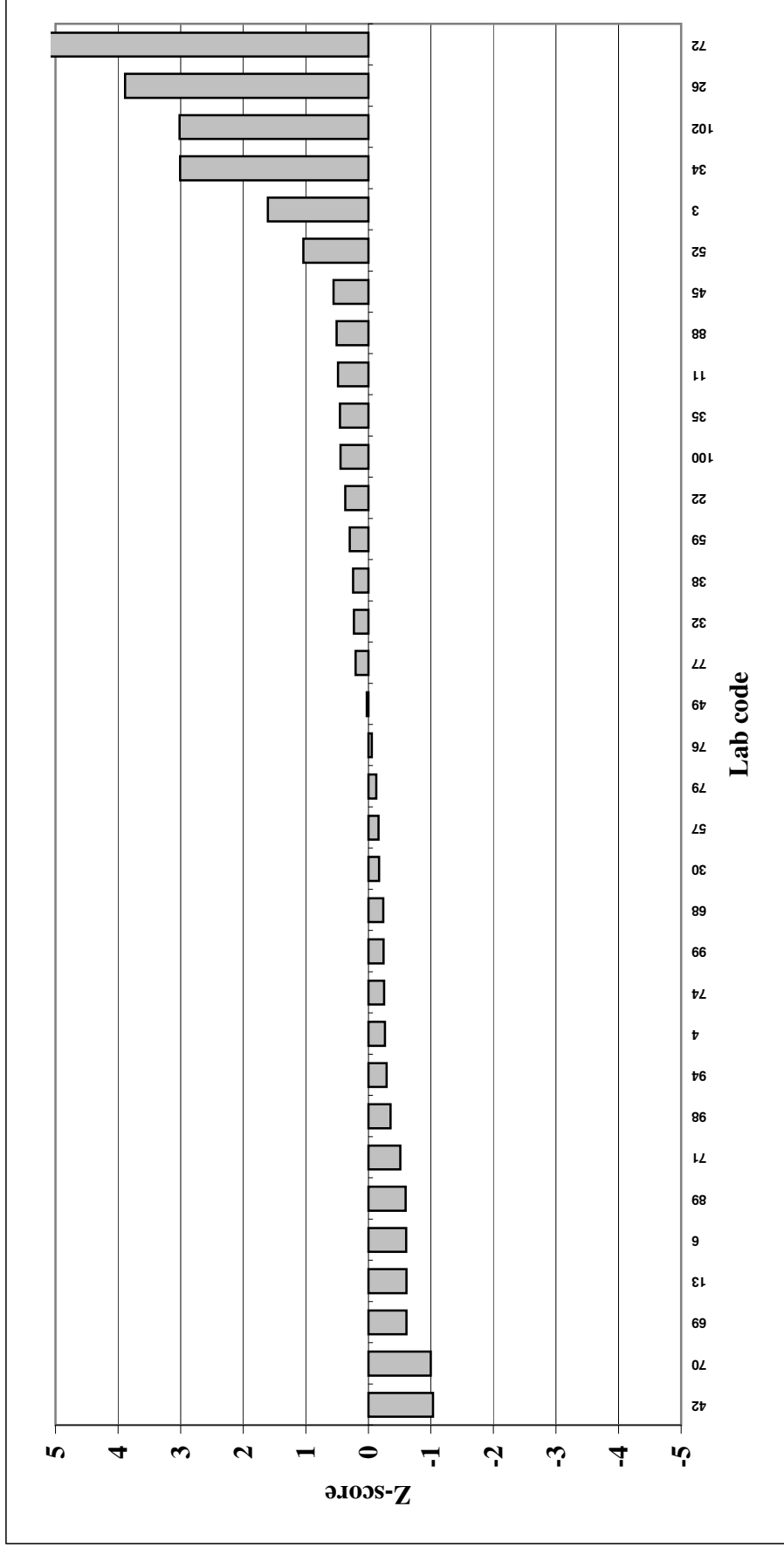
Z-score Butteroil; mono-ortho PCB TEQ



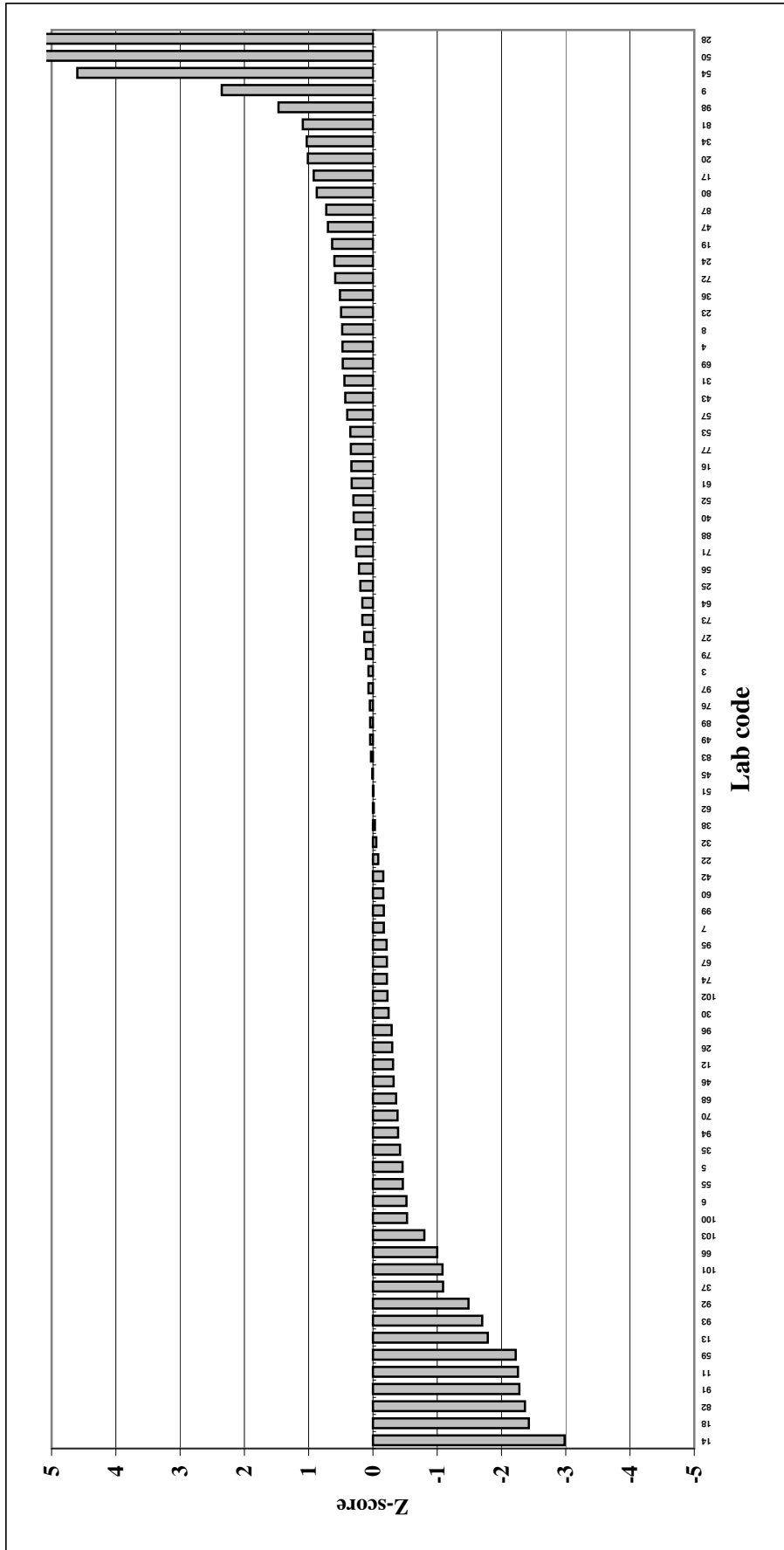
Z-score Butteroil; sum indicator PCB



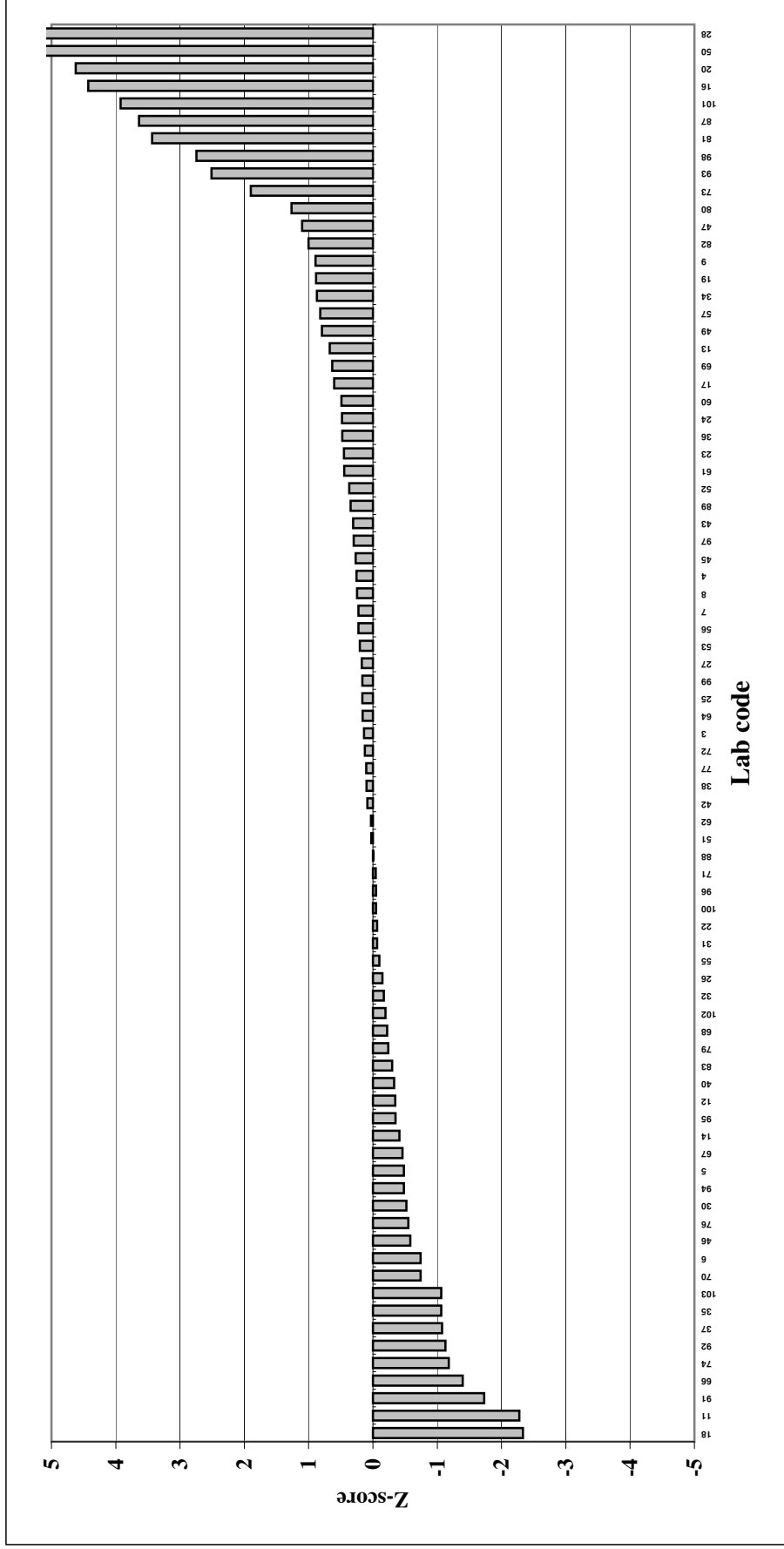
Z-score Butteroil; sum PBDE without BDE-209



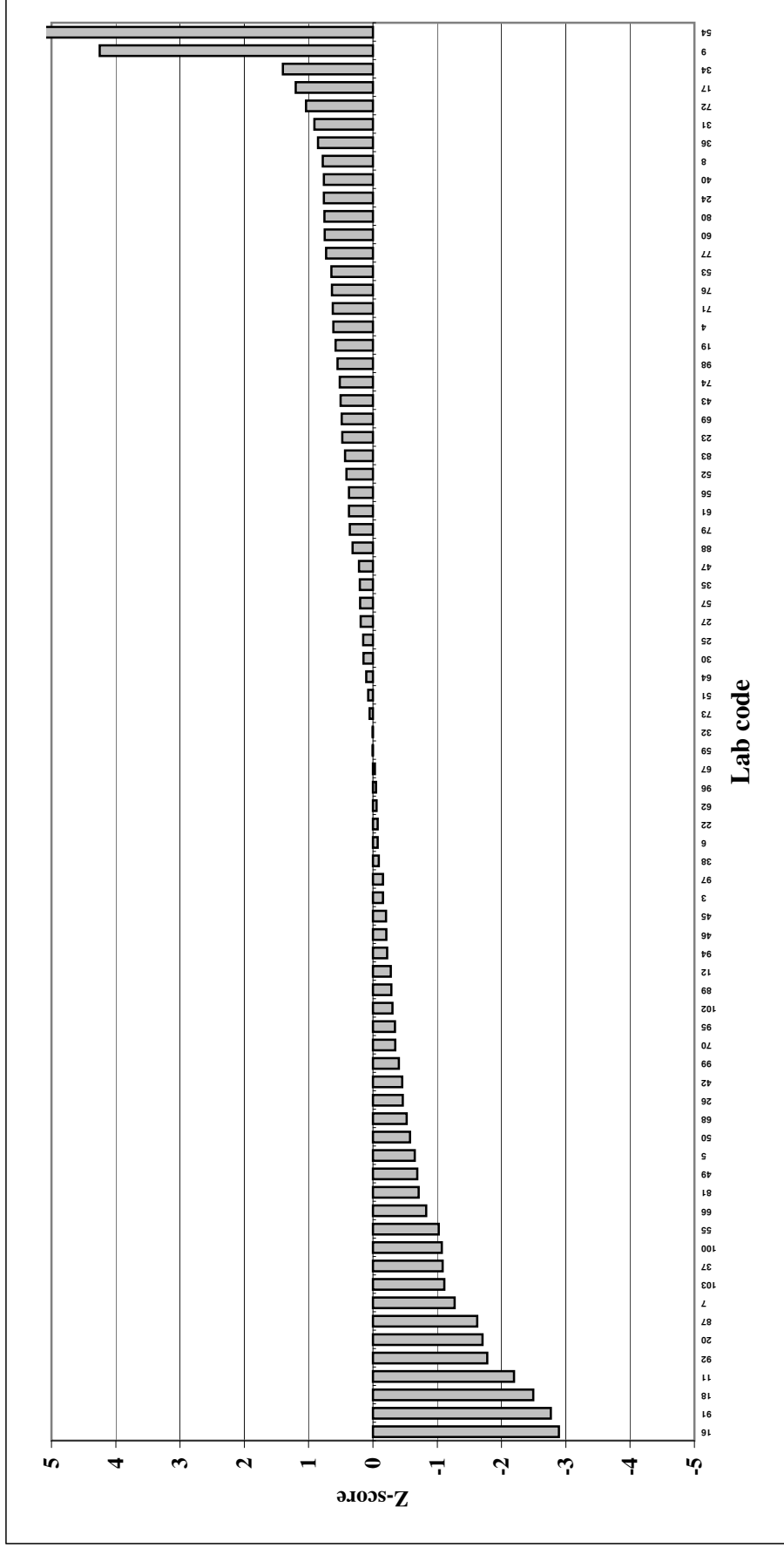
Z-score Herring; total TEQ



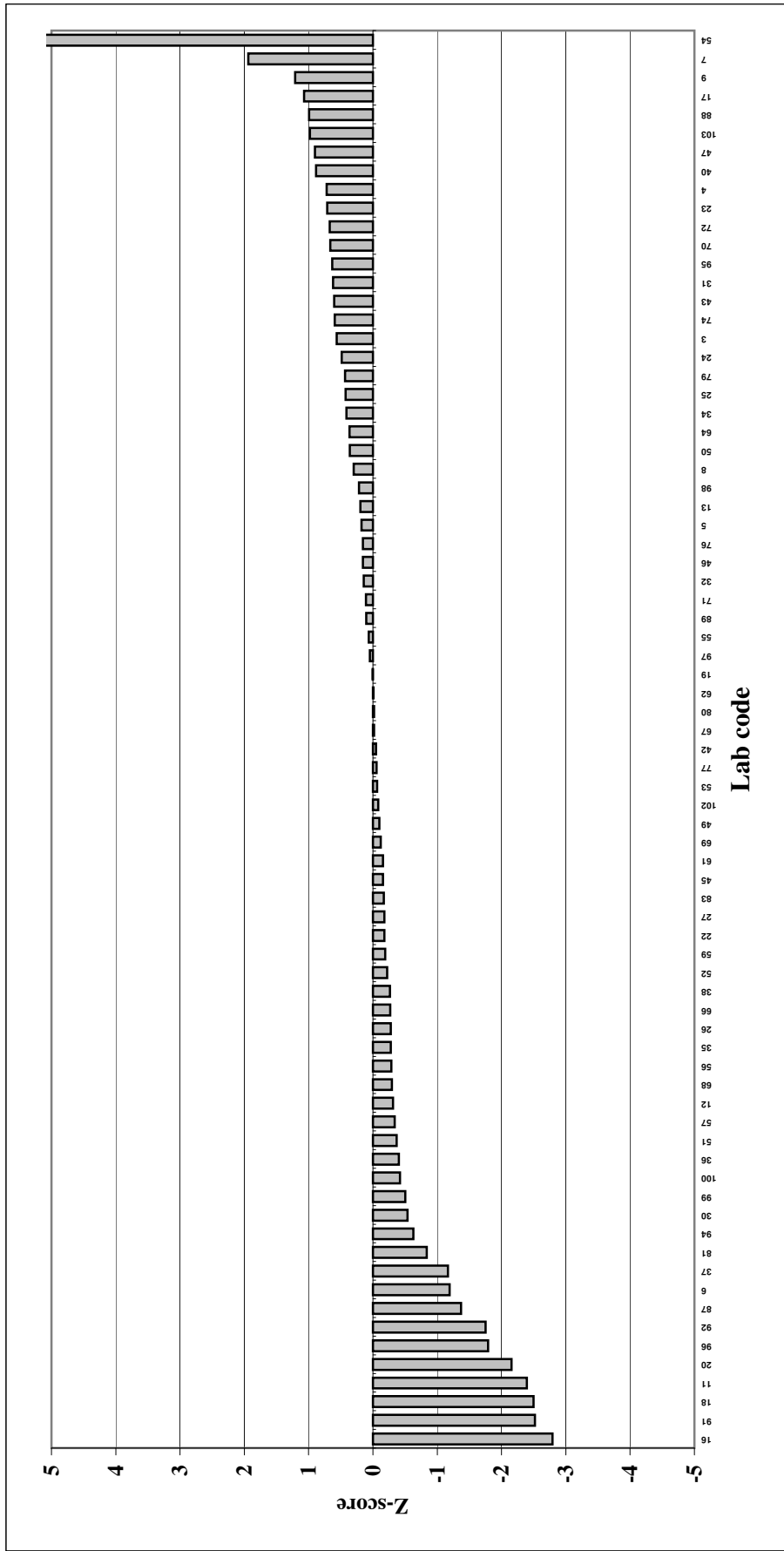
Z-score Herring; PCDD/PCDF TEQ



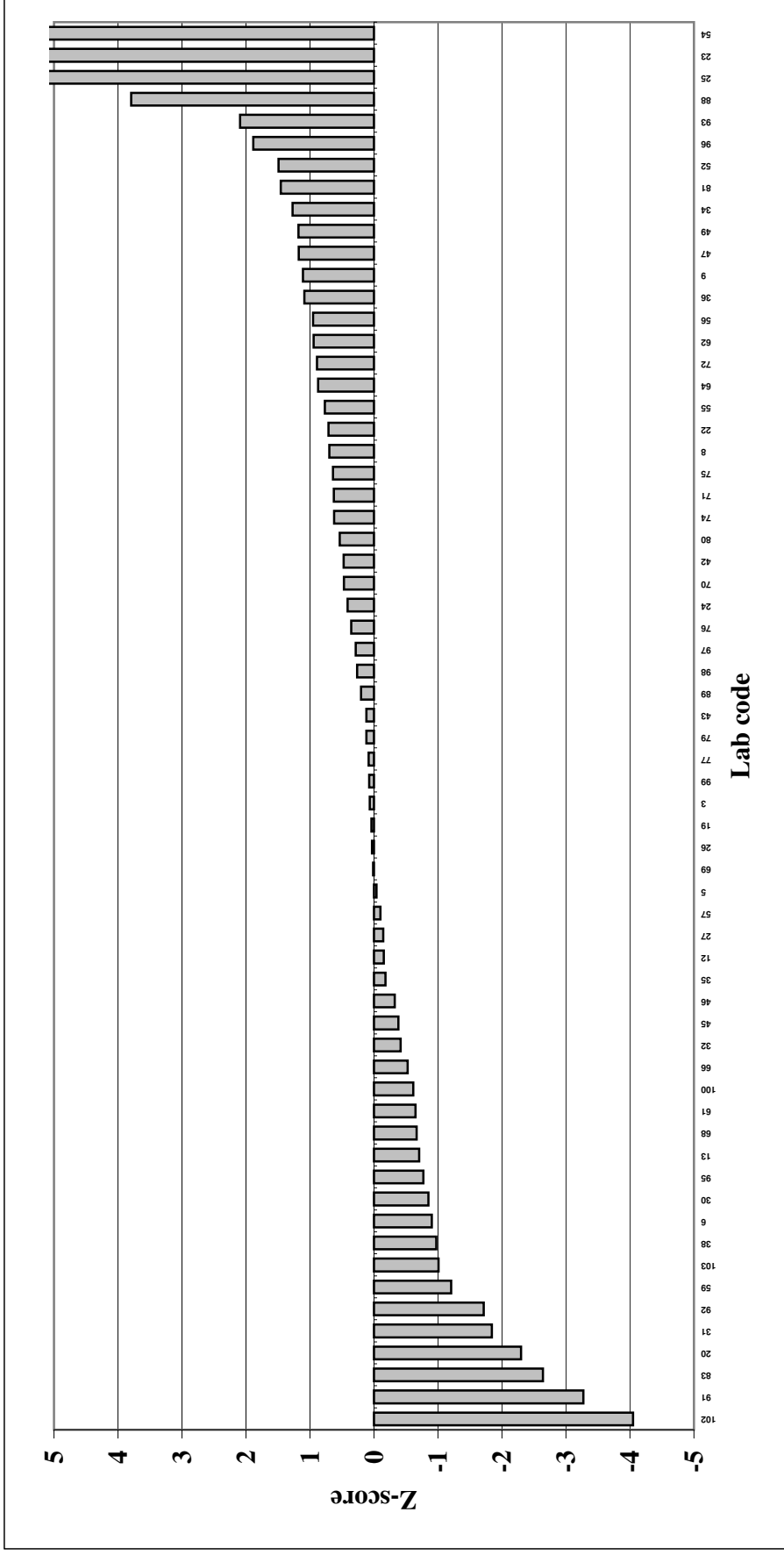
Z-score Herring; non-ortho PCB TEQ



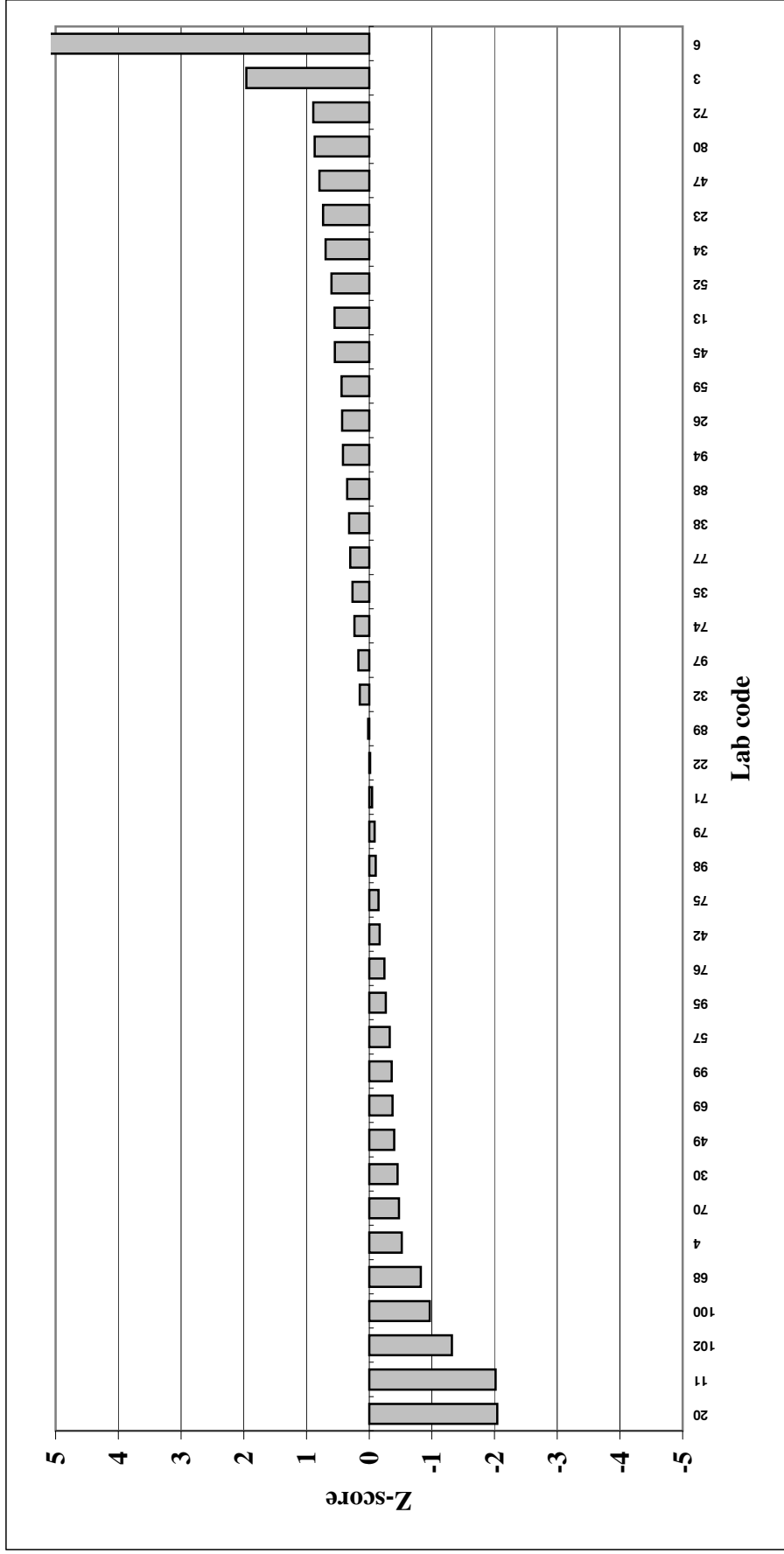
Z-score Herring; mono-ortho PCB TEQ



Z-score Herring; sum indicator PCB



Z-score Herring; sum PBDE without BDE-209



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

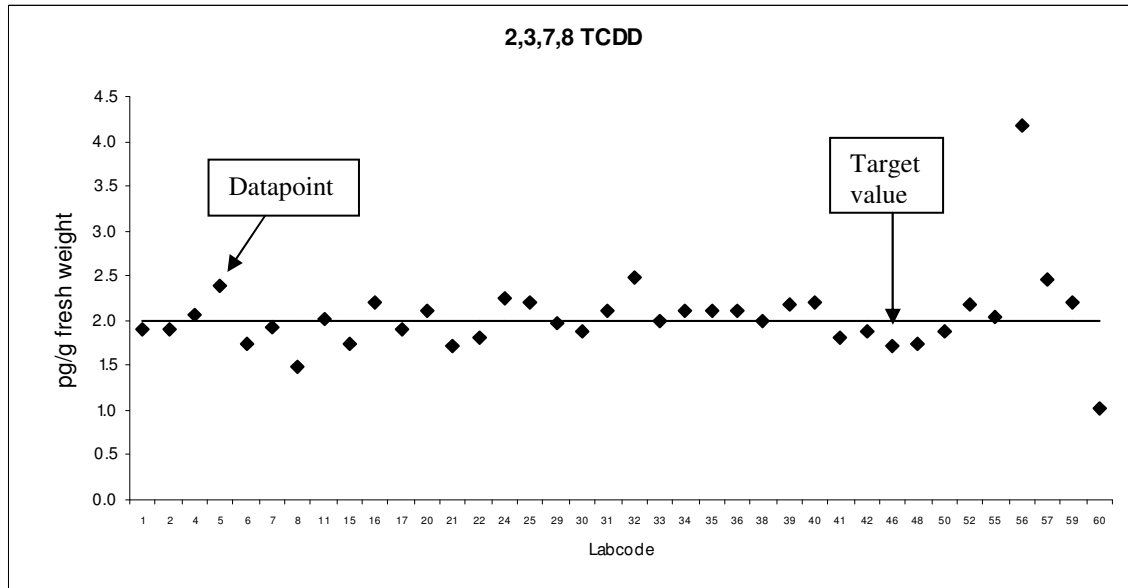
- PCDDs/PCDFs at concentrations of 2:5:10 pg/ μ l for tetra:penta-hexa-hepta:octa chlorinated dibenzodioxins/furans respectively.
- Non-ortho PCBs at concentration of 10 pg/ μ l.
- Mono-ortho PCBs and indicator PCBs at concentration of 100 pg/ μ l.
- PBDE at a concentration of 25 pg/ μ l, except BDE-209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

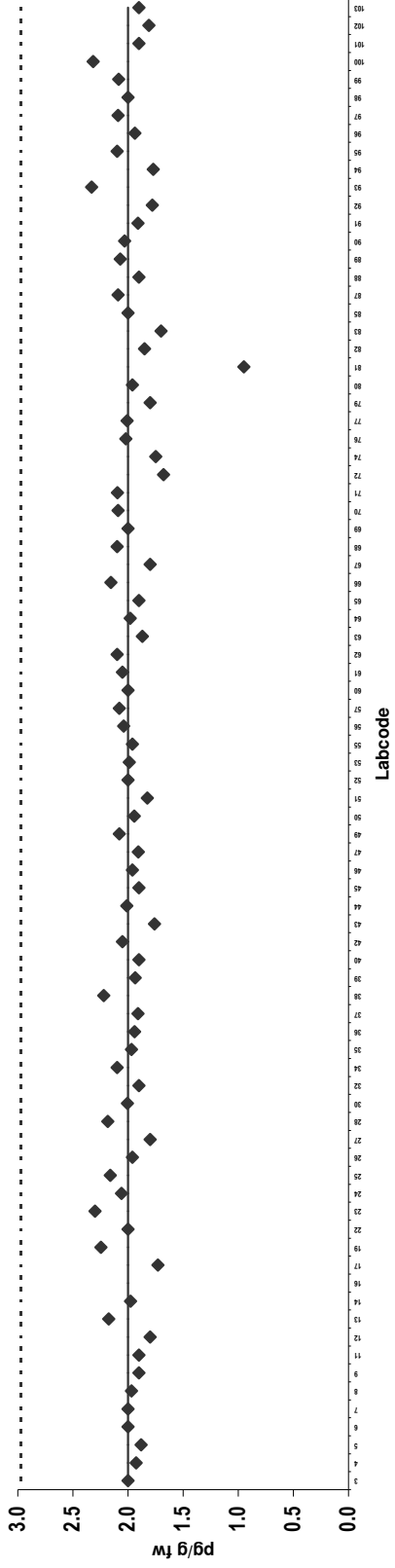
Analyte solution
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	2.0		61	2.1	
4	1.9		62	2.1	
5	1.9		63	1.9	
6	2.0		64	2.0	
7	2.0		65	1.9	
8	2.0		66	2.2	
9	1.9		67	1.8	
11	1.9		68	2.1	
12	1.8		69	2.0	
13	2.2		70	2.1	
14	2.0		71	2.1	
16	102	Outlier	72	1.7	
17	1.7		74	1.8	
19	2.2		76	2.0	
22	2.0		77	2.0	
23	2.3		79	1.8	
24	2.1		80	2.0	
25	2.2		81	0.95	Outlier
26	2.0		82	1.9	
27	1.8		83	1.7	
28	2.2		85	2.0	
30	2.0		87	2.1	
32	1.9		88	1.9	
34	2.1		89	2.1	
35	2.0		90	2.0	
36	1.9		91	1.9	
37	1.9		92	1.8	
38	2.2		93	2.3	
39	1.9		94	1.8	
40	1.9		95	2.1	
42	2.1		96	1.9	
43	1.8		97	2.1	
44	2.0		98	2.0	
45	1.9		99	2.1	
46	2.0		100	2.3	
47	1.9		101	1.9	
49	2.1		102	1.8	
50	1.8		103	1.9	
51	1.8				
52	2.0				
53	2.0				
55	2.0				
56	2.0				
57	2.1				
60	2.0				

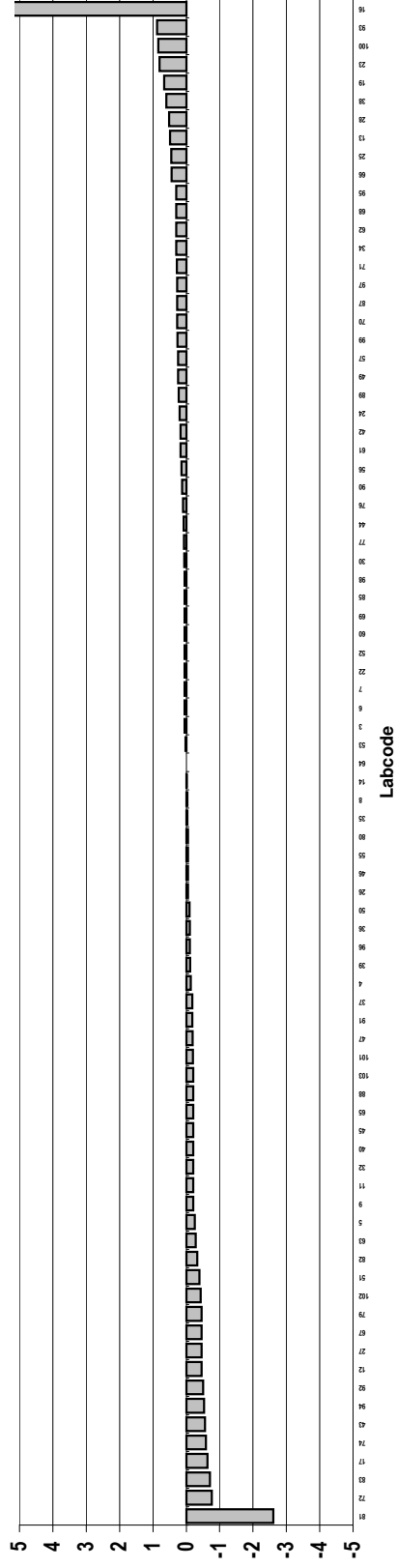
Consensus statistics

Consensus median, pg/g	2.0
Median all values pg/g	2.0
Consensus mean, pg/g	2.0
Standard deviation, pg/g	0.14
Relative standard deviation, %	6.9
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

2,3,7,8 TCDD



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



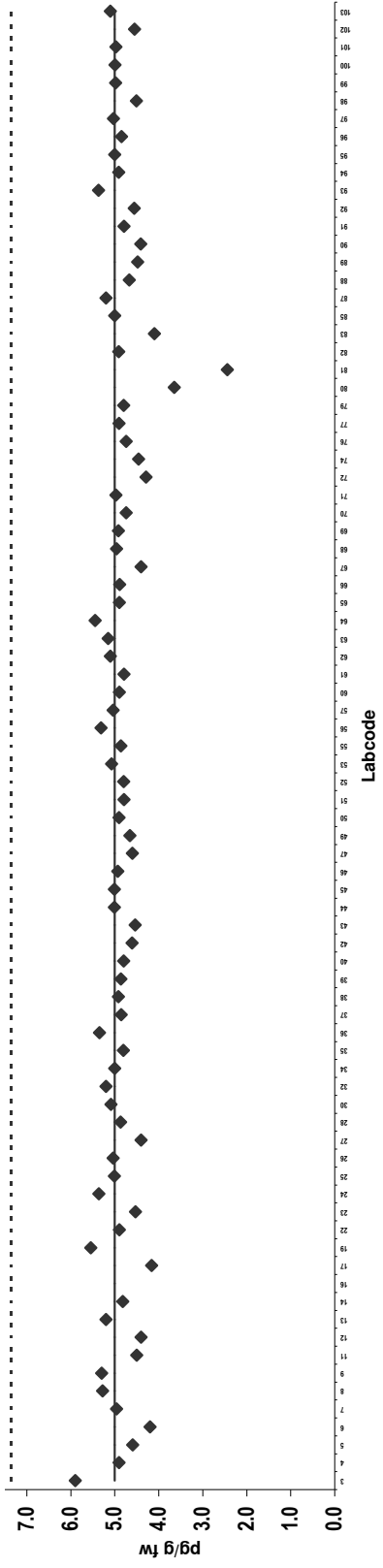
Analyte solution
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.9		61	4.8	
4	4.9		62	5.1	
5	4.6		63	5.2	
6	4.2		64	5.4	
7	5.0		65	4.9	
8	5.3		66	4.9	
9	5.3		67	4.4	
11	4.5		68	5.0	
12	4.4		69	4.9	
13	5.2		70	4.7	
14	4.8		71	5.0	
16	2.39		72	4.3	
17	4.2	Outlier	74	4.5	
19	5.5		76	4.7	
22	4.9		77	4.9	
23	4.5		79	4.8	
24	5.4		80	3.7	
25	5.0		81	2.4	
26	5.0		82	4.9	
27	4.4		83	4.1	
28	4.9		85	5.0	
30	5.1		87	5.2	
32	5.2		88	4.7	
34	5.0		89	4.5	
35	4.8		90	4.4	
36	5.4		91	4.8	
37	4.9		92	4.6	
38	4.9		93	5.4	
39	4.9		94	4.9	
40	4.8		95	5.0	
42	4.6		96	4.8	
43	4.5		97	5.0	
44	5.0		98	4.5	
45	5.0		99	5.0	
46	4.9		100	5.0	
47	4.6		101	5.0	
49	4.7		102	4.6	
50	4.9		103	5.1	
51	4.8				
52	4.8				
53	5.1				
55	4.9				
56	5.3				
57	5.0				
60	4.9				Outlier

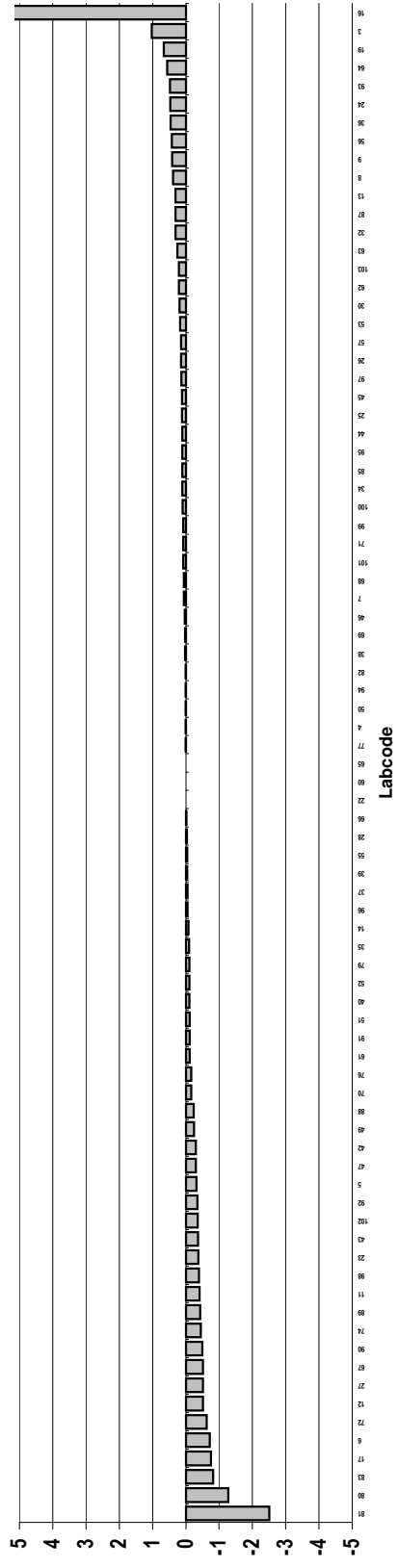
Consensus statistics

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.35
Relative standard deviation, %	7.1
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

1,2,3,7,8 PeCDD



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



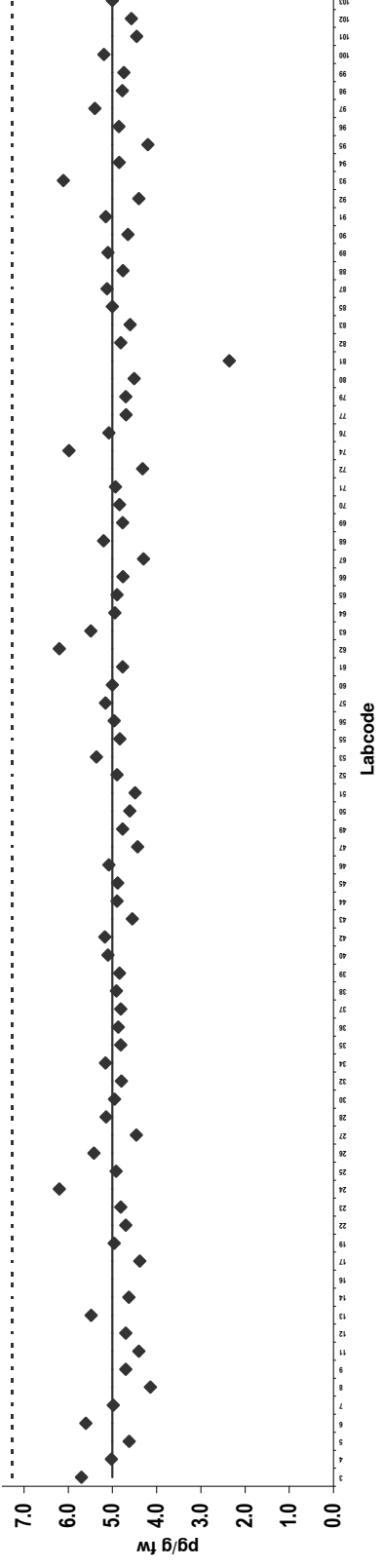
Analyte solution
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.7		61	4.8	
4	5.0		62	6.2	
5	4.6		63	5.5	
6	5.6		64	4.9	
7	5.0		65	4.9	
8	4.1		66	4.8	
9	4.7		67	4.3	
11	4.4		68	5.2	
12	4.7		69	4.8	
13	5.5		70	4.8	
14	4.6		71	4.9	
16	2.49		72	4.3	
17	4.4		74	6.0	
19	5.0		76	5.1	
22	4.7		77	4.7	
23	4.8		79	4.7	
24	6.2		80	4.5	
25	4.9		81	2.4	
26	5.4		82	4.8	
27	4.5		83	4.6	
28	5.1		85	5.0	
30	5.0		87	5.1	
32	4.8		88	4.8	
34	5.2		89	5.1	
35	4.8		90	4.7	
36	4.9		91	5.2	
37	4.8		92	4.4	
38	4.9		93	6.1	
39	4.8		94	4.9	
40	5.1		95	4.2	
42	5.2		96	4.9	
43	4.6		97	5.4	
44	4.9		98	4.8	
45	4.9		99	4.7	
46	5.1		100	5.2	
47	4.4		101	4.5	
49	4.8		102	4.6	
50	4.6		103	5.0	
51	4.5				
52	4.9				
53	5.4				
55	4.8				
56	5.0				
57	5.2				
60	5.0				

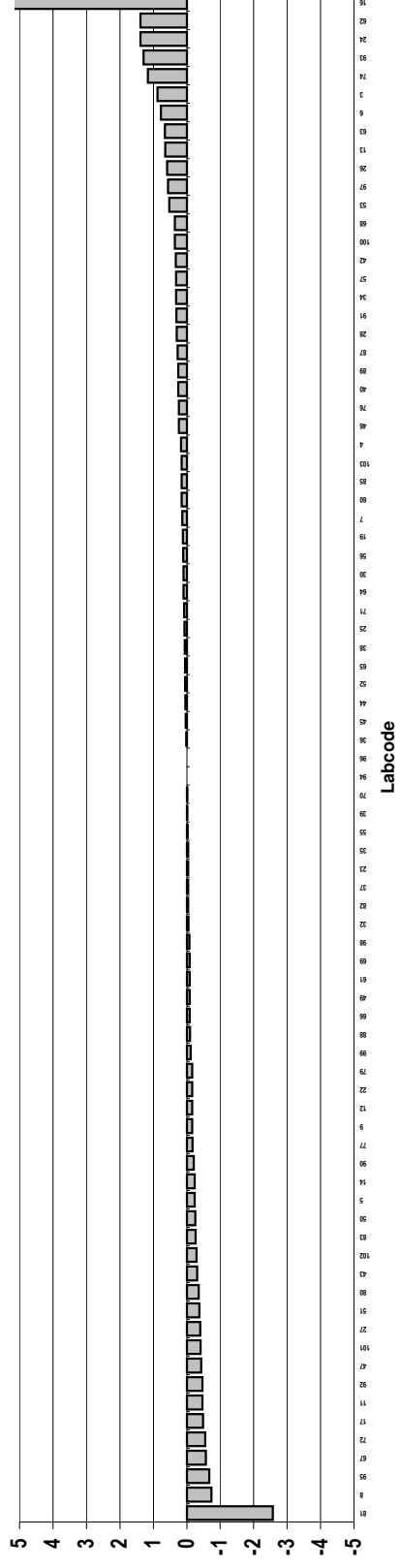
Consensus statistics

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.42
Relative standard deviation, %	8.4
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

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



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



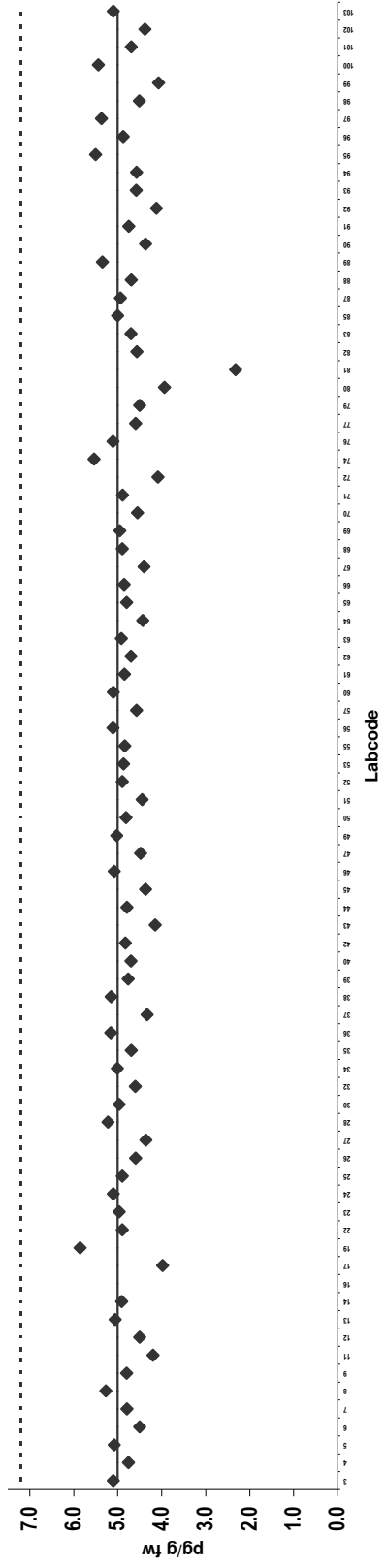
Analyte solution
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.1		61	4.9	
4	4.8		62	4.7	
5	5.1		63	4.9	
6	4.5		64	4.4	
7	4.8		65	4.8	
8	5.3		66	4.9	
9	4.8		67	4.4	
11	4.2		68	4.9	
12	4.5		69	5.0	
13	5.1		70	4.6	
14	4.9		71	4.9	
16	243	Outlier	72	4.1	
17	4.0		74	5.5	
19	5.9		76	5.1	
22	4.9		77	4.6	
23	5.0		79	4.5	
24	5.1		80	3.9	
25	4.9		81	2.3	Outlier
26	4.6		82	4.6	
27	4.4		83	4.7	
28	5.2		85	5.0	
30	5.0		87	4.9	
32	4.6		88	4.7	
34	5.0		89	5.4	
35	4.7		90	4.4	
36	5.2		91	4.8	
37	4.3		92	4.1	
38	5.2		93	4.6	
39	4.8		94	4.6	
40	4.7		95	5.5	
42	4.8		96	4.9	
43	4.2		97	5.4	
44	4.8		98	4.5	
45	4.4		99	4.1	
46	5.1		100	5.4	
47	4.5		101	4.7	
49	5.0		102	4.4	
50	4.8		103	5.1	
51	4.4				
52	4.9				
53	4.9				
55	4.8				
56	5.1				
57	4.6				
60	5.1				

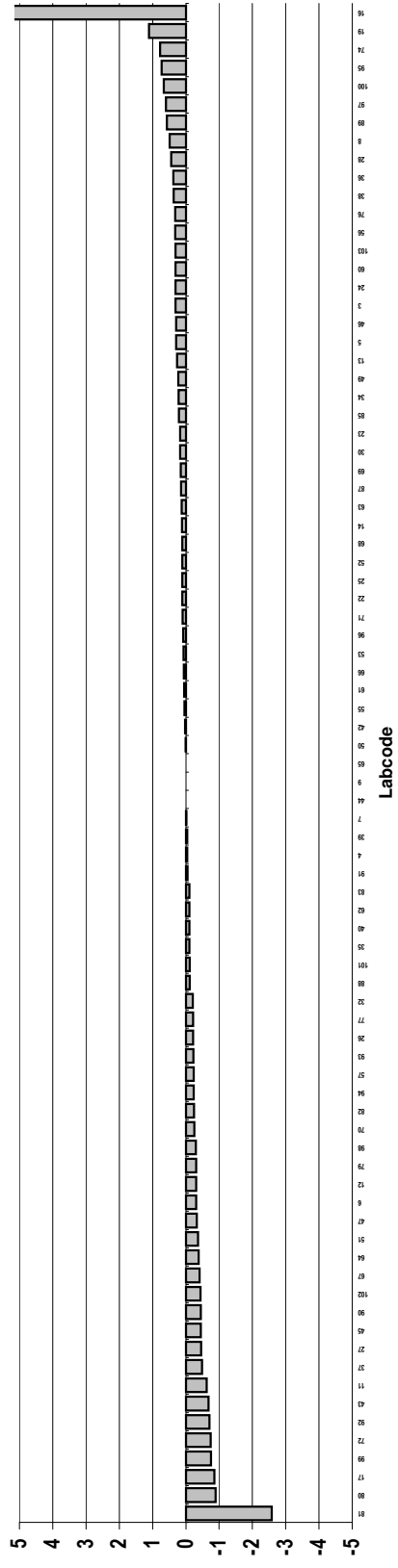
Consensus statistics

Consensus median, pg/g	4.8
Median all values pg/g	4.8
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.37
Relative standard deviation, %	7.7
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

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



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



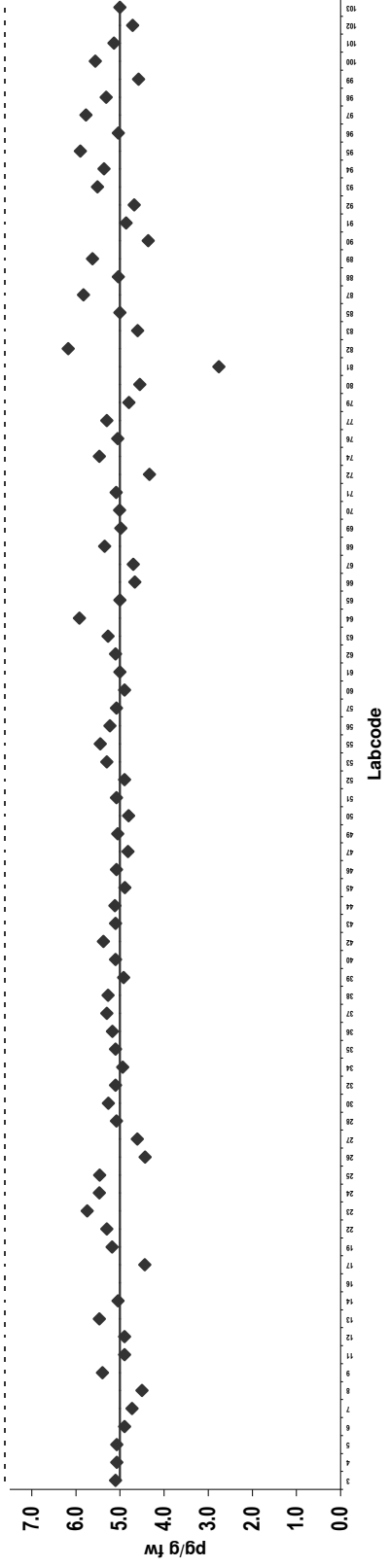
Analyte solution
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.1		61	5.0	
4	5.1		62	5.1	
5	5.1		63	5.3	
6	4.9		64	5.9	
7	4.7		65	5.0	
8	4.5		66	4.7	
9	5.4		67	4.7	
11	4.9		68	5.4	
12	4.9		69	5.0	
13	5.5		70	5.0	
14	5.0		71	5.1	
16	253	Outlier	72	4.3	
17	4.4		74	5.5	
19	5.2		76	5.1	
22	5.3		77	5.3	
23	5.7		79	4.8	
24	5.5		80	4.6	
25	5.5		81	2.8	
26	4.4		82	6.2	
27	4.6		83	4.6	
28	5.1		85	5.0	
30	5.3		87	5.8	
32	5.1		88	5.0	
34	4.9		89	5.6	
35	5.1		90	4.4	
36	5.2		91	4.9	
37	5.3		92	4.7	
38	5.3		93	5.5	
39	4.9		94	5.4	
40	5.1		95	5.9	
42	5.4		96	5.0	
43	5.1		97	5.8	
44	5.1		98	5.3	
45	4.9		99	4.6	
46	5.1		100	5.6	
47	4.8		101	5.1	
49	5.1		102	4.7	
50	4.8		103	5.0	
51	5.1				
52	4.9				
53	5.3				
55	5.5				
56	5.2				
57	5.1				
60	4.9				

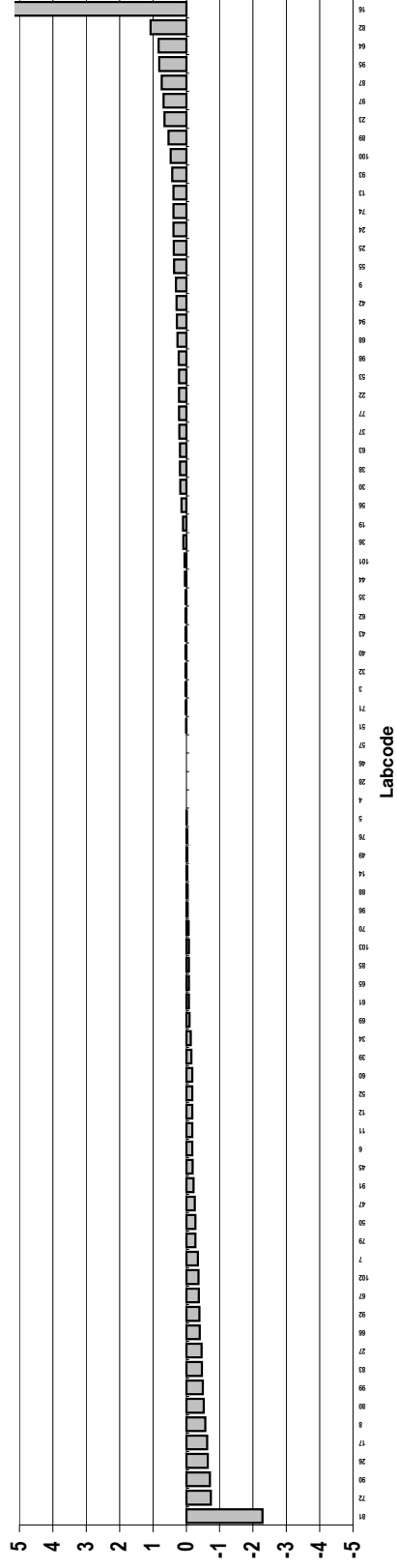
Consensus statistics

Consensus median, pg/g	5.1
Median all values pg/g	5.1
Consensus mean, pg/g	5.1
Standard deviation, pg/g	0.45
Relative standard deviation, %	8.8
No. of values reported	83
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



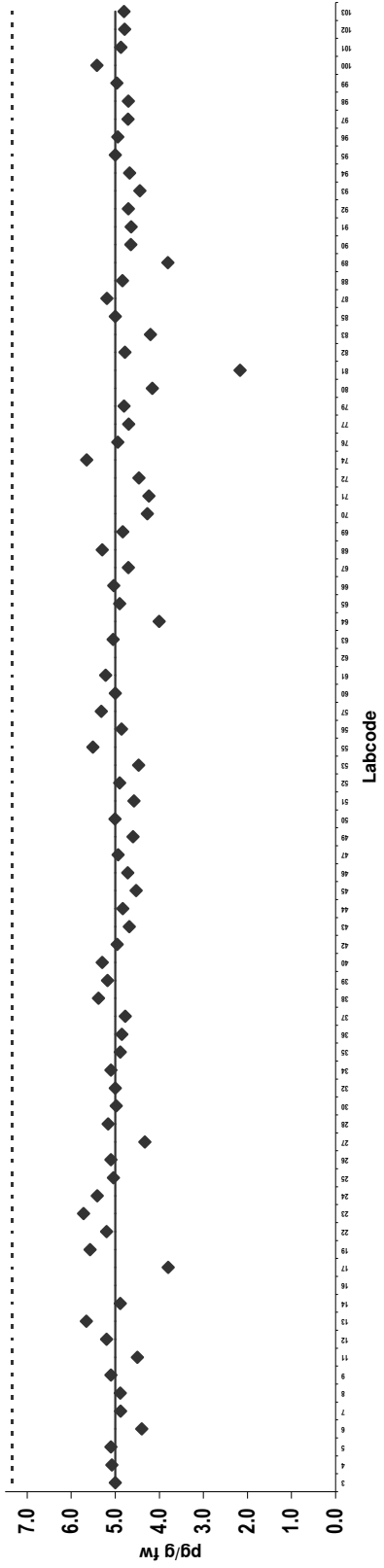
Analyte solution
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.0		61	5.2	
4	5.1		62	8.0	Outlier
5	5.1		63	5.1	
6	4.4		64	4.0	
7	4.9		65	4.9	
8	4.9		66	5.0	
9	5.1		67	4.7	
11	4.5		68	5.3	
12	5.2		69	4.8	
13	5.7		70	4.3	
14	4.9		71	4.2	
16	2.42		72	4.5	
17	3.8	Outlier	74	5.7	
19	5.6		76	4.9	
22	5.2		77	4.7	
23	5.7		79	4.8	
24	5.4		80	4.2	
25	5.0		81	2.2	
26	5.1		82	4.8	
27	4.3		83	4.2	
28	5.2		85	5.0	
30	5.0		87	5.2	
32	5.0		88	4.8	
34	5.1		89	3.8	
35	4.9		90	4.7	
36	4.9		91	4.6	
37	4.8		92	4.7	
38	5.4		93	4.4	
39	5.2		94	4.7	
40	5.3		95	5.0	
42	5.0		96	4.9	
43	4.7		97	4.7	
44	4.8		98	4.7	
45	4.5		99	5.0	
46	4.7		100	5.4	
47	4.9		101	4.9	
49	4.6		102	4.8	
50	5.0		103	4.8	
51	4.6				
52	4.9				
53	4.5				
55	5.5				
56	4.9				
57	5.3				
60	5.0				

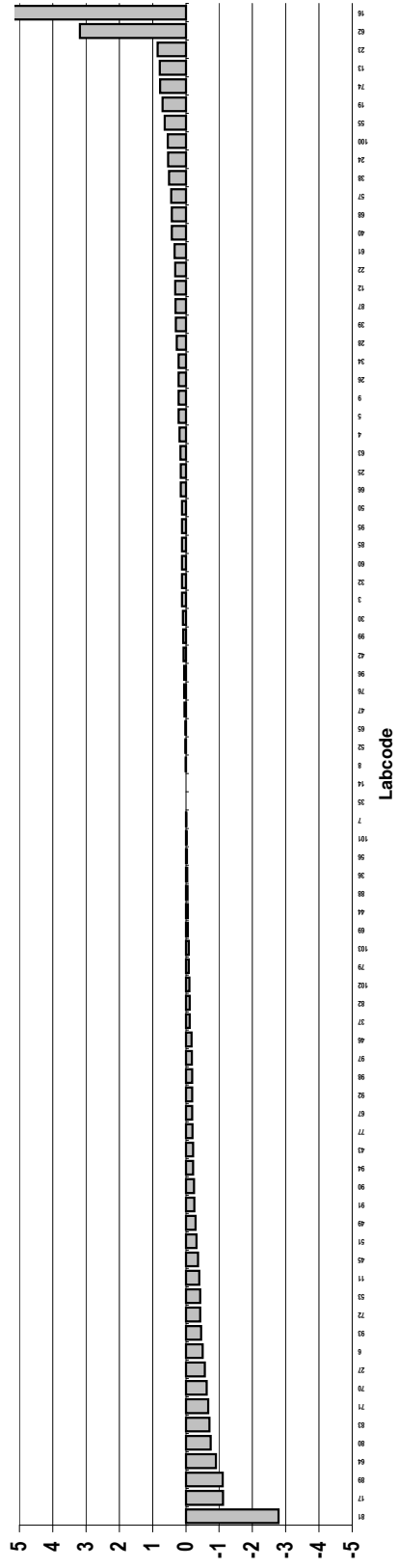
Consensus statistics

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.39
Relative standard deviation, %	8
No. of values reported	83
No. of values removed	3
No. of reported non-detects	0

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



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



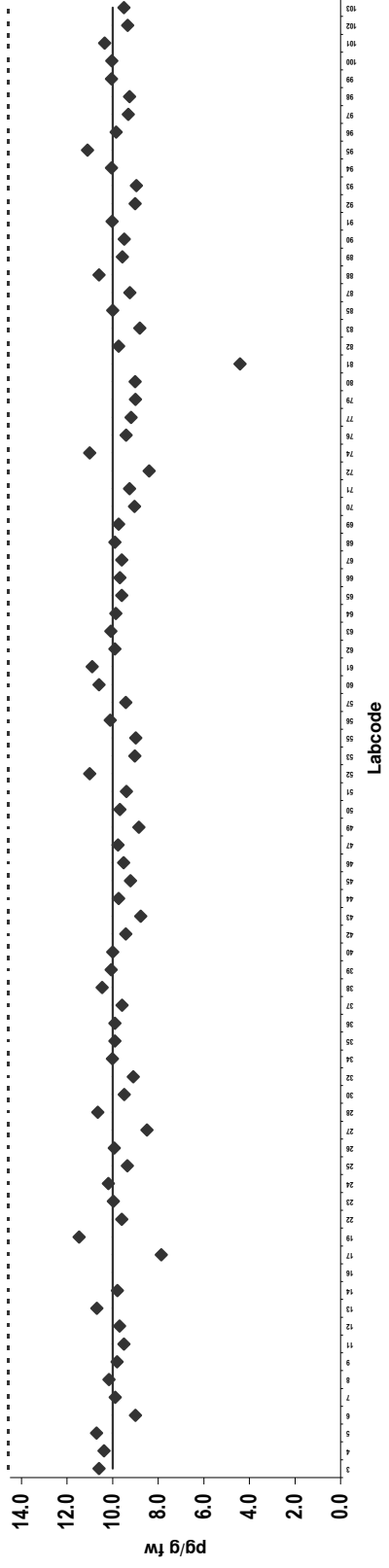
Analyte solution
Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	11		61	11	
4	10		62	9.9	
5	11		63	10	
6	9.0		64	9.9	
7	9.9		65	9.6	
8	10		66	9.7	
9	9.8		67	9.6	
11	9.5		68	9.9	
12	9.7		69	9.7	
13	11		70	9.0	
14	9.8		71	9.3	
16	446	Outlier	72	8.4	
17	7.9		74	11	
19	11		76	9.4	
22	9.6		77	9.2	
23	10		79	9.0	
24	10		80	9.0	
25	9.4		81	4.4	
26	9.9		82	9.7	Outlier
27	8.5		83	8.8	
28	11		85	10	
30	9.5		87	9.2	
32	9.1		88	11	
34	10		89	9.6	
35	9.9		90	9.5	
36	9.9		91	10	
37	9.6		92	9.0	
38	10		93	9.0	
39	10		94	10	
40	10		95	11	
42	9.4		96	9.8	
43	8.8		97	9.3	
44	9.7		98	9.3	
45	9.2		99	10	
46	9.5		100	10	
47	9.8		101	10	
49	8.9		102	9.3	
50	9.7		103	9.5	
51	9.4				
52	11				
53	9.0				
55	9.0				
56	10				
57	9.4				
60	11				

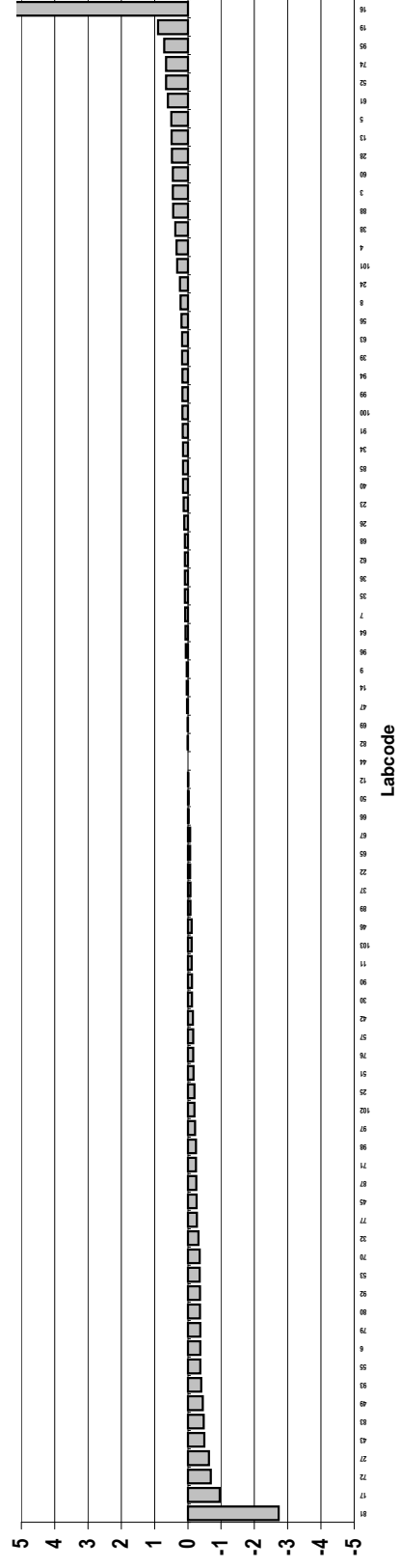
Consensus statistics

Consensus median, pg/g	9.7
Median all values pg/g	9.7
Consensus mean, pg/g	9.7
Standard deviation, pg/g	0.65
Relative standard deviation, %	6.7
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

OCDD



Z-score: OCDD



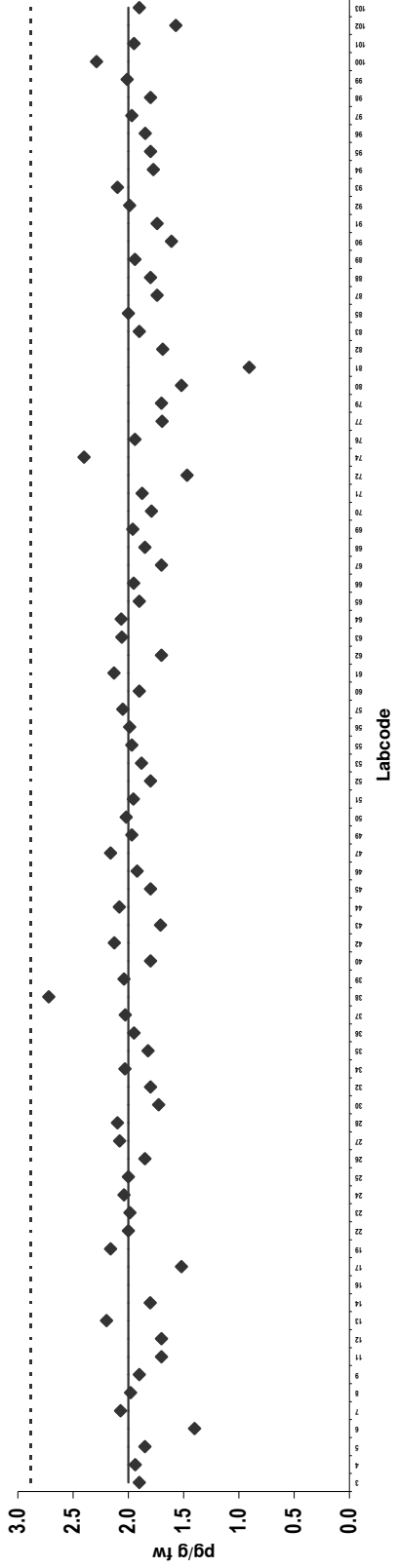
Analyte solution
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	1.9		61	2.1	
4	1.9		62	1.7	
5	1.9		63	2.1	
6	1.4		64	2.1	
7	2.1		65	1.9	
8	2.0		66	2.0	
9	1.9		67	1.7	
11	1.7		68	1.9	
12	1.7		69	2.0	
13	2.2		70	1.8	
14	1.8		71	1.9	
16	99	Outlier	72	1.5	
17	1.5		74	2.4	
19	2.2		76	1.9	
22	2.0		77	1.7	
23	2.0		79	1.7	
24	2.0		80	1.5	
25	2.0		81	0.91	
26	1.9		82	1.7	
27	2.1		83	1.9	
28	2.1		85	2.0	
30	1.7		87	1.7	
32	1.8		88	1.8	
34	2.0		89	1.9	
35	1.8		90	1.6	
36	2.0		91	1.7	
37	2.0		92	2.0	
38	2.7		93	2.1	
39	2.0		94	1.8	
40	1.8		95	1.8	
42	2.1		96	1.8	
43	1.7		97	2.0	
44	2.1		98	1.8	
45	1.8		99	2.0	
46	1.9		100	2.3	
47	2.2		101	1.9	
49	2.0		102	1.6	
50	2.0		103	1.9	
51	2.0				
52	1.8				
53	1.9				
55	2.0				
56	2.0				
57	2.1				
60	1.9				

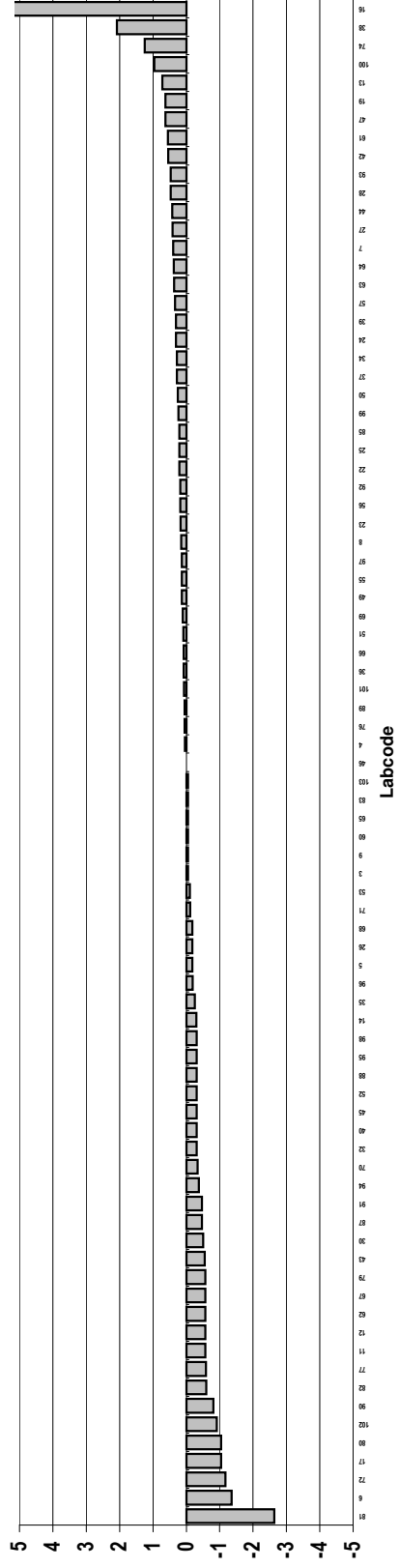
Consensus statistics

Consensus median, pg/g	1.9
Median all values pg/g	1.9
Consensus mean, pg/g	1.9
Standard deviation, pg/g	0.20
Relative standard deviation, %	11
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

2,3,7,8 TCDF



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



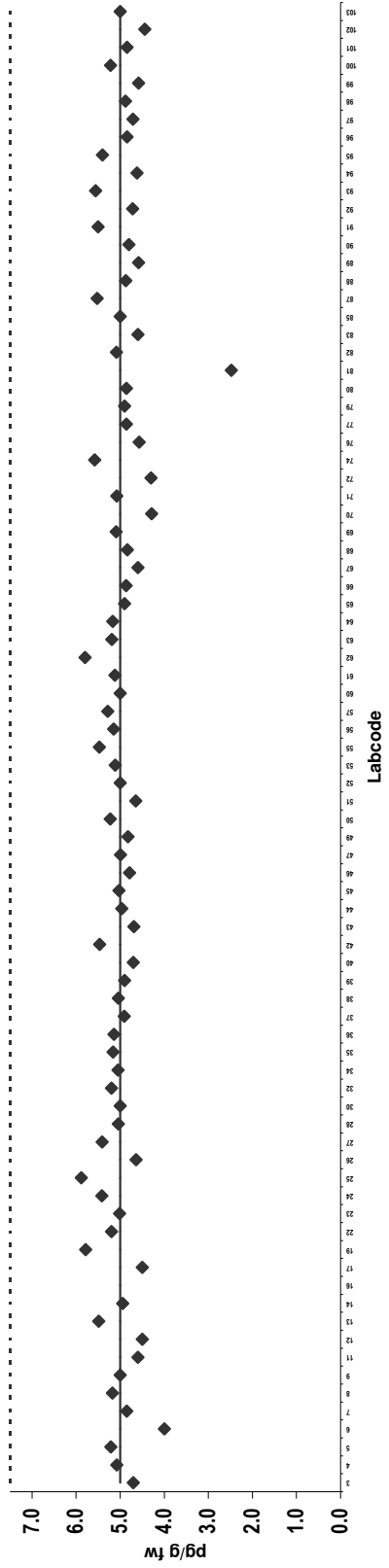
Analyte solution
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	4.7		61	5.1	
4	5.1		62	5.8	
5	5.2		63	5.2	
6	4.0		64	5.2	
7	4.9		65	4.9	
8	5.2		66	4.9	
9	5.0		67	4.6	
11	4.6		68	4.8	
12	4.5		69	5.1	
13	5.5		70	4.3	
14	4.9		71	5.1	
16	258	Outlier	72	4.3	
17	4.5		74	5.6	
19	5.8		76	4.6	
22	5.2		77	4.9	
23	5.0		79	4.9	
24	5.4		80	4.9	
25	5.9		81	2.5	
26	4.6		82	5.1	Outlier
27	5.4		83	4.6	
28	5.0		85	5.0	
30	5.0		87	5.5	
32	5.2		88	4.9	
34	5.1		89	4.6	
35	5.2		90	4.8	
36	5.1		91	5.5	
37	4.9		92	4.7	
38	5.0		93	5.6	
39	4.9		94	4.6	
40	4.7		95	5.4	
42	5.5		96	4.8	
43	4.7		97	4.7	
44	5.0		98	4.9	
45	5.0		99	4.6	
46	4.8		100	5.2	
47	5.0		101	4.8	
49	4.8		102	4.4	
50	5.2		103	5.0	
51	4.6				
52	5.0				
53	5.1				
55	5.5				
56	5.2				
57	5.3				
60	5.0				

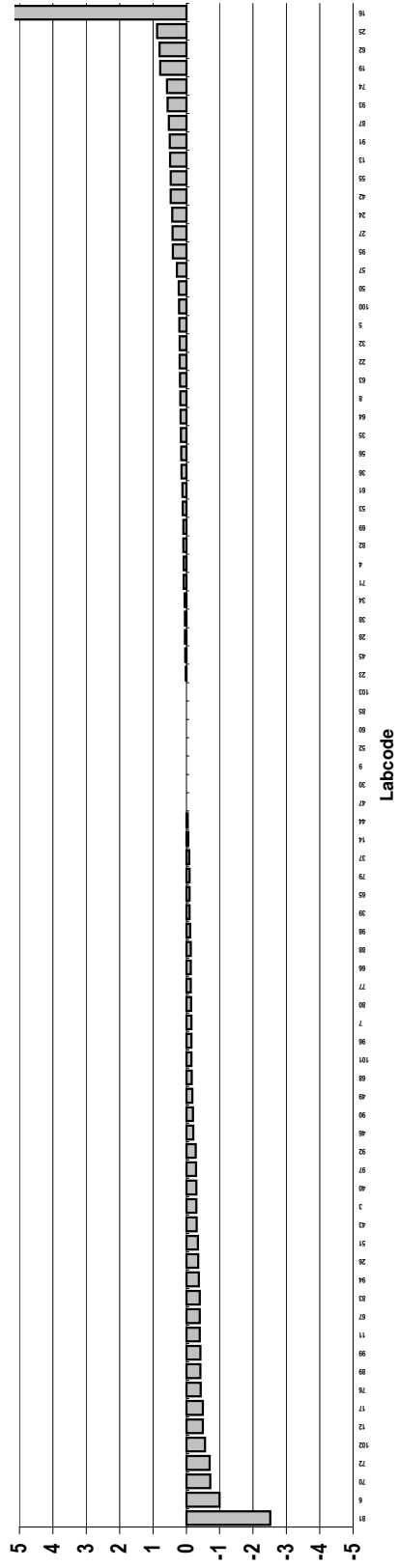
Consensus statistics

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.35
Relative standard deviation, %	7.1
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

1,2,3,7,8 PeCDF



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



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

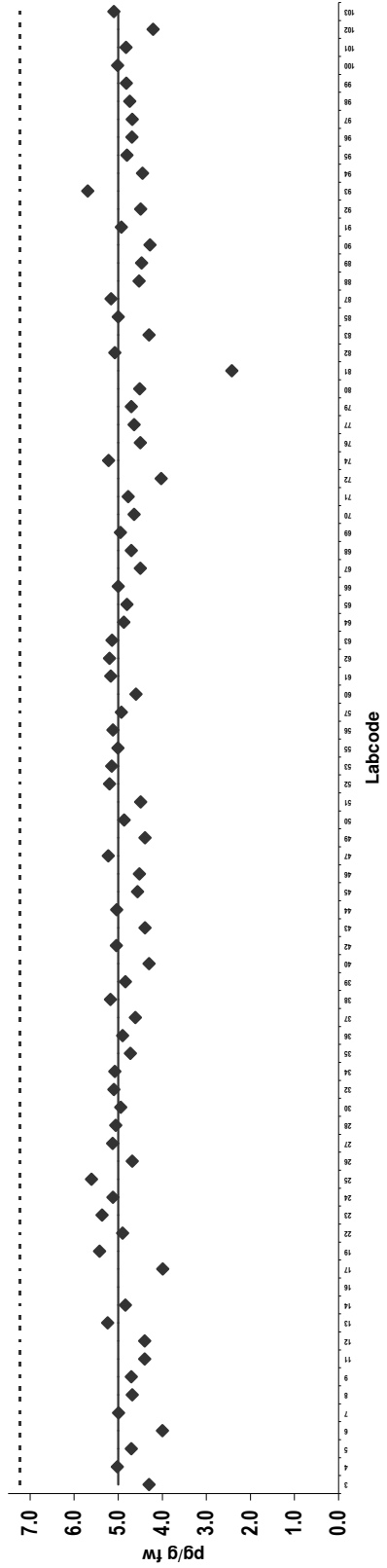
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	4.3		61	5.2	
4	5.0		62	5.2	
5	4.7		63	5.1	
6	4.0		64	4.9	
7	5.0		65	4.8	
8	4.7		66	5.0	
9	4.7		67	4.5	
11	4.4		68	4.7	
12	4.4		69	5.0	
13	5.2		70	4.6	
14	4.8		71	4.8	
16	2.45		72	4.0	
17	4.0		74	5.2	
19	5.4		76	4.5	
22	4.9		77	4.6	
23	5.4		79	4.7	
24	5.1		80	4.5	
25	5.6		81	2.4	
26	4.7		82	5.1	
27	5.1		83	4.3	
28	5.1		85	5.0	
30	4.9		87	5.2	
32	5.1		88	4.5	
34	5.1		89	4.5	
35	4.7		90	4.3	
36	4.9		91	4.9	
37	4.6		92	4.5	
38	5.2		93	5.7	
39	4.8		94	4.5	
40	4.3		95	4.8	
42	5.0		96	4.7	
43	4.4		97	4.7	
44	5.0		98	4.7	
45	4.6		99	4.8	
46	4.5		100	5.0	
47	5.2		101	4.8	
49	4.4		102	4.2	
50	4.9		103	5.1	
51	4.5				
52	5.2				
53	5.2				
55	5.0				
56	5.1				
57	4.9				
60	4.6				

Outlier

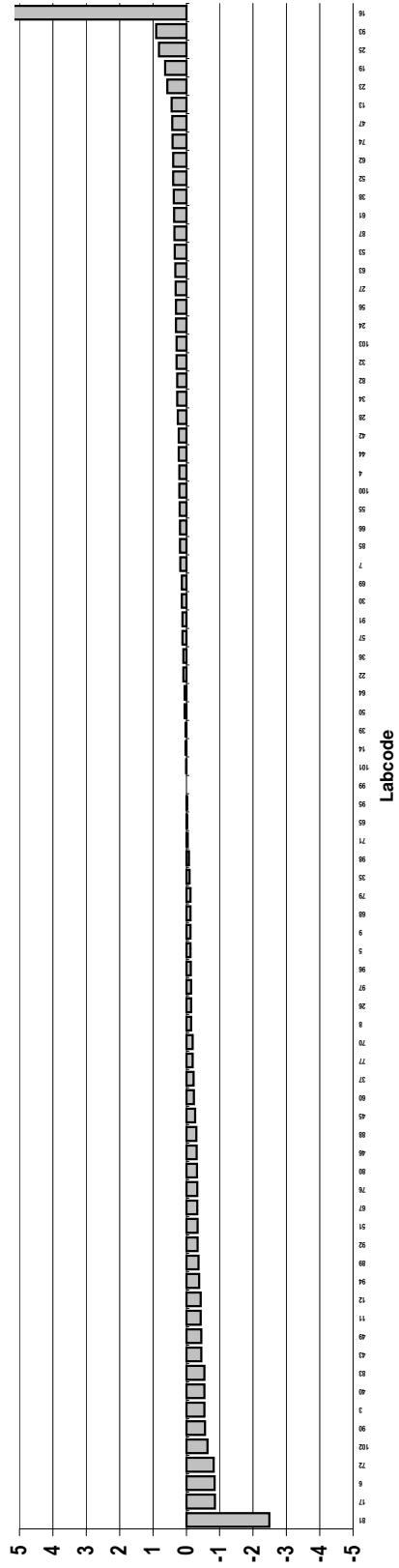
Consensus statistics

Consensus median, pg/g	4.8
Median all values pg/g	4.8
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.44
Relative standard deviation, %	9.2
No. of values reported	83
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



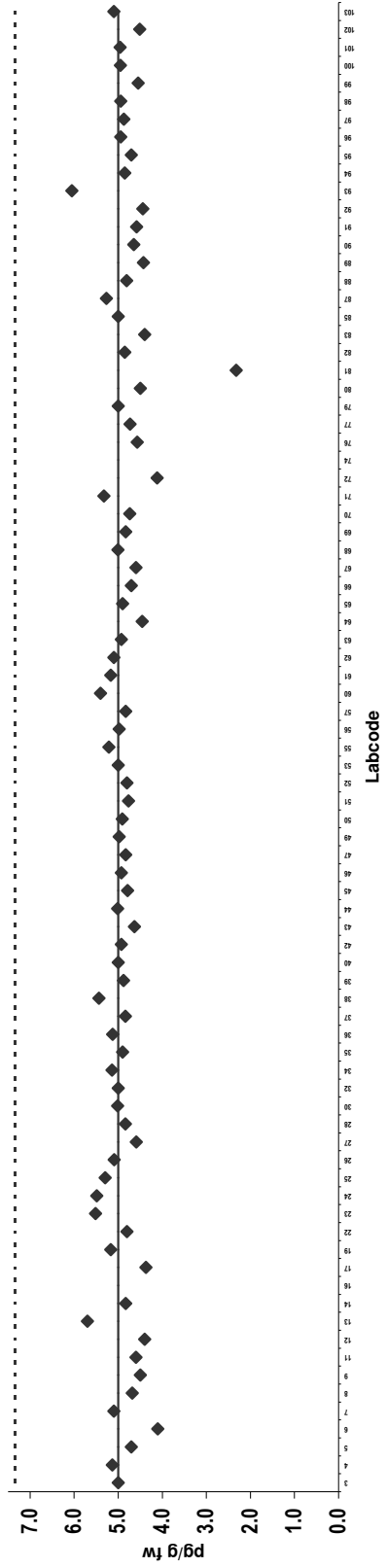
Analyte solution
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.0		61	5.2	
4	5.1		62	5.1	
5	4.7		63	4.9	
6	4.1		64	4.5	
7	5.1		65	4.9	
8	4.7		66	4.7	
9	4.5		67	4.6	
11	4.6		68	5.0	
12	4.4		69	4.8	
13	5.7		70	4.7	
14	4.8		71	5.3	
16	2.46		72	4.1	
17	4.4		74	8.0	Outlier
19	5.2		76	4.6	
22	4.8		77	4.7	
23	5.5		79	5.0	
24	5.5		80	4.5	
25	5.3		81	2.3	
26	5.1		82	4.9	
27	4.6		83	4.4	
28	4.8		85	5.0	
30	5.0		87	5.3	
32	5.0		88	4.8	
34	5.1		89	4.4	
35	4.9		90	4.7	
36	5.1		91	4.6	
37	4.8		92	4.4	
38	5.4		93	6.1	
39	4.9		94	4.9	
40	5.0		95	4.7	
42	4.9		96	4.9	
43	4.6		97	4.9	
44	5.0		98	4.9	
45	4.8		99	4.5	
46	4.9		100	4.9	
47	4.8		101	5.0	
49	5.0		102	4.5	
50	4.9		103	5.1	
51	4.8				
52	4.8				
53	5.0				
55	5.2				
56	5.0				
57	4.8				
60	5.4				

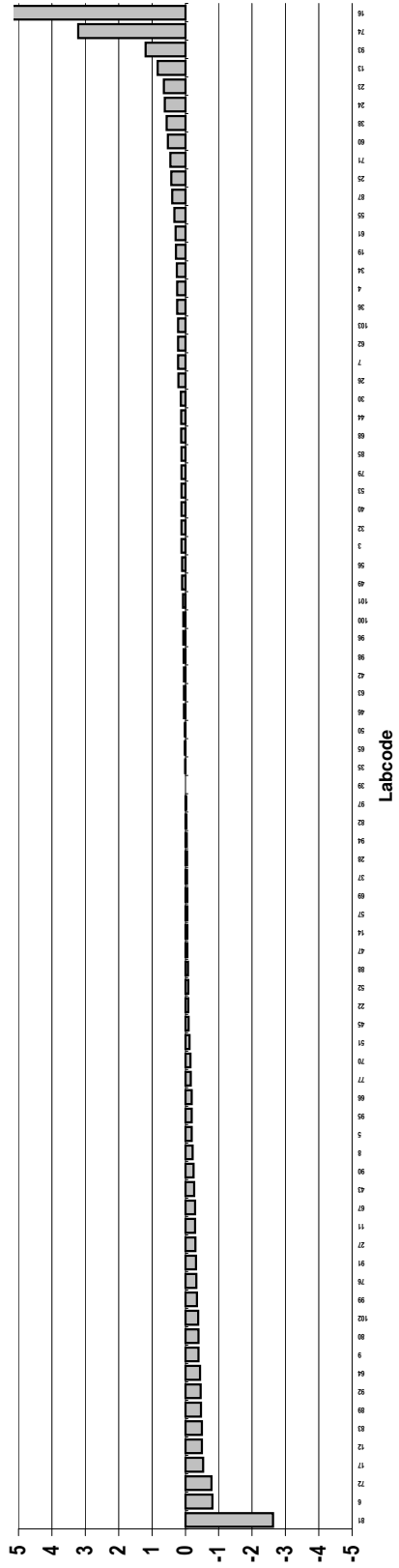
Consensus statistics

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.33
Relative standard deviation, %	6.7
No. of values reported	83
No. of values removed	3
No. of reported non-detects	0

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



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



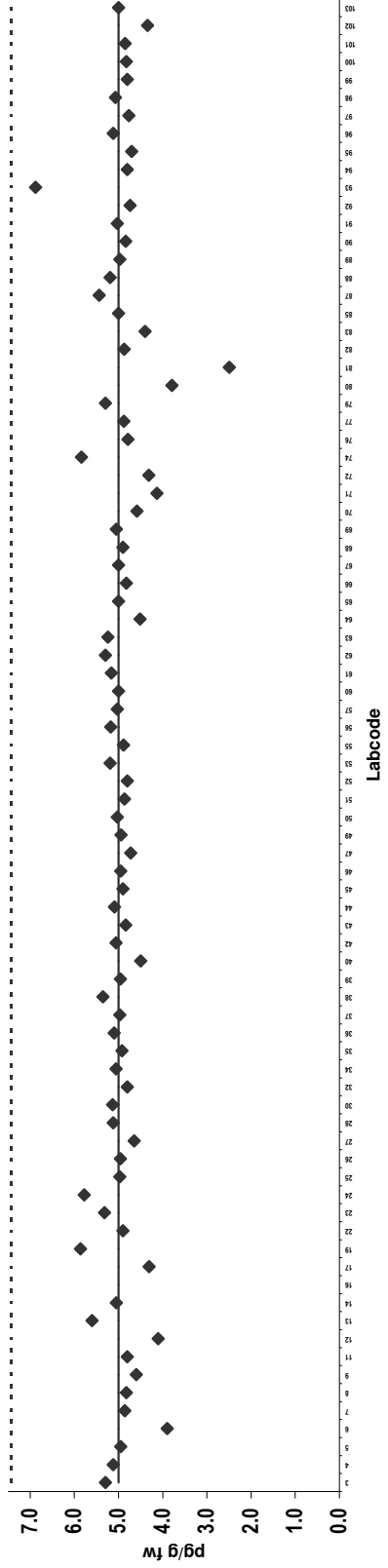
Analyte solution
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.3		61	5.2	
4	5.1		62	5.3	
5	5.0		63	5.2	
6	3.9		64	4.5	
7	4.9		65	5.0	
8	4.8		66	4.8	
9	4.6		67	5.0	
11	4.8		68	4.9	
12	4.1		69	5.1	
13	5.6		70	4.6	
14	5.0		71	4.1	
16	2.44		72	4.3	
17	4.3	Outlier	74	5.8	
19	5.9		76	4.8	
22	4.9		77	4.9	
23	5.3		79	5.3	
24	5.8		80	3.8	
25	5.0		81	2.5	
26	5.0		82	4.9	
27	4.7		83	4.4	
28	5.1		85	5.0	
30	5.1		87	5.4	
32	4.8		88	5.2	
34	5.1		89	5.0	
35	4.9		90	4.8	
36	5.1		91	5.0	
37	5.0		92	4.7	
38	5.4		93	6.9	
39	5.0		94	4.8	
40	4.5		95	4.7	
42	5.1		96	5.1	
43	4.8		97	4.8	
44	5.1		98	5.1	
45	4.9		99	4.8	
46	5.0		100	4.8	
47	4.7		101	4.9	
49	4.9		102	4.3	
50	5.0		103	5.0	
51	4.9				
52	4.8				
53	5.2				
55	4.9				
56	5.2				
57	5.0				
60	5.0				

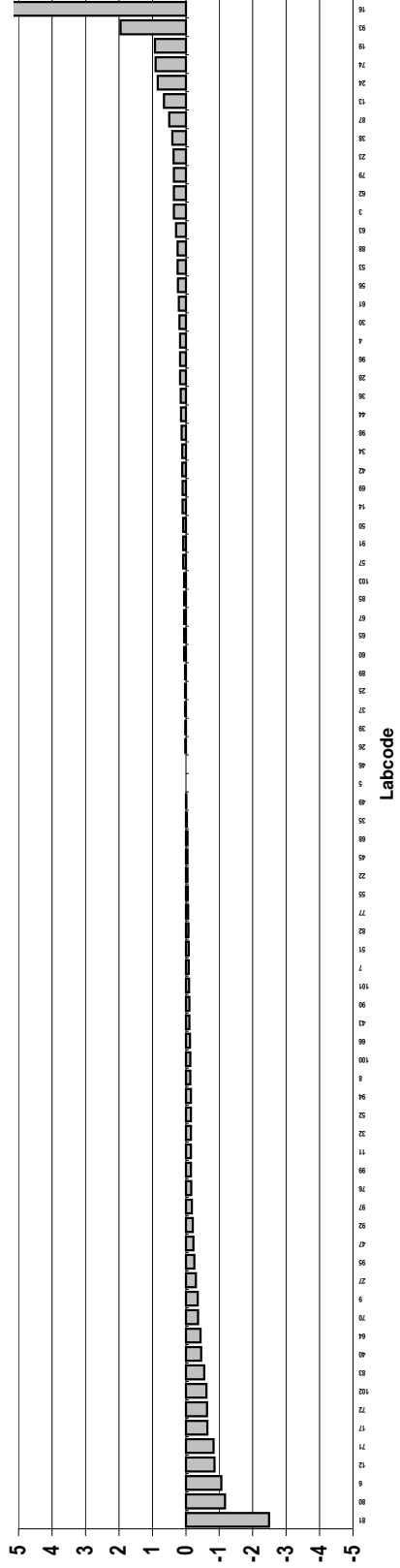
Consensus statistics

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.50
Relative standard deviation, %	10
No. of values reported	83
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

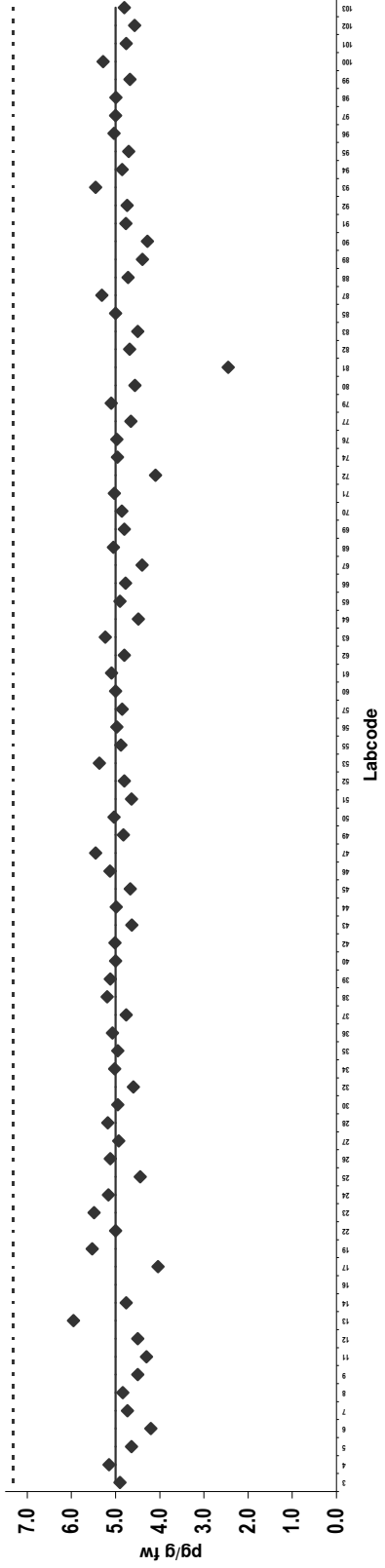
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	4.9		61	5.1	
4	5.1		62	4.8	
5	4.6		63	5.2	
6	4.2		64	4.5	
7	4.7		65	4.9	
8	4.8		66	4.8	
9	4.5		67	4.4	
11	4.3		68	5.1	
12	4.5		69	4.8	
13	6.0		70	4.9	
14	4.8		71	5.0	
16	248		72	4.1	
17	4.0		74	5.0	
19	5.5		76	5.0	
22	5.0		77	4.7	
23	5.5		79	5.1	
24	5.2		80	4.6	
25	4.4		81	2.5	
26	5.1		82	4.7	
27	4.9		83	4.5	
28	5.2		85	5.0	
30	4.9		87	5.3	
32	4.6		88	4.7	
34	5.0		89	4.4	
35	4.9		90	4.3	
36	5.1		91	4.8	
37	4.8		92	4.7	
38	5.2		93	5.5	
39	5.1		94	4.9	
40	5.0		95	4.7	
42	5.0		96	5.0	
43	4.6		97	5.0	
44	5.0		98	5.0	
45	4.7		99	4.7	
46	5.1		100	5.3	
47	5.5		101	4.8	
49	4.8		102	4.6	
50	5.0		103	4.8	
51	4.6				
52	4.8				
53	5.4				
55	4.9				
56	5.0				
57	4.9				
60	5.0				

Outlier

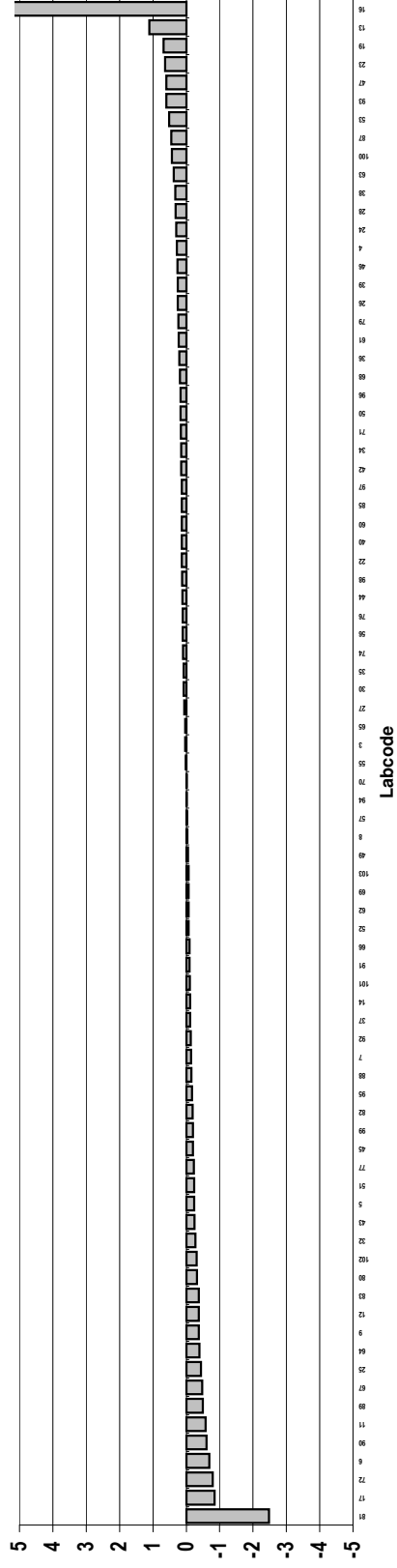
Consensus statistics

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.42
Relative standard deviation, %	8.8
No. of values reported	83
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



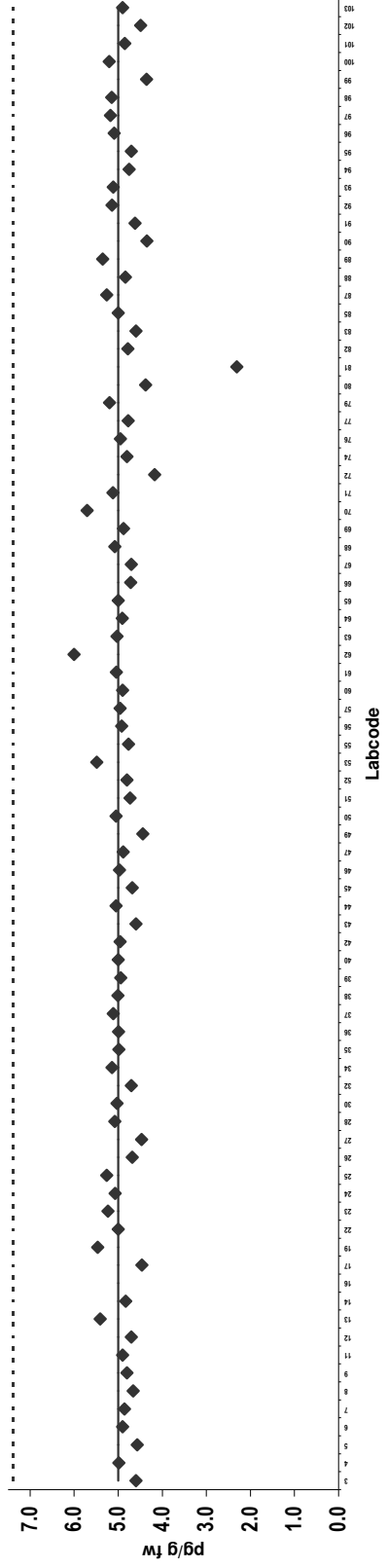
Analyte solution
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	4.6		61	5.0	
4	5.0		62	6.0	
5	4.6		63	5.0	
6	4.9		64	4.9	
7	4.9		65	5.0	
8	4.7		66	4.7	
9	4.8		67	4.7	
11	4.9		68	5.1	
12	4.7		69	4.9	
13	5.4		70	5.7	
14	4.8		71	5.1	
16	2.47	Outlier	72	4.2	
17	4.5		74	4.8	
19	5.5		76	5.0	
22	5.0		77	4.8	
23	5.2		79	5.2	
24	5.1		80	4.4	
25	5.3		81	2.3	
26	4.7		82	4.8	
27	4.5		83	4.6	
28	5.1		85	5.0	
30	5.0		87	5.3	
32	4.7		88	4.8	
34	5.1		89	5.4	
35	5.0		90	4.4	
36	5.0		91	4.6	
37	5.1		92	5.1	
38	5.0		93	5.1	
39	4.9		94	4.8	
40	5.0		95	4.7	
42	5.0		96	5.1	
43	4.6		97	5.2	
44	5.1		98	5.2	
45	4.7		99	4.4	
46	5.0		100	5.2	
47	4.9		101	4.9	
49	4.4		102	4.5	
50	5.0		103	4.9	
51	4.7				
52	4.8				
53	5.5				
55	4.8				
56	4.9				
57	5.0				
60	4.9				

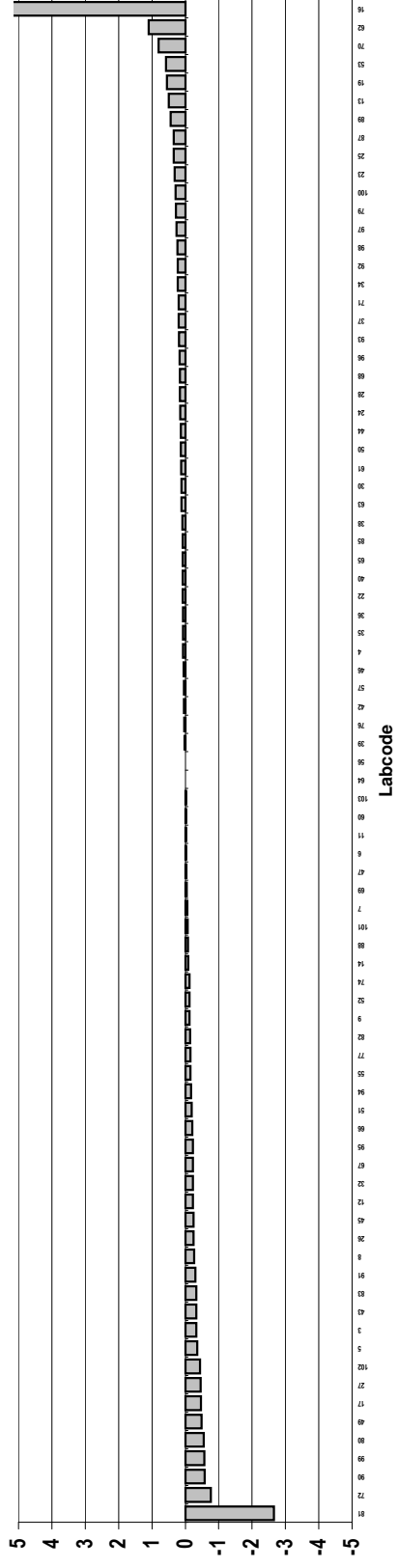
Consensus statistics

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.30
Relative standard deviation, %	6.2
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

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



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



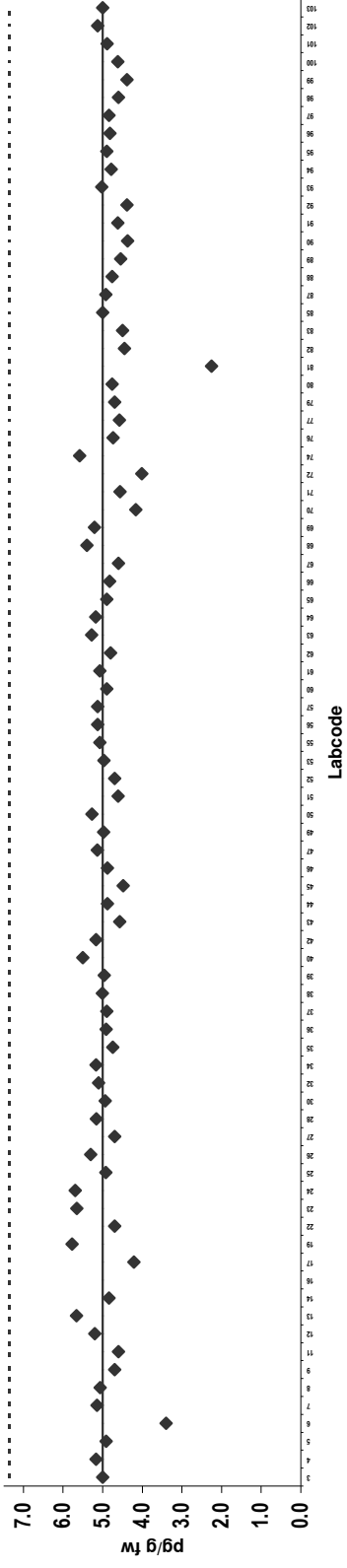
Analyte solution
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.0		61	5.1	
4	5.2		62	4.8	
5	4.9		63	5.3	
6	3.4		64	5.2	
7	5.1		65	4.9	
8	5.1		66	4.8	
9	4.7		67	4.6	
11	4.6		68	5.4	
12	5.2		69	5.2	
13	5.7		70	4.2	
14	4.8		71	4.6	
16	2.53		72	4.0	
17	4.2		74	5.6	
19	5.8		76	4.7	
22	4.7		77	4.6	
23	5.7		79	4.7	
24	5.7		80	4.8	
25	4.9		81	2.3	
26	5.3		82	4.5	
27	4.7		83	4.5	
28	5.2		85	5.0	
30	4.9		87	4.9	
32	5.1		88	4.8	
34	5.2		89	4.6	
35	4.7		90	4.4	
36	4.9		91	4.6	
37	4.9		92	4.4	
38	5.0		93	5.0	
39	5.0		94	4.8	
40	5.5		95	4.9	
42	5.2		96	4.8	
43	4.6		97	4.8	
44	4.9		98	4.6	
45	4.5		99	4.4	
46	4.9		100	4.6	
47	5.1		101	4.9	
49	5.0		102	5.1	
50	5.3		103	5.0	
51	4.6				
52	4.7				
53	5.0				
55	5.1				
56	5.1				
57	5.1				
60	4.9				

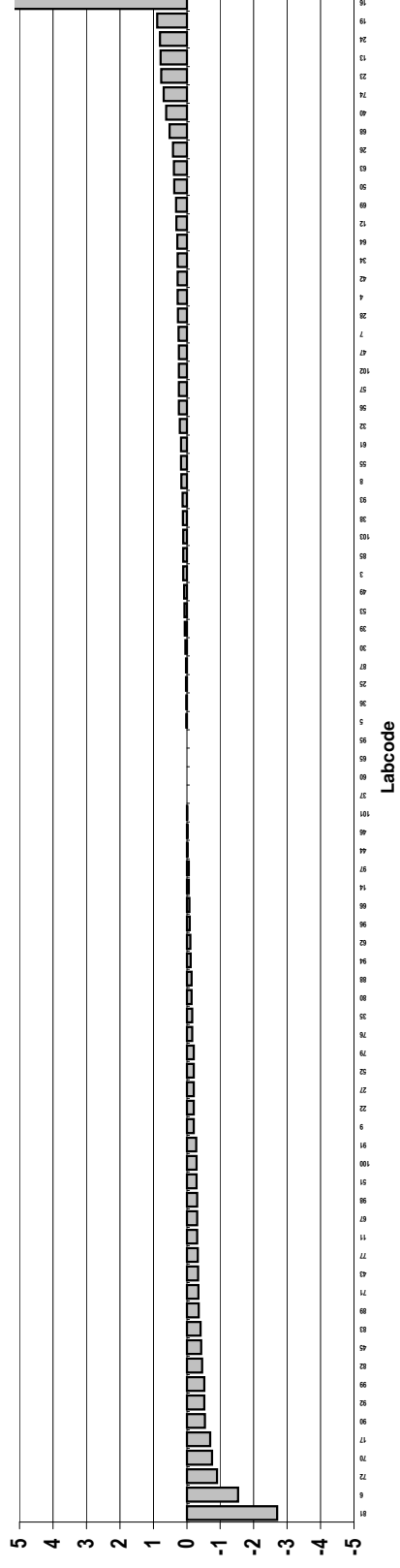
Consensus statistics

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.38
Relative standard deviation, %	7.8
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

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



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



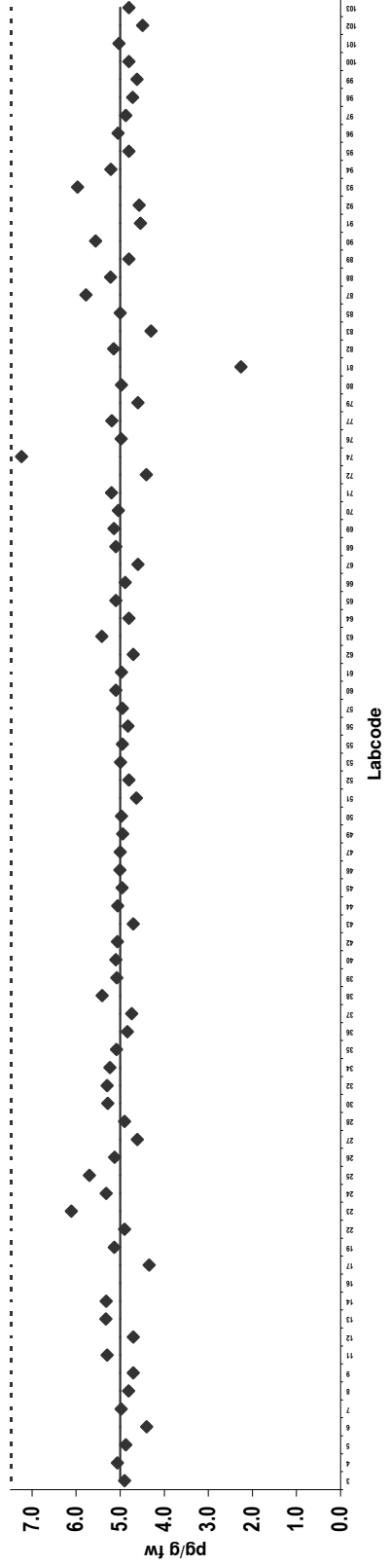
Analyte solution
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	4.9		61	5.0	
4	5.1		62	4.7	
5	4.9		63	5.4	
6	4.4		64	4.8	
7	5.0		65	5.1	
8	4.8		66	4.9	
9	4.7		67	4.6	
11	5.3		68	5.1	
12	4.7		69	5.1	
13	5.3		70	5.0	
14	5.3		71	5.2	
16	2.48	Outlier	72	4.4	
17	4.3		74	7.2	
19	5.1		76	5.0	
22	4.9		77	5.2	
23	6.1		79	4.6	
24	5.3		80	5.0	
25	5.7		81	2.3	
26	5.1		82	5.1	Outlier
27	4.6		83	4.3	
28	4.9		85	5.0	
30	5.3		87	5.8	
32	5.3		88	5.2	
34	5.2		89	4.8	
35	5.1		90	5.6	
36	4.8		91	4.5	
37	4.7		92	4.6	
38	5.4		93	6.0	
39	5.1		94	5.2	
40	5.1		95	4.8	
42	5.1		96	5.0	
43	4.7		97	4.9	
44	5.1		98	4.7	
45	5.0		99	4.6	
46	5.0		100	4.8	
47	5.0		101	5.0	
49	4.9		102	4.5	
50	5.0		103	4.8	
51	4.6				
52	4.8				
53	5.0				
55	5.0				
56	4.8				
57	5.0				
60	5.1				

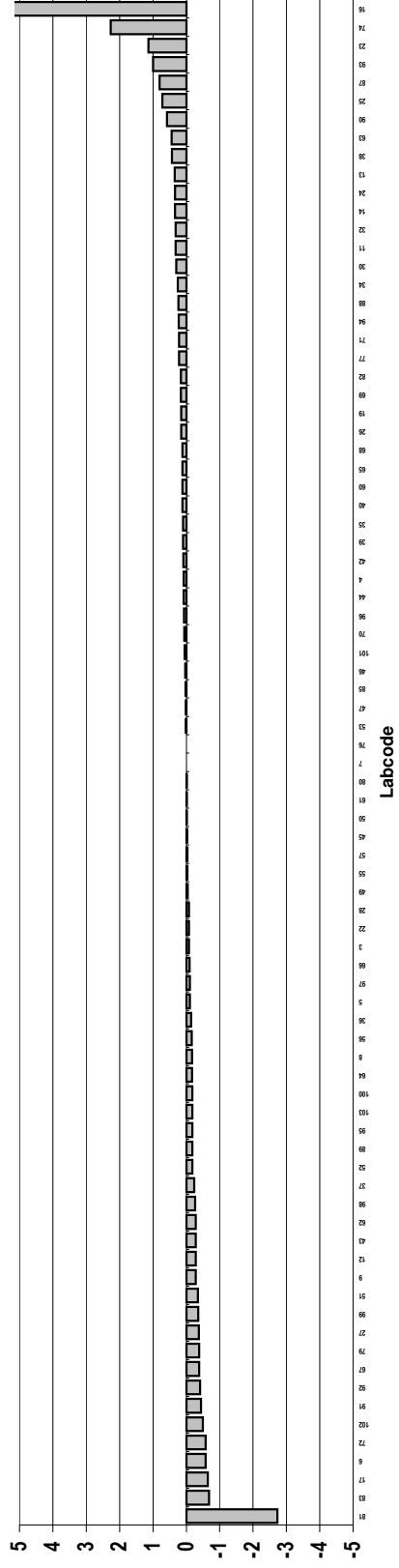
Consensus statistics

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.42
Relative standard deviation, %	8.3
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

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



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



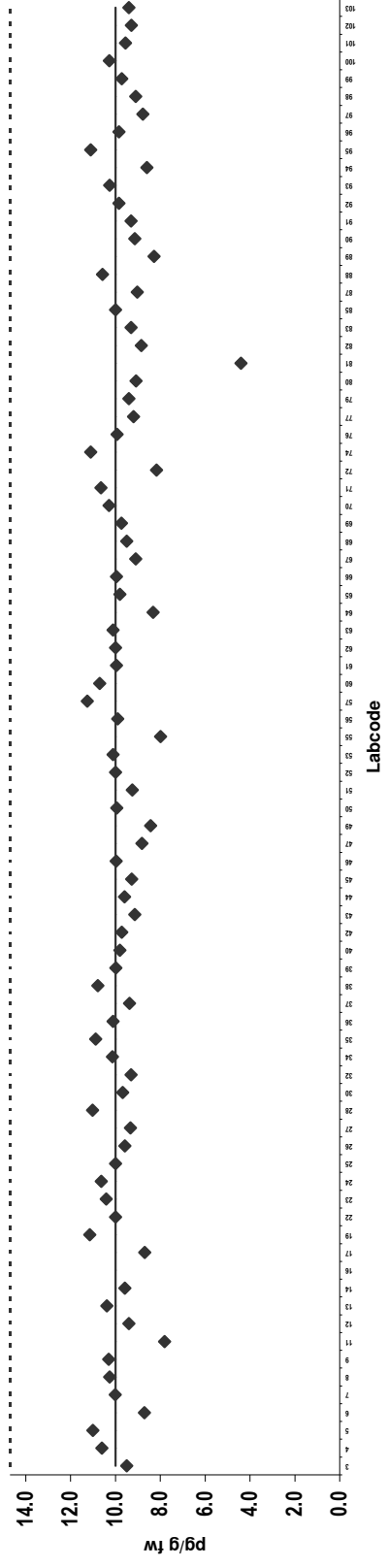
Analyte solution
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	9.5		61	10	
4	11		62	10	
5	11		63	10	
6	8.7		64	8.3	
7	10		65	9.8	
8	10		66	9.9	
9	10		67	9.1	
11	7.8		68	9.5	
12	9.4		69	9.7	
13	10		70	10	
14	9.6		71	11	
16	498	Outlier	72	8.2	
17	8.7		74	11	
19	11		76	9.9	
22	10		77	9.2	
23	10		79	9.4	
24	11		80	9.1	
25	10		81	4.4	Outlier
26	9.6		82	8.9	
27	9.3		83	9.3	
28	11		85	10	
30	9.7		87	9.0	
32	9.3		88	11	
34	10		89	8.3	
35	11		90	9.1	
36	10		91	9.3	
37	9.4		92	9.8	
38	11		93	10	
39	10		94	8.6	
40	9.8		95	11	
42	9.7		96	9.8	
43	9.1		97	8.8	
44	9.6		98	9.1	
45	9.3		99	9.7	
46	10		100	10	
47	8.8		101	9.6	
49	8.4		102	9.3	
50	9.9		103	9.4	
51	9.3				
52	10				
53	10				
55	8.0				
56	9.9				
57	11				
60	11				

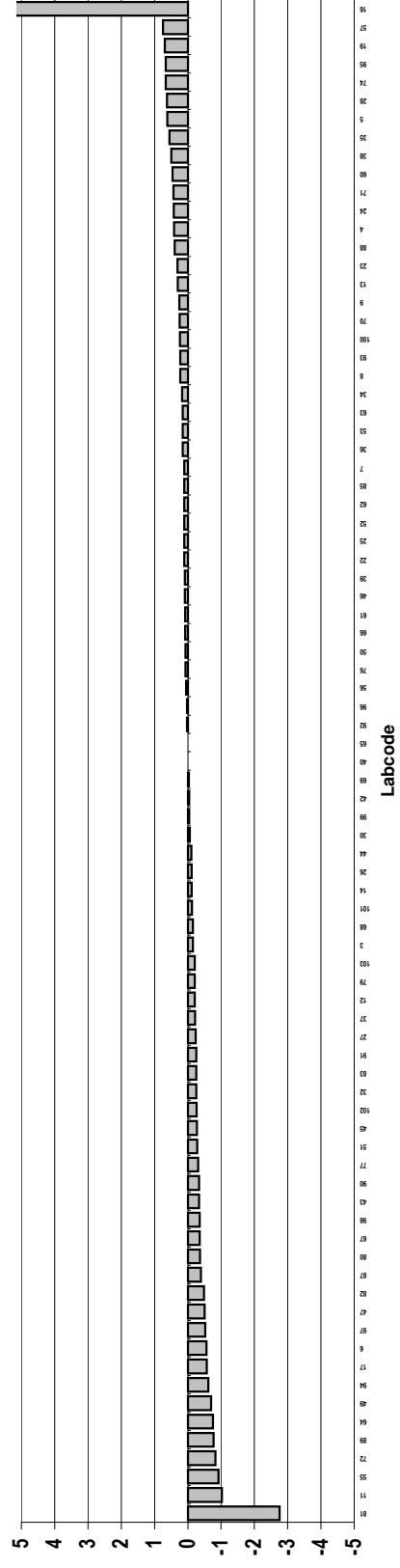
Consensus statistics

Consensus median, pg/g	9.8
Median all values pg/g	9.8
Consensus mean, pg/g	9.7
Standard deviation, pg/g	0.77
Relative standard deviation, %	7.9
No. of values reported	83
No. of values removed	2
No. of reported non-detects	0

OCDF



Z-score: OCDF



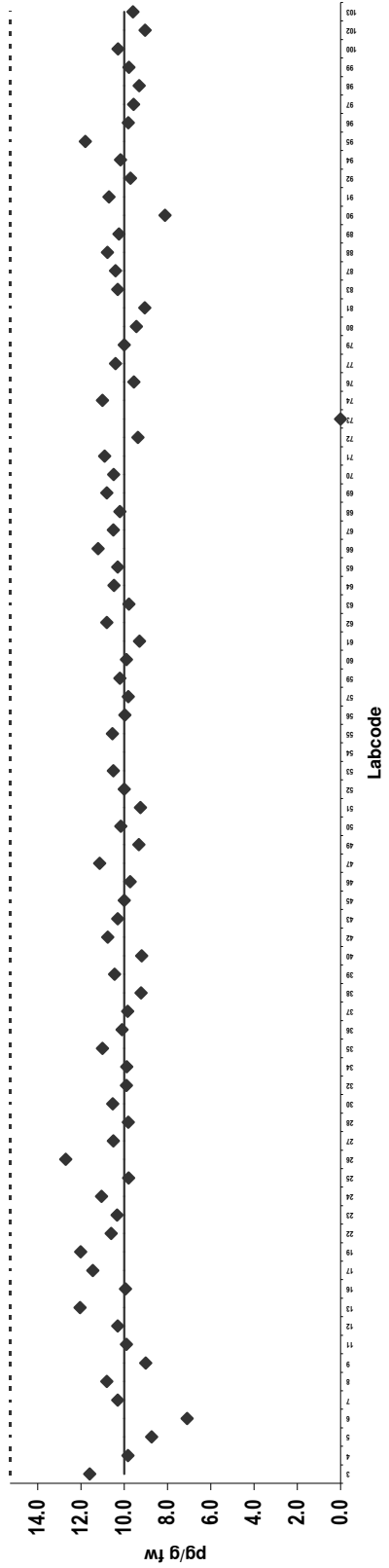
Analyte solution
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	12		61	9.3	
4	9.8		62	11	
5	8.7		63	9.8	
6	7.1		64	10	
7	10		65	10	
8	11		66	11	
9	9.0		67	11	
11	9.9		68	10	
12	10		69	11	
13	12		70	10	
16	9.9		71	11	
17	11		72	9.4	
19	12		73	0.0055	Outlier
22	11		74	11	
23	10		76	9.6	
24	11		77	10	
25	9.8		79	10	
26	13		80	9.4	
27	11		81	9.1	
28	9.8		83	10	
30	11		87	10	
32	9.9		88	11	
34	9.9		89	10	
35	11		90	8.1	
36	10		91	11	
37	9.8		92	9.7	
38	9.2		94	10	
39	10		95	12	
40	9.2		96	9.8	
42	11		97	9.6	
43	10		98	9.3	
45	10		99	9.8	
46	9.7		100	10	
47	11		102	9.0	
49	9.3		103	9.6	
50	10				
51	9.2				
52	10				
53	11				
54	10800				
55	11				
56	10				
57	9.8				
59	10				
60	9.9				

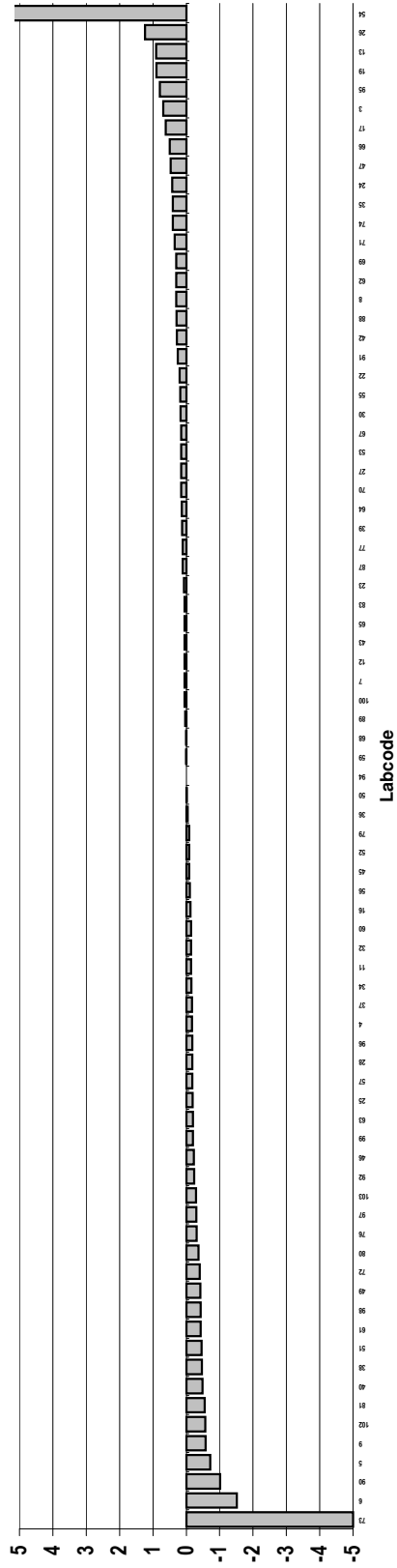
Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.86
Relative standard deviation, %	8.4
No. of values reported	80
No. of values removed	2
No. of reported non-detects	0

PCB 77



Z-score: PCB 77



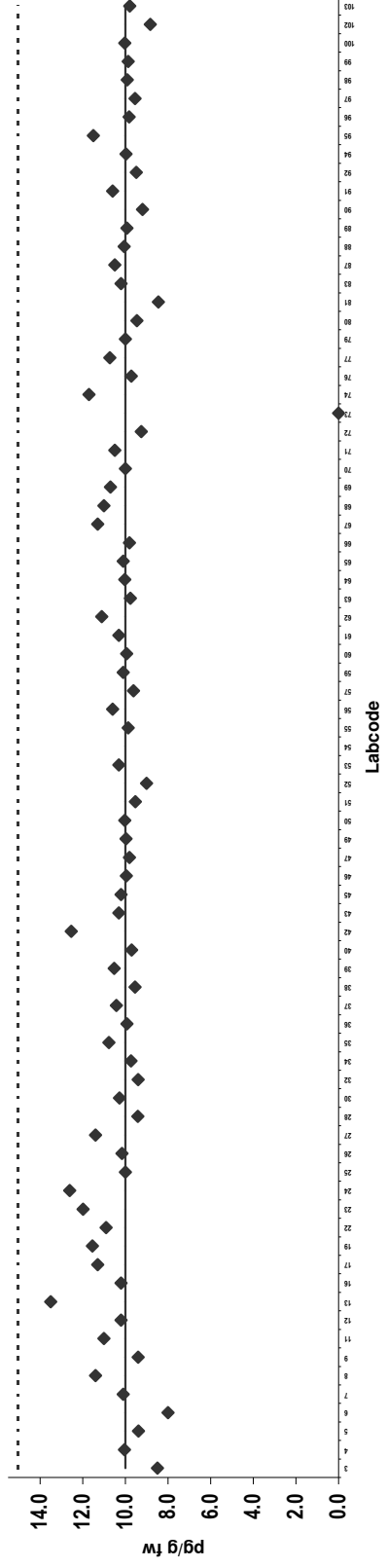
Analyte solution
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	8.5		61	10	
4	10		62	11	
5	9.4		63	9.8	
6	8.0		64	10	
7	10		65	10	
8	11		66	9.8	
9	9.4		67	11	
11	11		68	11	
12	10		69	11	
13	13		70	10	
16	10		71	11	
17	11		72	9.3	
19	12		73	0.0053	Outlier
22	11		74	12	
23	12		76	9.7	
24	13		77	11	
25	10		79	10	
26	10		80	9.5	
27	11		81	8.4	
28	9.4		83	10	
30	10		87	11	
32	9.4		88	10	
34	9.7		89	9.9	
35	11		90	9.2	
36	9.9		91	11	
37	10		92	9.5	
38	9.5		94	10	
39	11		95	12	
40	9.7		96	9.8	
42	13		97	9.6	
43	10		98	9.9	
45	10		99	9.9	
46	10		100	10	
47	9.8		102	8.8	
49	10		103	9.8	
50	10				
51	9.5				
52	9.0				
53	10				
54	10200				
55	9.9				
56	11				
57	9.6				
59	10				
60	9.9				

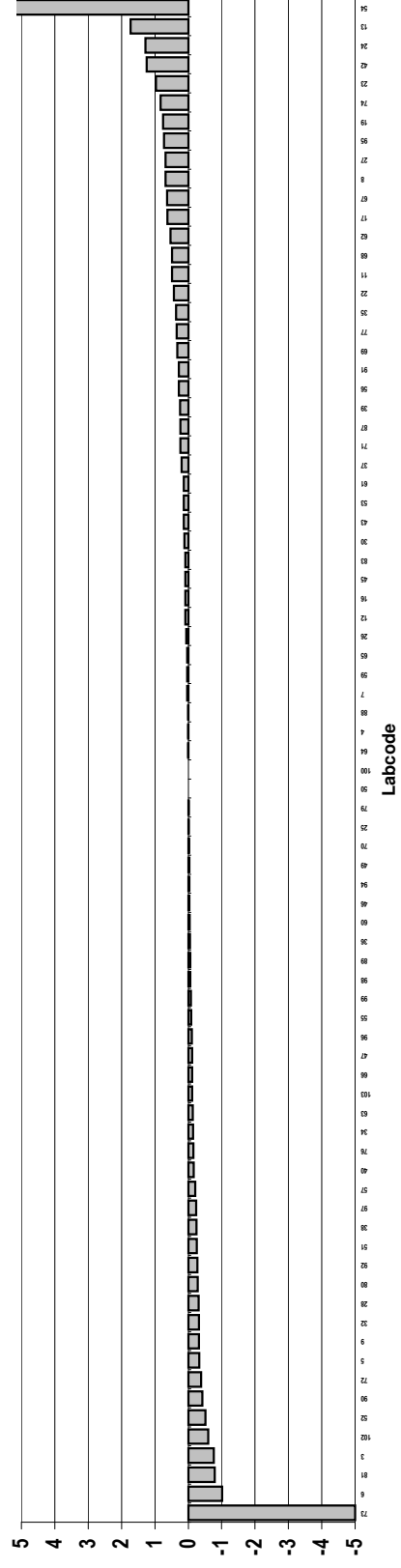
Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.91
Relative standard deviation, %	9
No. of values reported	80
No. of values removed	2
No. of reported non-detects	0

PCB 126



Z-score: PCB 126



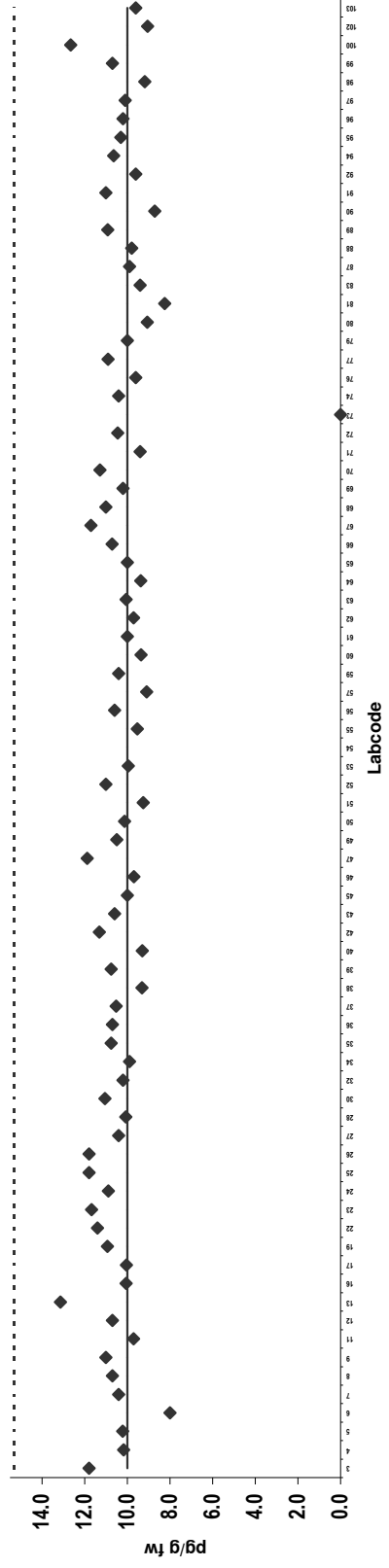
Analyte solution
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	12		61	10	
4	10		62	9.7	
5	10		63	10	
6	8.0		64	9.4	
7	10		65	10	
8	11		66	11	
9	11		67	12	
11	9.7		68	11	
12	11		69	10	
13	13		70	11	
16	10		71	9.4	
17	10		72	10	
19	11		73	0.0058	Outlier
22	11		74	10	
23	12		76	9.6	
24	11		77	11	
25	12		79	10	
26	12		80	9.1	
27	10		81	8.3	
28	10		83	9.4	
30	11		87	9.9	
32	10		88	9.8	
34	9.9		89	11	
35	11		90	8.7	
36	11		91	11	
37	11		92	9.6	
38	9.3		94	11	
39	11		95	10	
40	9.3		96	10	
42	11		97	10	
43	11		98	9.2	
45	10		99	11	
46	9.7		100	13	
47	12		102	9.1	
49	11		103	9.6	
50	10				
51	9.3				
52	11				
53	10				
54	9880	Outlier			
55	9.5				
56	11				
57	9.1				
59	10				
60	9.4				

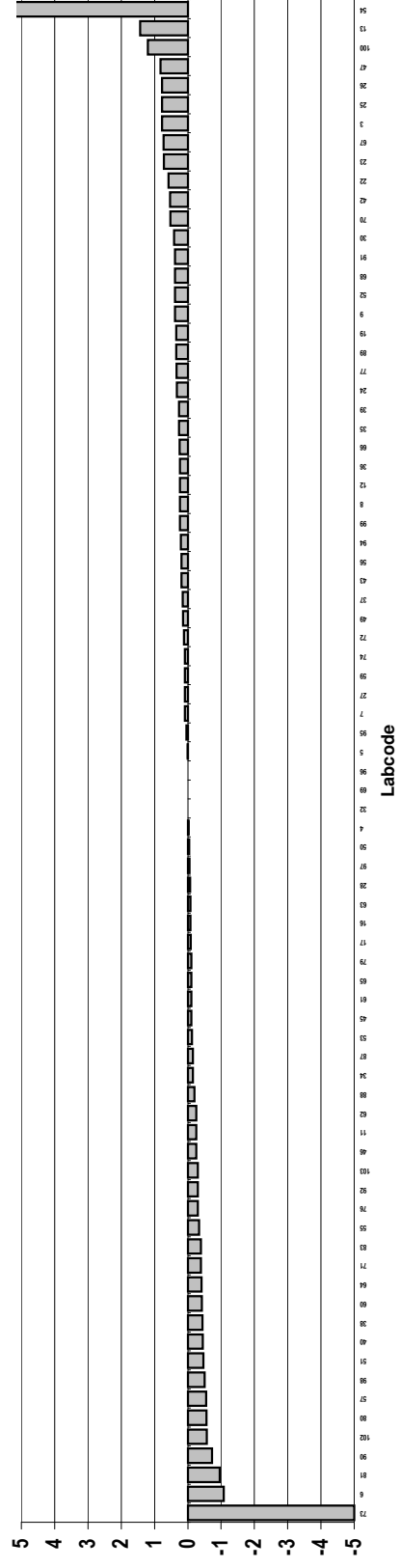
Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.91
Relative standard deviation, %	9
No. of values reported	80
No. of values removed	2
No. of reported non-detects	0

PCB 169



Z-score: PCB 169



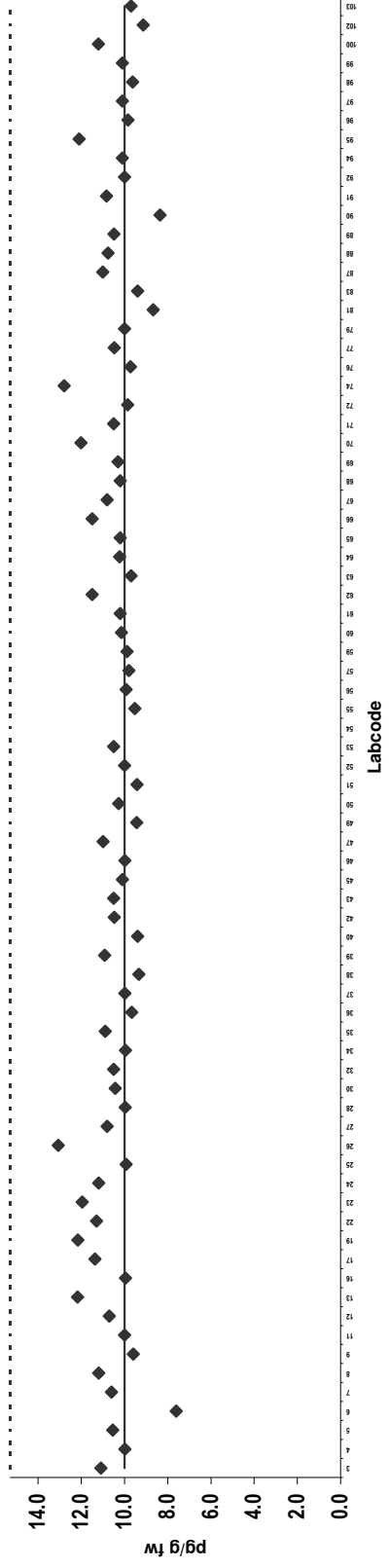
Analyte solution
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	11		61	10	
4	10		62	12	
5	11		63	9.7	
6	7.6		64	10	
7	11		65	10	
8	11		66	12	
9	9.6		67	11	
11	10		68	10	
12	11		69	10	
13	12		70	12	
16	10		71	11	
17	11		72	9.9	
19	12		74	13	
22	11		76	9.7	
23	12		77	10	
24	11		79	10	
25	9.9		81	8.7	
26	13		83	9.4	
27	11		87	11	
28	10		88	11	
30	10		89	10	
32	11		90	8.4	
34	10		91	11	
35	11		92	10	
36	9.7		94	10	
37	10		95	12	
38	9.3		96	9.8	
39	11		97	10	
40	9.4		98	9.6	
42	10		99	10	
43	11		100	11	
45	10		102	9.1	
46	10		103	9.7	
47	11				
49	9.4				
50	10				
51	9.4				
52	10				
53	11				
54	10200				
55	9.5				
56	9.9				
57	9.8				
59	9.9				
60	10				

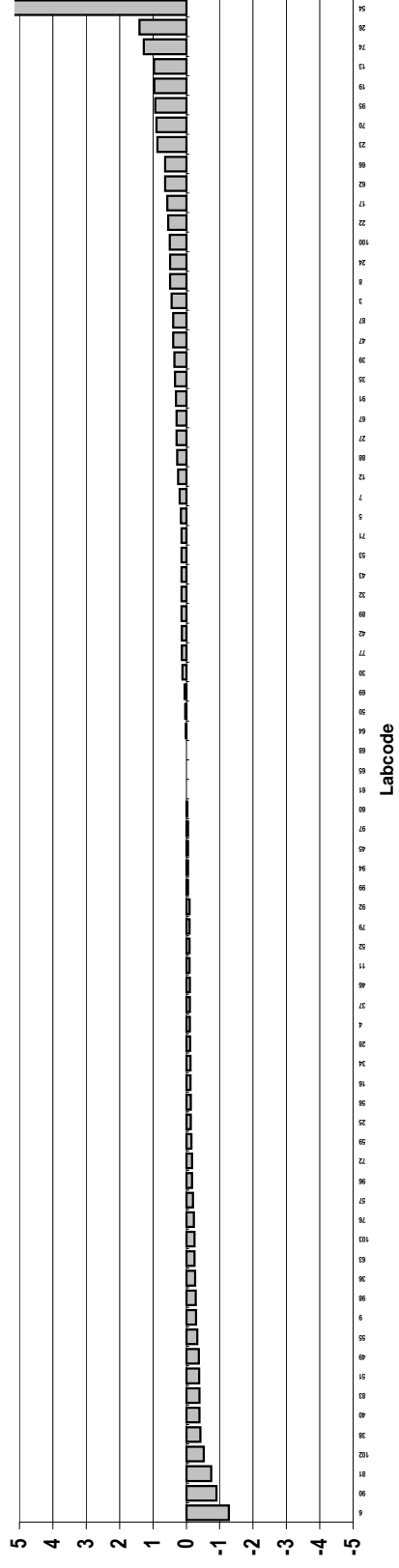
Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.93
Relative standard deviation, %	8.9
No. of values reported	78
No. of values removed	1
No. of reported non-detects	0

PCB 81



Z-score: PCB 81



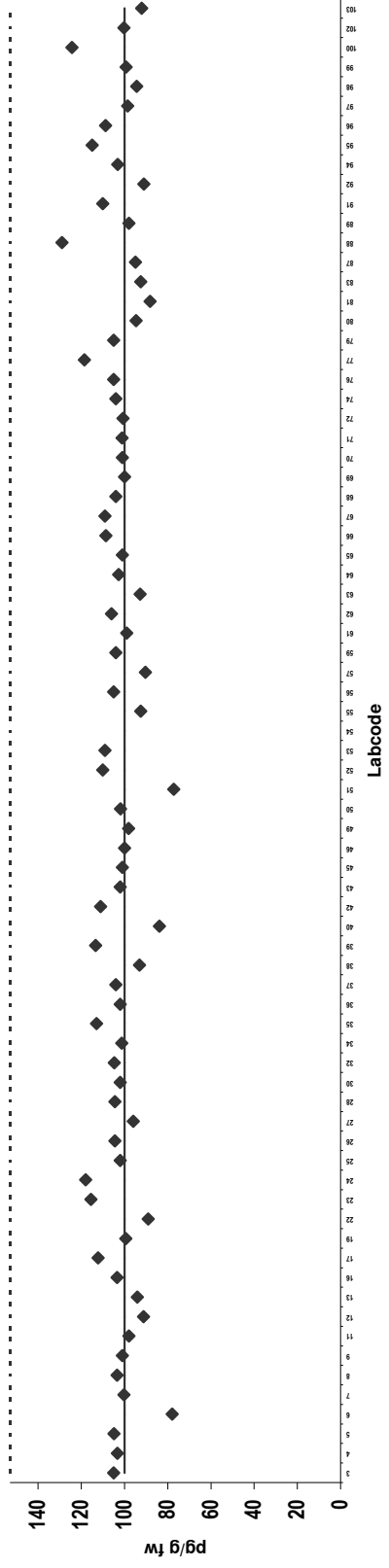
Analyte solution
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	105		63	93	
4	103		64	103	
5	105		65	101	
6	78		66	109	
7	100		67	109	
8	103		68	104	
9	101		69	100	
11	98		70	101	
12	91		71	101	
13	94		72	101	
16	104		74	104	
17	112		76	105	
19	99		77	119	
22	89		79	105	
23	116		80	95	
24	118		81	88	
25	102		83	93	
26	105		87	95	
27	96		88	129	
28	105		89	98	
30	102		91	110	
32	105		92	91	
34	101		94	103	
35	113		95	115	
36	102		96	109	
37	104		97	99	
38	93		98	94	
39	113		99	99	
40	84		100	124	
42	111		102	100	
43	102		103	92	
45	101				
46	100				
49	98				
50	102				
51	77				
52	110				
53	109				
54	91200	Outlier			
55	93				
56	105				
57	90				
59	104				
61	99				
62	106				

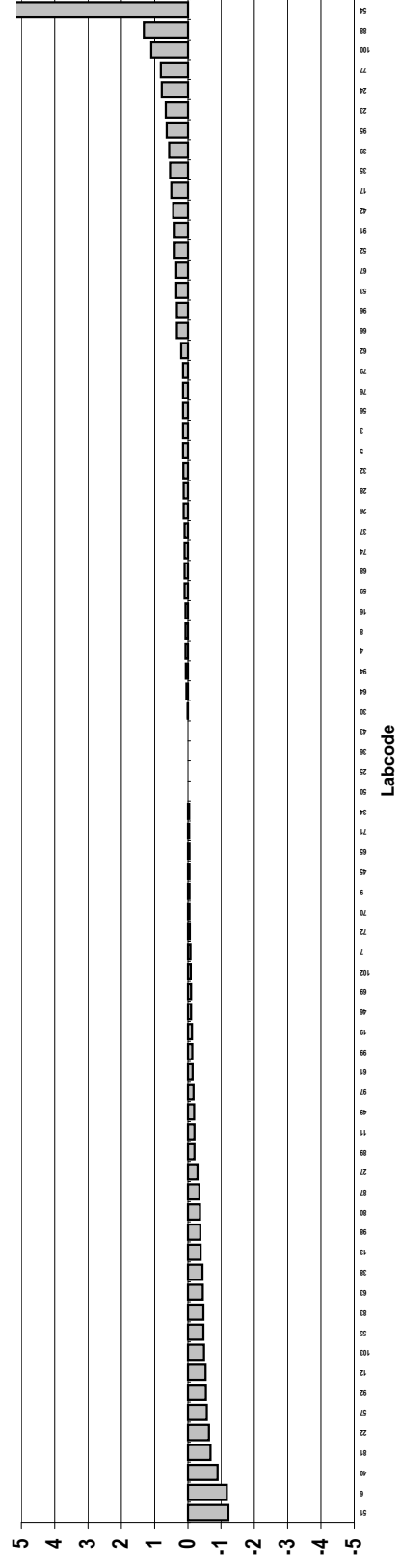
Consensus statistics

Consensus median, pg/g	102
Median all values pg/g	102
Consensus mean, pg/g	102
Standard deviation, pg/g	9.0
Relative standard deviation, %	8.9
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 105



Z-score: PCB 105



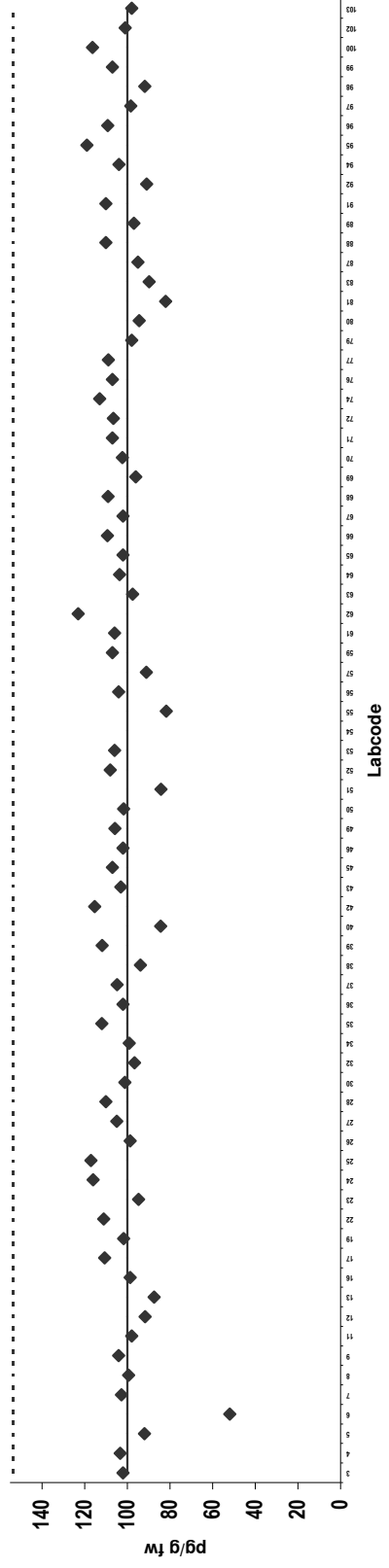
Analyte solution
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	102		63	97	
4	103		64	104	
5	92		65	102	
6	52		66	109	
7	103		67	102	
8	99		68	109	
9	104		69	96	
11	98		70	102	
12	92		71	107	
13	87		72	106	
16	99		74	113	
17	111		76	107	
19	102		77	109	
22	111		79	98	
23	95		80	95	
24	116		81	82	
25	117		83	90	
26	99		87	95	
27	105		88	110	
28	110		89	97	
30	101		91	110	
32	97		92	91	
34	99		94	104	
35	112		95	119	
36	102		96	109	
37	105		97	98	
38	94		98	92	
39	112		99	107	
40	84		100	116	
42	115		102	101	
43	103		103	98	
45	107				
46	102				
49	106				
50	102				
51	84				
52	108				
53	106				
54	91100	Outlier			
55	82				
56	104				
57	91				
59	107				
61	106				
62	123				

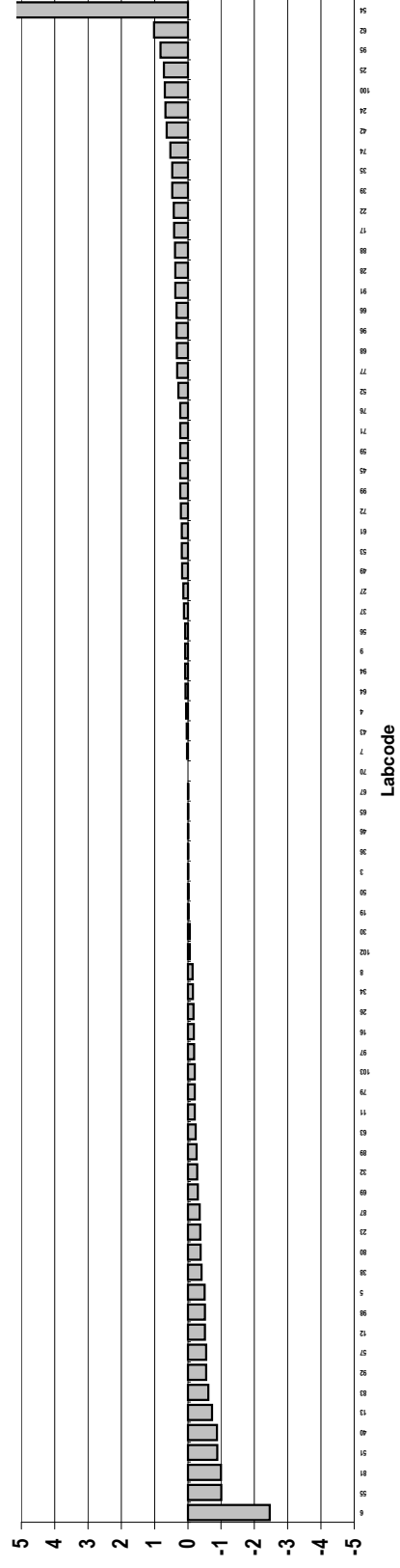
Consensus statistics

Consensus median, pg/g	102
Median all values pg/g	103
Consensus mean, pg/g	102
Standard deviation, pg/g	10
Relative standard deviation, %	10
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 114



Z-score: PCB 114



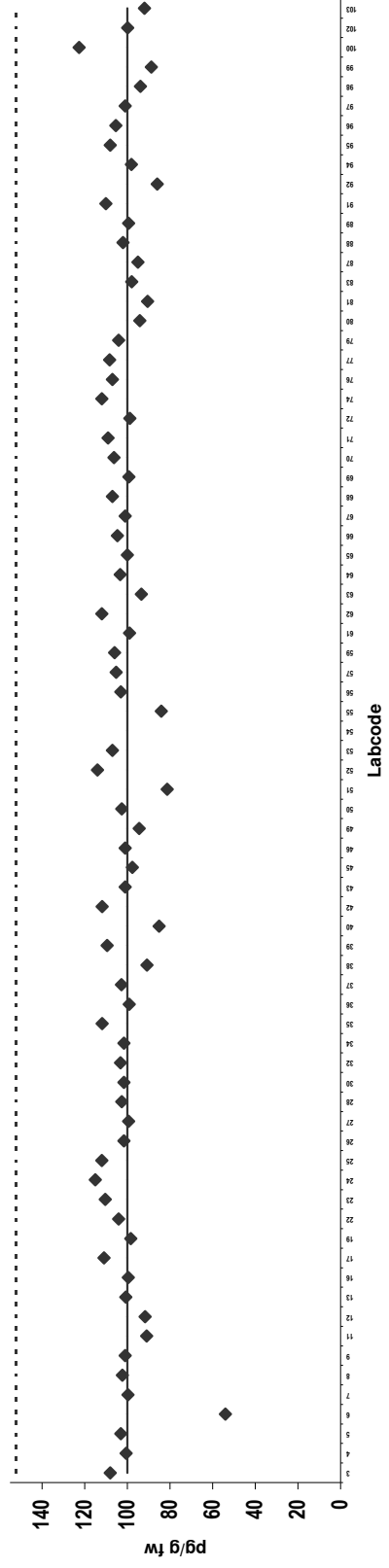
Analyte solution
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	108		63	93	
4	101		64	103	
5	103		65	100	
6	54		66	105	
7	100		67	101	
8	102		68	107	
9	101		69	99	
11	91		70	106	
12	92		71	109	
13	101		72	99	
16	100		74	112	
17	111		76	107	
19	98		77	108	
22	104		79	104	
23	110		80	94	
24	115		81	90	
25	112		83	98	
26	102		87	95	
27	99		88	102	
28	103		89	99	
30	102		91	110	
32	103		92	86	
34	102		94	98	
35	112		95	108	
36	99		96	105	
37	103		97	101	
38	91		98	94	
39	109		99	89	
40	85		100	123	
42	112		102	100	
43	101		103	92	
45	98				
46	101				
49	94				
50	103				
51	81				
52	114				
53	107				
54	84900	Outlier			
55	84				
56	103				
57	105				
59	106				
61	99				
62	112				

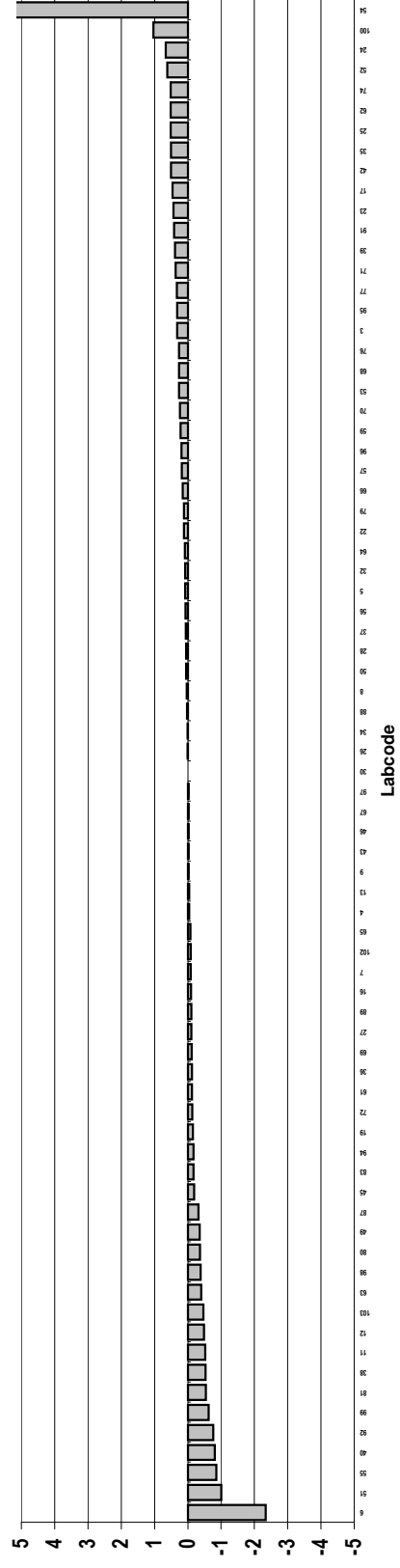
Consensus statistics

Consensus median, pg/g	102
Median all values pg/g	102
Consensus mean, pg/g	101
Standard deviation, pg/g	9.4
Relative standard deviation, %	9.3
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 118



Z-score: PCB 118



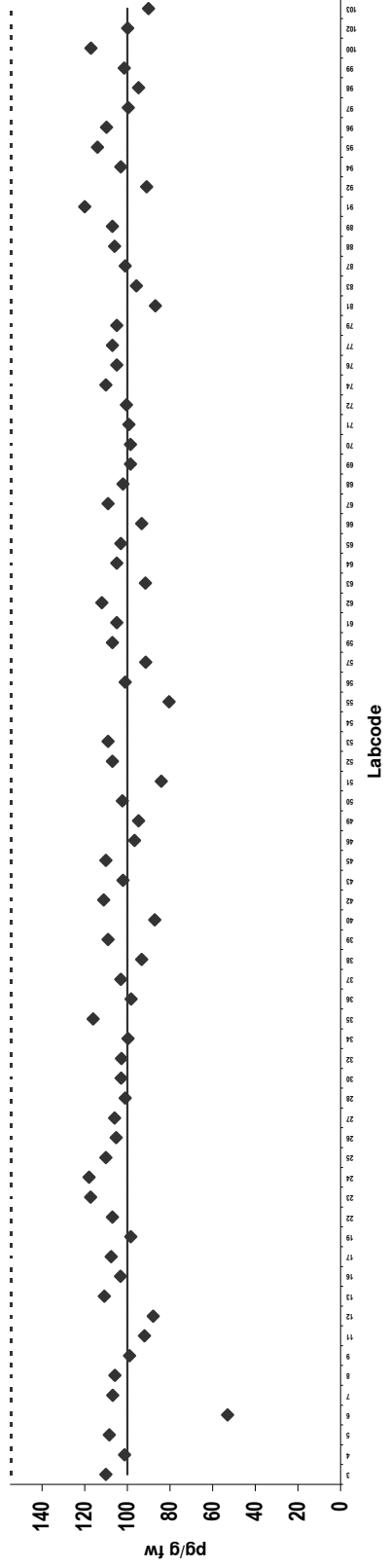
Analyte solution
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	110		63	92	
4	101		64	105	
5	109		65	103	
6	53		66	93	
7	107		67	109	
8	106		68	102	
9	99		69	99	
11	92		70	98	
12	88		71	99	
13	111		72	100	
16	103		74	110	
17	108		76	105	
19	98		77	107	
22	107		79	105	
23	117		81	87	
24	118		83	96	
25	110		87	101	
26	105		88	106	
27	106		89	107	
28	101		91	120	
30	103		92	91	
32	103		94	103	
34	100		95	114	
35	116		96	110	
36	98		97	100	
37	103		98	95	
38	93		99	101	
39	109		100	117	
40	87		102	100	
42	111		103	90	
43	102				
44	110				
45	110				
46	97				
49	95				
50	102				
51	84				
52	107				
53	109				
54	93200	Outlier			
55	80				
56	101				
57	91				
59	107				
61	105				
62	112				

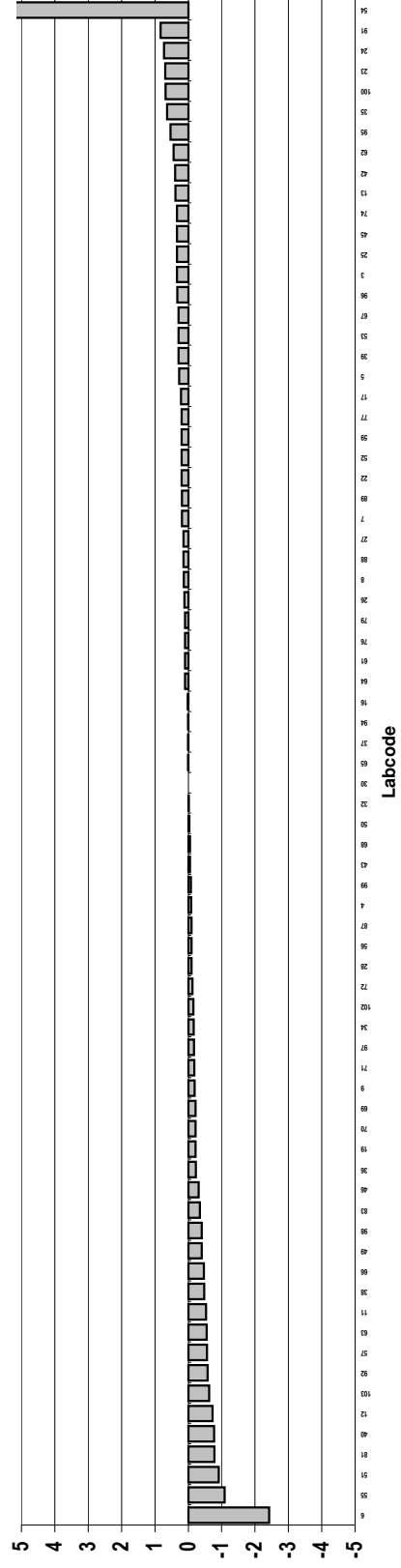
Consensus statistics

Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	102
Standard deviation, pg/g	10
Relative standard deviation, %	10
No. of values reported	75
No. of values removed	1
No. of reported non-detects	0

PCB 123



Z-score: PCB 123



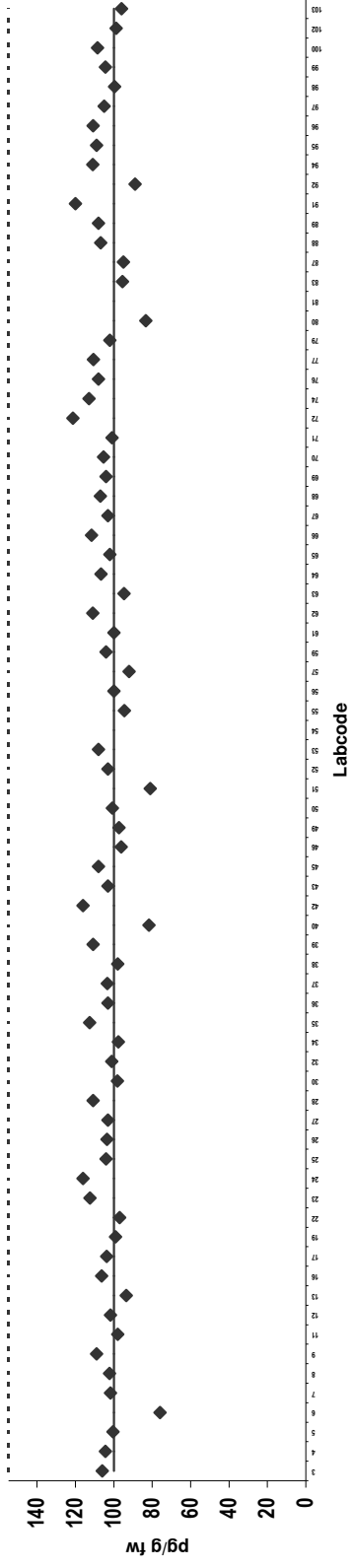
Analyte solution
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	106		63	95	
4	104		64	107	
5	101		65	102	
6	76		66	112	
7	102		67	103	
8	102		68	107	
9	109		69	104	
11	98		70	105	
12	102		71	101	
13	94		72	121	
16	106		74	113	
17	104		76	108	
19	99		77	111	
22	97		79	102	
23	112		80	83	
24	116		81	177	
25	104		83	96	
26	104		87	95	
27	103		88	107	
28	111		89	108	
30	98		91	120	
32	101		92	89	
34	98		94	111	
35	113		95	109	
36	103		96	111	
37	103		97	105	
38	98		98	100	
39	111		99	104	
40	82		100	108	
42	116		102	99	
43	103		103	96	
45	108				
46	96				
49	97				
50	101				
51	81				
52	103				
53	108				
54	88800				
55	94				
56	100				
57	92				
59	104				
61	100				
62	111				

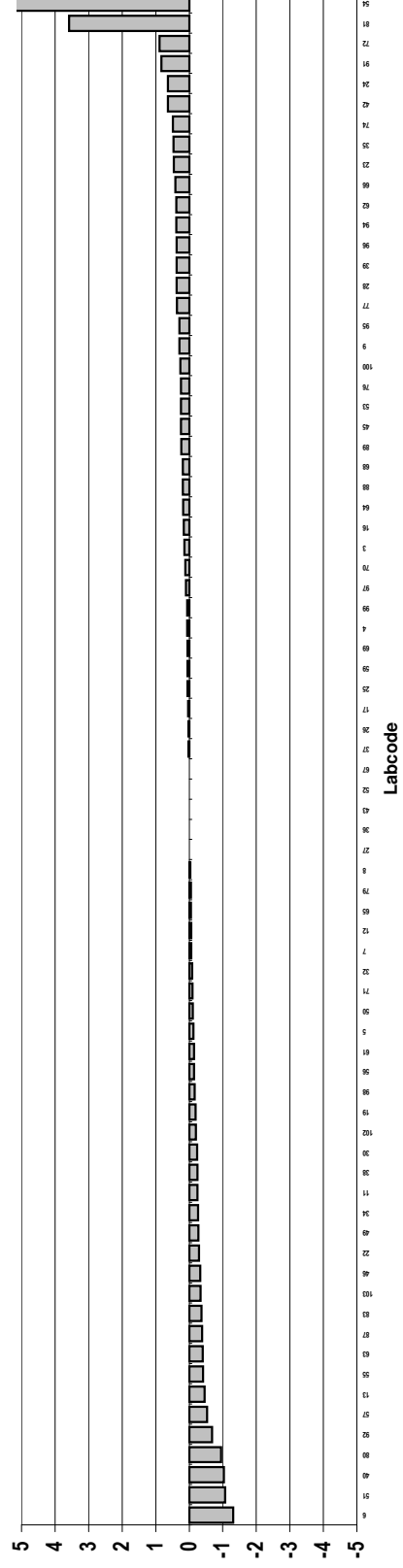
Consensus statistics

Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	103
Standard deviation, pg/g	8.3
Relative standard deviation, %	8.1
No. of values reported	76
No. of values removed	2
No. of reported non-detects	0

PCB 156



Z-score: PCB 156



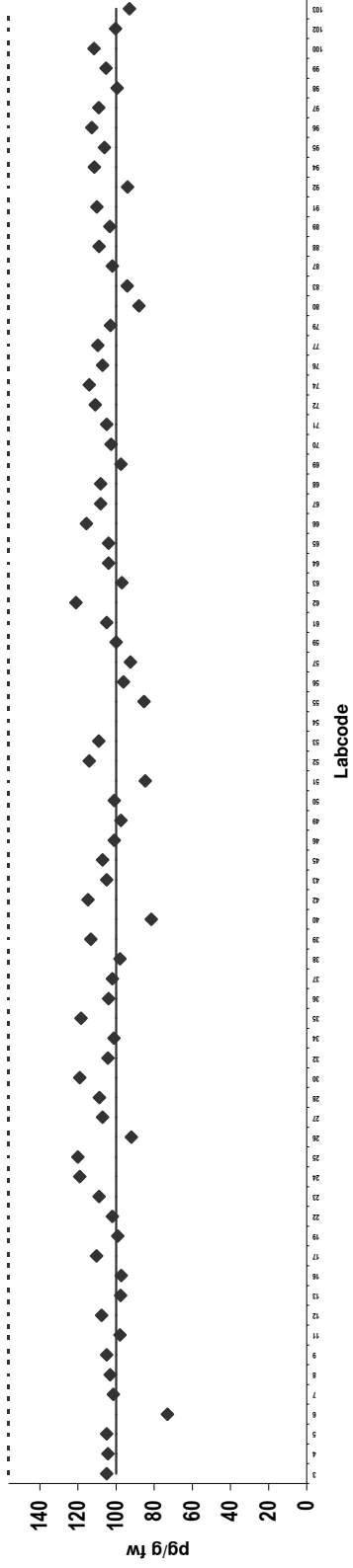
Analyte solution
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	105		63	97	
4	104		64	104	
5	105		65	104	
6	73		66	115	
7	102		67	108	
8	103		68	108	
9	105		69	98	
11	98		70	103	
12	108		71	105	
13	98		72	111	
16	97		74	114	
17	110		76	107	
19	99		77	110	
22	102		79	103	
23	109		80	88	
24	119		83	94	
25	120		87	102	
26	92		88	109	
27	107		89	103	
28	109		91	110	
30	119		92	94	
32	104		94	111	
34	101		95	106	
35	118		96	113	
36	104		97	109	
37	102		98	100	
38	98		99	105	
39	113		100	112	
40	82		102	100	
42	115		103	93	
43	105				
45	107				
46	101				
49	98				
50	101				
51	85				
52	114				
53	109				
54	88600	Outlier			
55	85				
56	96				
57	92				
59	100				
61	105				
62	121				

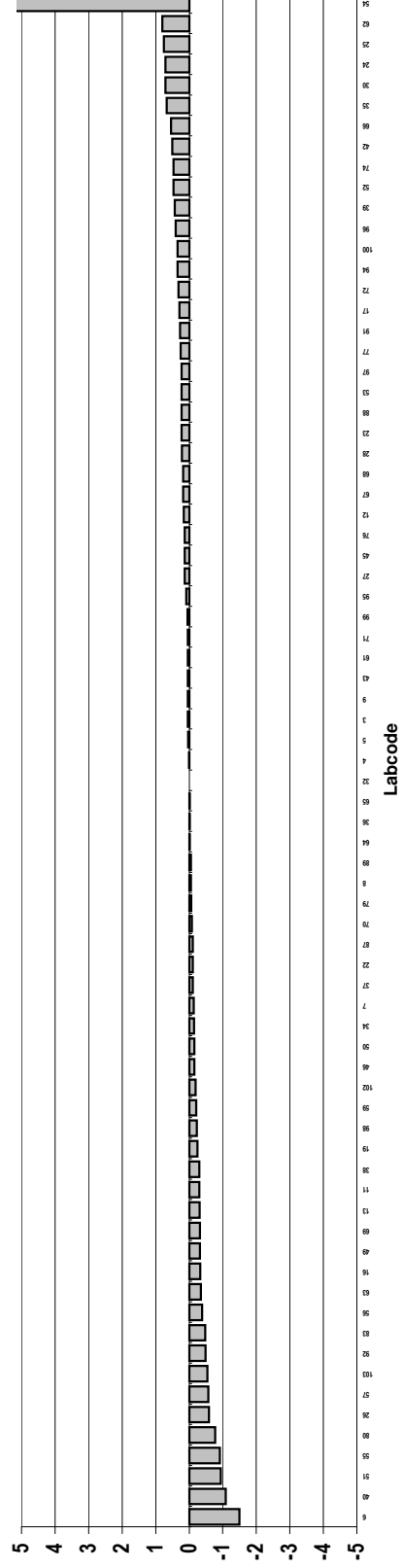
Consensus statistics

Consensus median, pg/g	104
Median all values pg/g	104
Consensus mean, pg/g	104
Standard deviation, pg/g	8.9
Relative standard deviation, %	8.6
No. of values reported	75
No. of values removed	1
No. of reported non-detects	0

PCB 157



Z-score: PCB 157



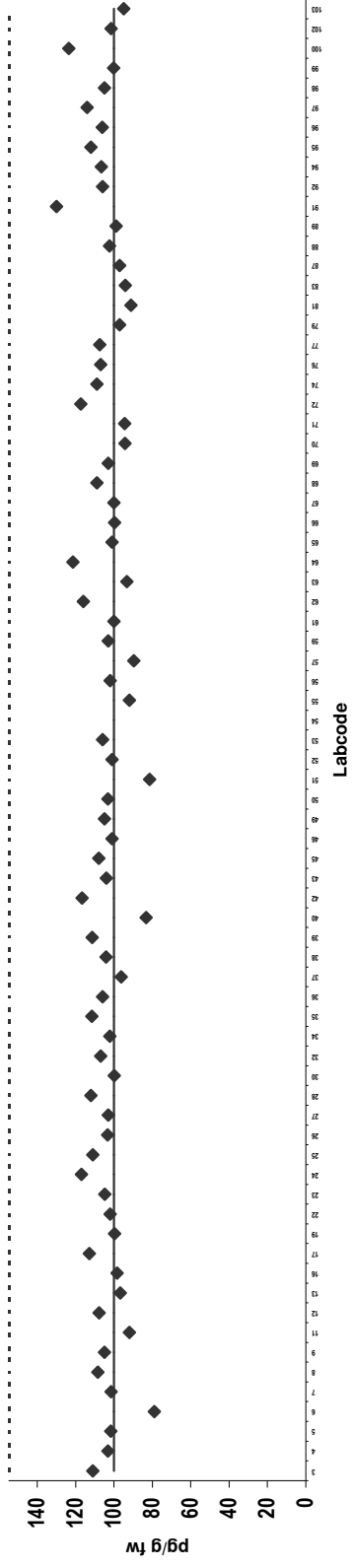
Analyte solution
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	111		63	93	
4	103		64	121	
5	102		65	101	
6	79		66	100	
7	102		67	100	
8	108		68	109	
9	105		69	103	
11	92		70	94	
12	108		71	95	
13	97		72	117	
16	98		74	109	
17	113		76	107	
19	100		77	107	
22	102		79	97	
23	105		81	91	
24	117		83	94	
25	111		87	97	
26	103		88	102	
27	103		89	99	
28	112		91	130	
30	100		92	106	
32	107		94	107	
34	102		95	112	
35	112		96	106	
36	106		97	114	
37	96		98	105	
38	104		99	100	
39	111		100	124	
40	83		102	102	
42	117		103	95	
43	104				
45	108				
46	101				
49	105				
50	103				
51	81				
52	101				
53	106				
54	90700	Outlier			
55	92				
56	102				
57	90				
59	103				
61	100				
62	116				

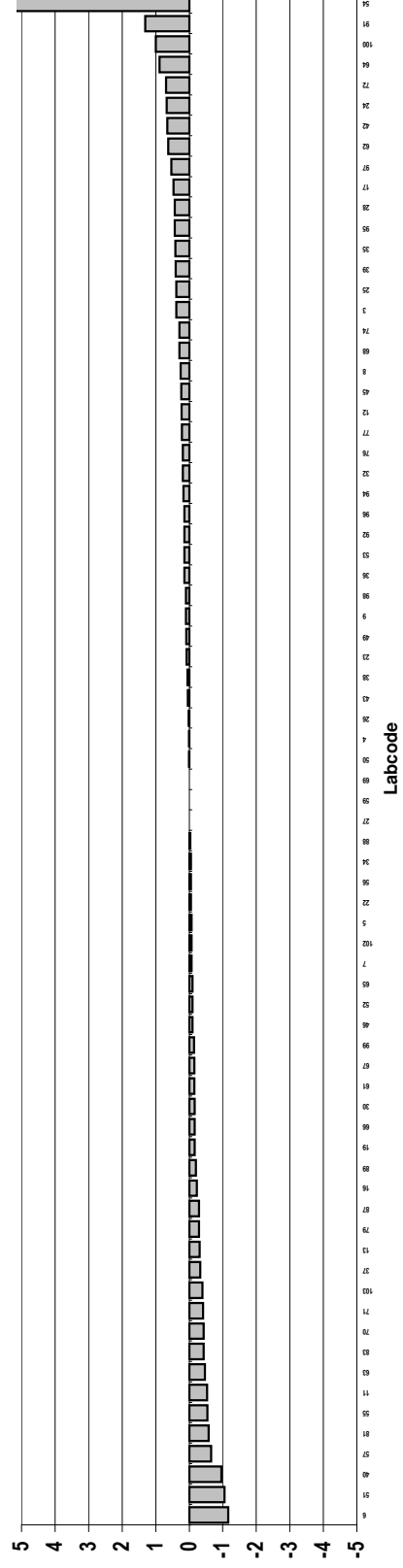
Consensus statistics

Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	103
Standard deviation, pg/g	8.9
Relative standard deviation, %	8.6
No. of values reported	75
No. of values removed	1
No. of reported non-detects	0

PCB 167



Z-score: PCB 167



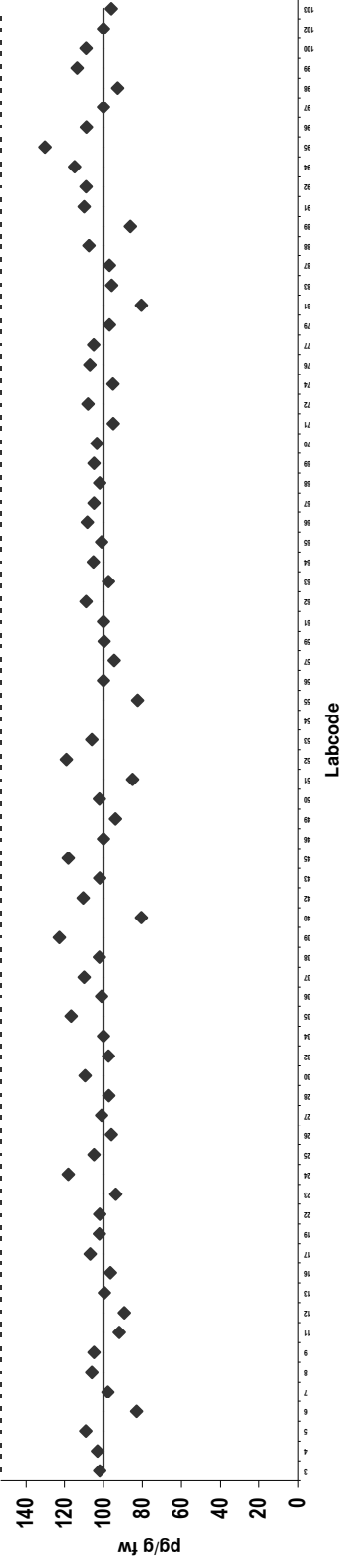
Analyte solution
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	102		63	97	
4	103		64	105	
5	109		65	101	
6	83		66	108	
7	98		67	105	
8	106		68	102	
9	105		69	105	
11	92		70	103	
12	89		71	95	
13	100		72	108	
16	96		74	95	
17	107		76	107	
19	102		77	105	
22	102		79	97	
23	94		81	81	
24	118		83	96	
25	105		87	97	
26	96		88	108	
27	101		89	86	
28	97		91	110	
30	110		92	109	
32	98		94	115	
34	100		95	130	
35	117		96	109	
36	101		97	100	
37	110		98	93	
38	102		99	113	
39	123		100	109	
40	81		102	100	
42	111		103	96	
43	102				
45	118				
46	100				
49	94				
50	102				
51	85				
52	119				
53	106				
54	98200	Outlier			
55	82				
56	100				
57	95				
59	100				
61	100				
62	109				

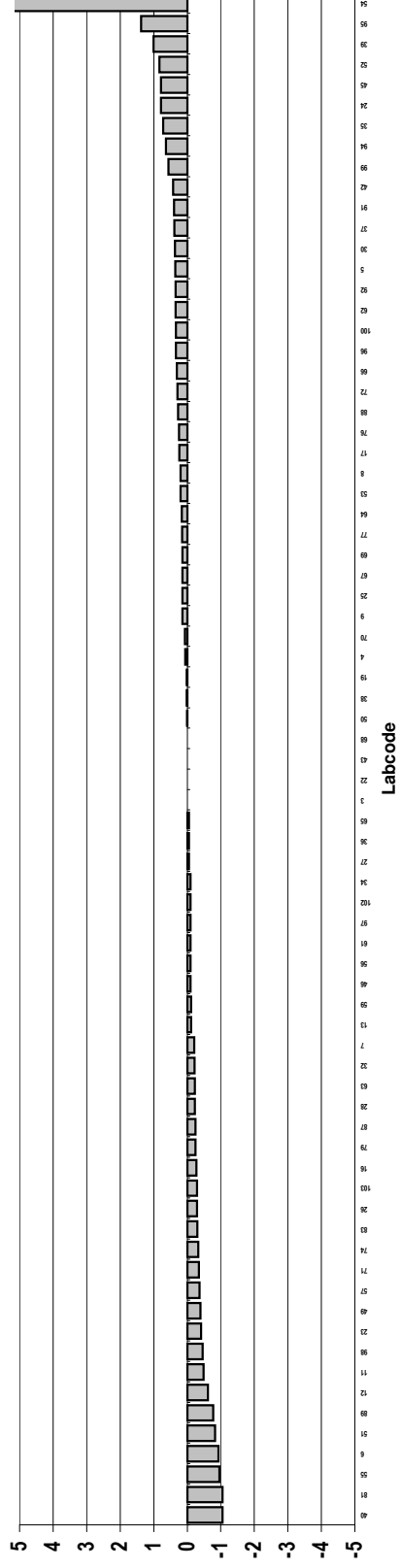
Consensus statistics

Consensus median, pg/g	102
Median all values pg/g	102
Consensus mean, pg/g	102
Standard deviation, pg/g	9.4
Relative standard deviation, %	9.2
No. of values reported	75
No. of values removed	1
No. of reported non-detects	0

PCB 189



Z-score: PCB 189



Analyte solution

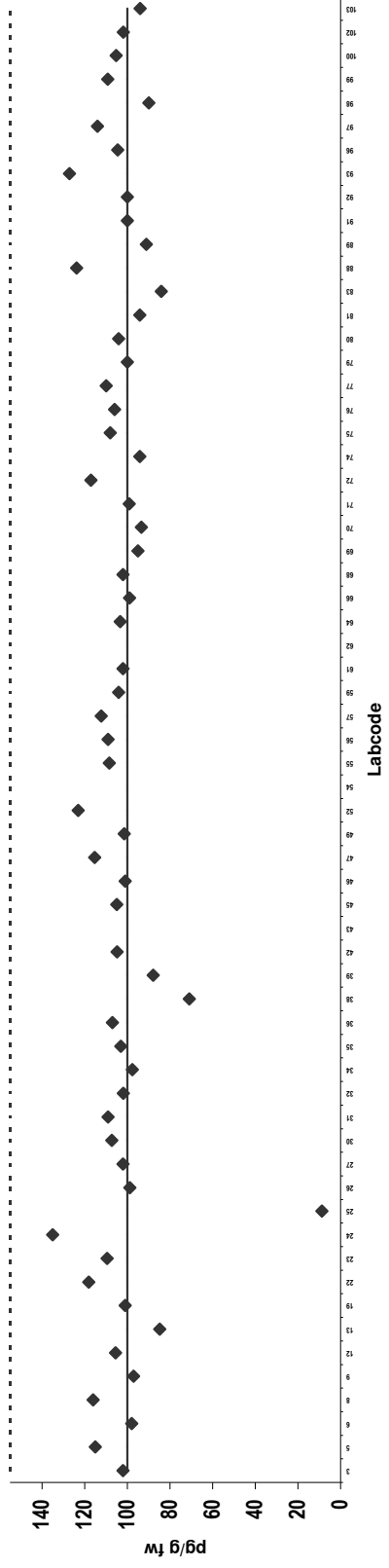
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	102		76	106	
5	115		77	110	
6	98		79	100	
8	116		80	104	
9	97		81	94	
12	106		83	84	
13	85		88	124	
19	101		89	91	
22	118		91	100	
23	109		92	100	
24	135		93	127	
25	8.8	Outlier	96	105	
26	99		97	114	
27	102		98	90	
30	107		99	109	
31	109		100	105	
32	102		102	102	
34	98		103	94	
35	103				
36	107				
38	71				
39	88				
42	105				
43	3550	Outlier			
45	105				
46	101				
47	115				
49	102				
52	123				
54	103000	Outlier			
55	108				
56	109				
57	112				
59	104				
61	102				
62	172				
64	103				
66	99				
68	102				
69	95				
70	93				
71	99				
72	117				
74	94				
75	108				

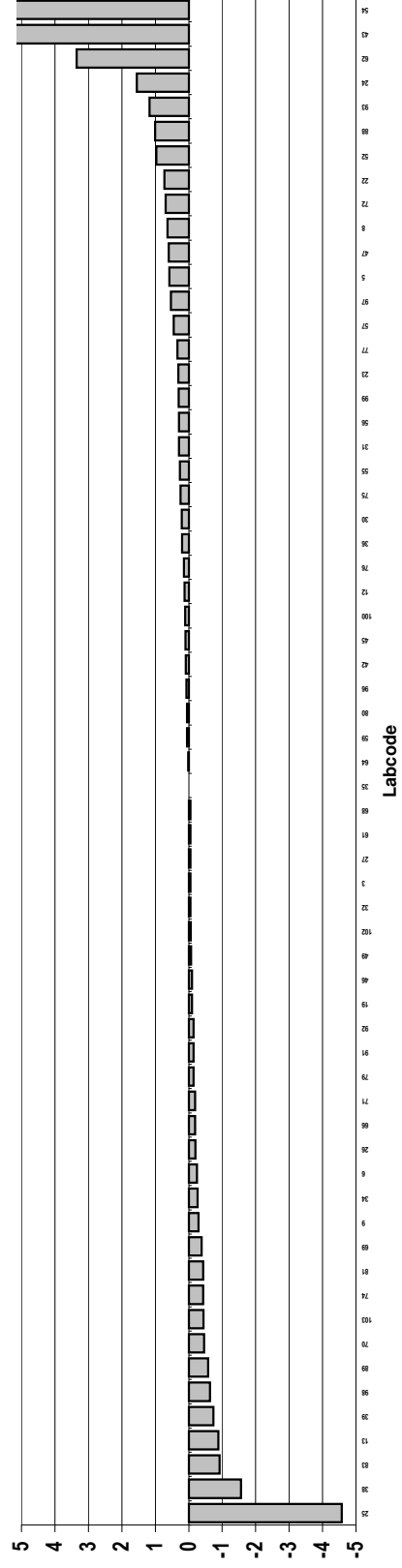
Consensus statistics

Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	104
Standard deviation, pg/g	11
Relative standard deviation, %	10
No. of values reported	63
No. of values removed	4
No. of reported non-detects	0

CB 28



Z-score: CB 28



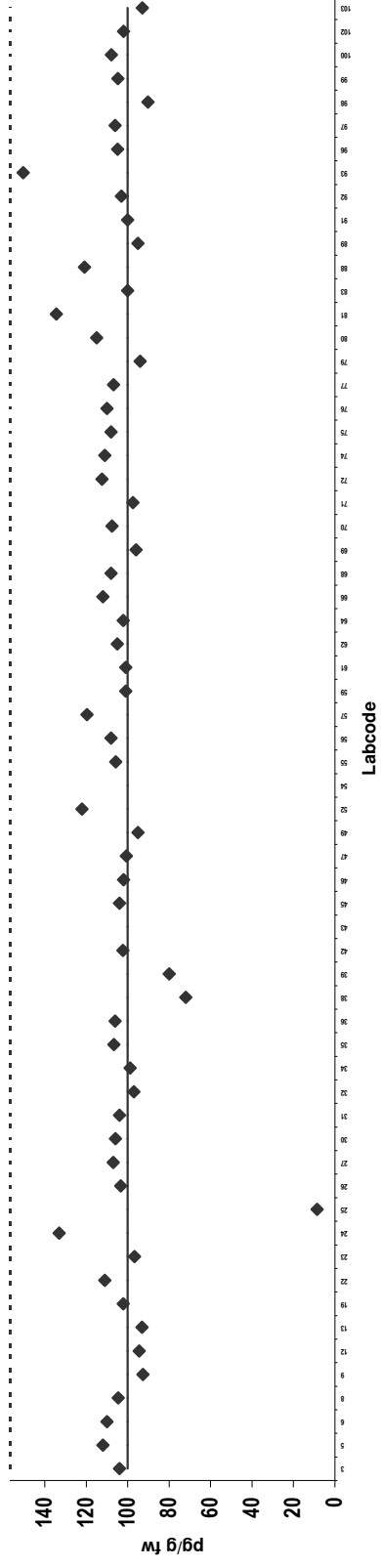
Analyte solution
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	104		76	110	
5	112		77	107	
6	110		79	94	
8	105		80	115	
9	93		81	134	
12	95		83	100	
13	93		88	121	
19	102		89	95	
22	111		91	100	
23	97		92	103	
24	133		93	150	
25	8.6	Outlier	96	105	
26	103		97	106	
27	107		98	90	
30	106		99	105	
31	104		100	108	
32	97		102	102	
34	99		103	93	
35	107				
36	106				
38	72				
39	80				
42	102				
43	3670	Outlier			
45	104				
46	102				
47	101				
49	95				
52	122				
54	124000	Outlier			
55	106				
56	108				
57	120				
59	101				
61	101				
62	105				
64	102				
66	112				
68	108				
69	96				
70	108				
71	97				
72	112				
74	111				
75	108				

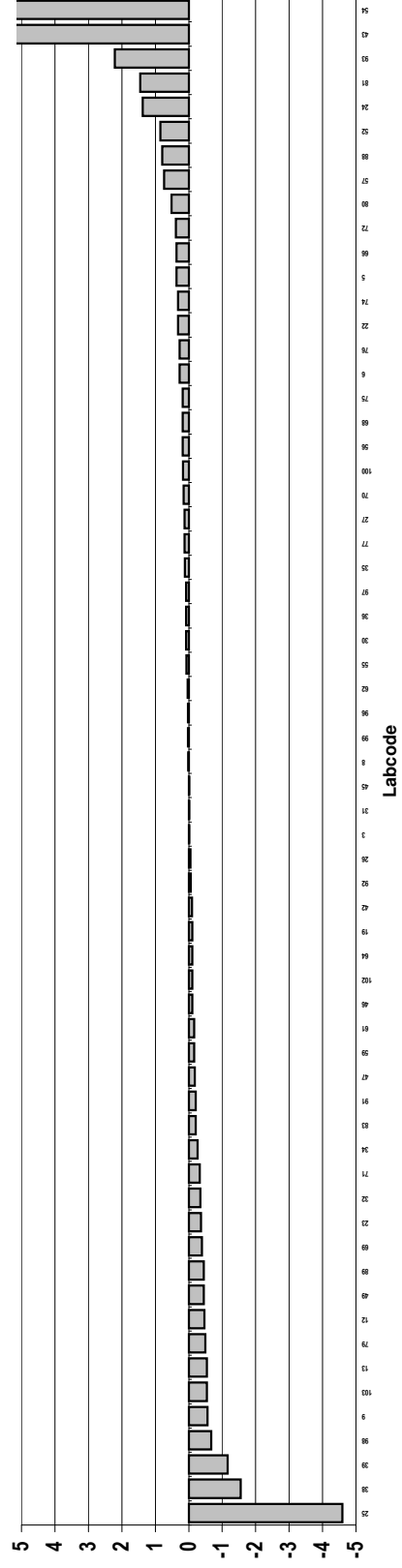
Consensus statistics

Consensus median, pg/g	104
Median all values pg/g	105
Consensus mean, pg/g	105
Standard deviation, pg/g	12
Relative standard deviation, %	11
No. of values reported	63
No. of values removed	3
No. of reported non-detects	0

CB 52



Z-score: CB 52



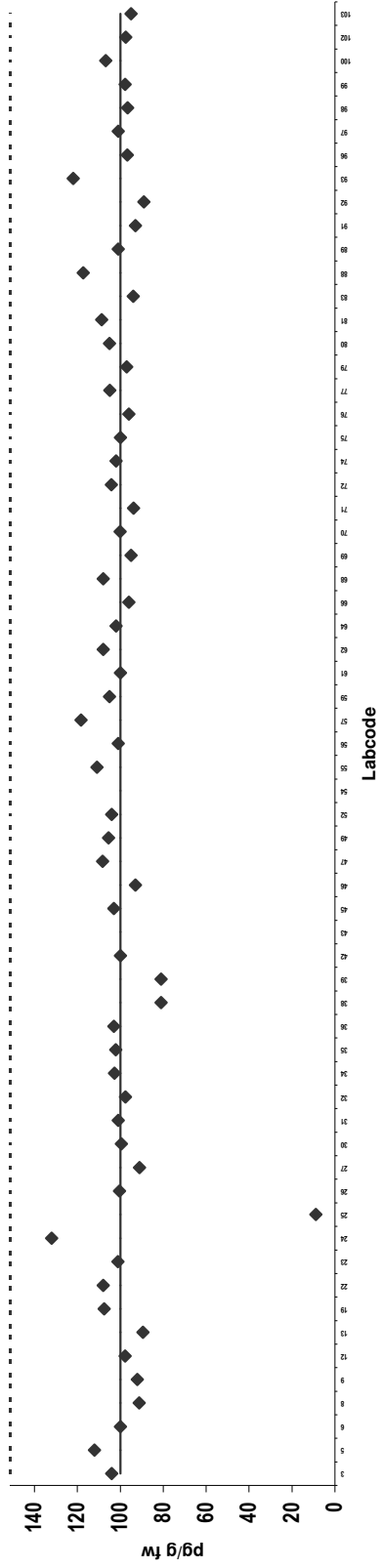
Analyte solution
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	104		76	96	
5	112		77	105	
6	100		79	97	
8	91		80	105	
9	92		81	109	
12	98		83	94	
13	89		88	117	
19	107		89	101	
22	108		91	93	
23	101		92	89	
24	132		93	122	
25	8.9	Outlier	96	97	
26	100		97	101	
27	91		98	97	
30	99		99	98	
31	101		100	107	
32	98		102	97	
34	103		103	95	
35	102				
36	103				
38	81				
39	81				
42	100				
43	3440	Outlier			
45	103				
46	93				
47	108				
49	106				
52	104				
54	113000	Outlier			
55	111				
56	101				
57	118				
59	105				
61	100				
62	108				
64	102				
66	96				
68	108				
69	95				
70	100				
71	94				
72	104				
74	102				
75	100				

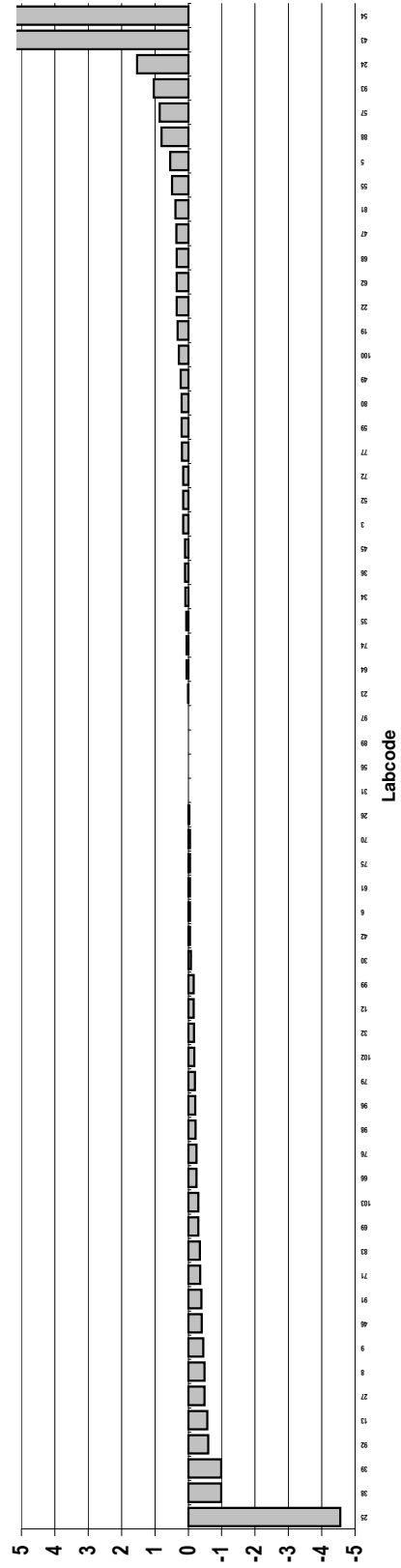
Consensus statistics

Consensus median, pg/g	101
Median all values pg/g	101
Consensus mean, pg/g	101
Standard deviation, pg/g	8.7
Relative standard deviation, %	8.6
No. of values reported	63
No. of values removed	3
No. of reported non-detects	0

CB 101



Z-score: CB 101



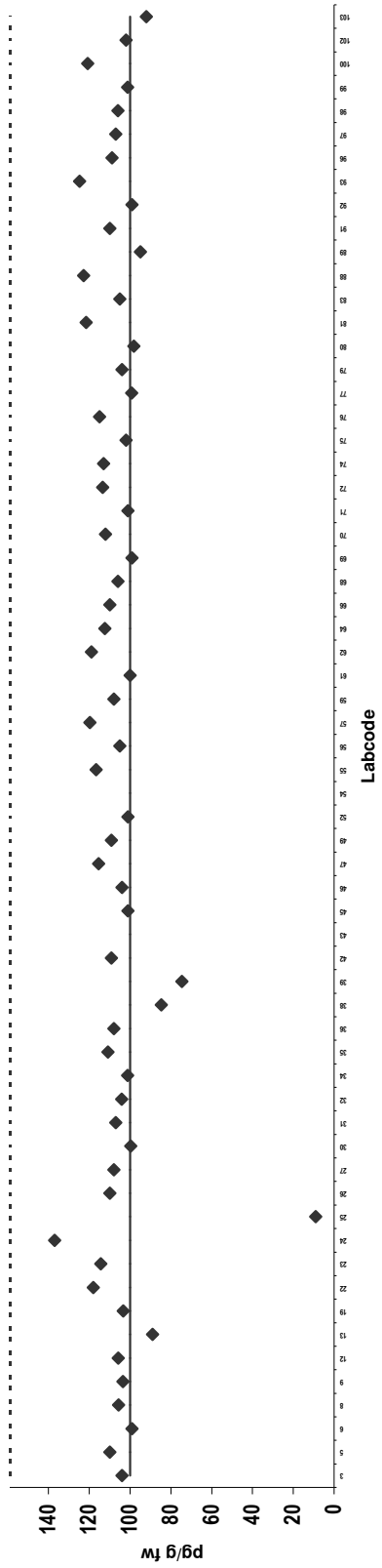
Analyte solution
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	104		76	115	
5	110		77	99	
6	99		79	104	
8	106		80	98	
9	104		81	122	
12	106		83	105	
13	89		88	123	
19	103		89	95	
22	118		91	110	
23	114		92	99	
24	137		93	125	
25	9.0		96	109	
26	110	Outlier	97	107	
27	108		98	106	
30	100		99	101	
31	107		100	121	
32	104		102	102	
34	101		103	92	
35	111				
36	108				
38	85				
39	75				
42	109				
43	3430	Outlier			
45	101				
46	104				
47	115				
49	109				
52	101				
54	115000	Outlier			
55	117				
56	105				
57	120				
59	108				
61	100				
62	119				
64	112				
66	110				
68	106				
69	99				
70	112				
71	101				
72	114				
74	113				
75	102				

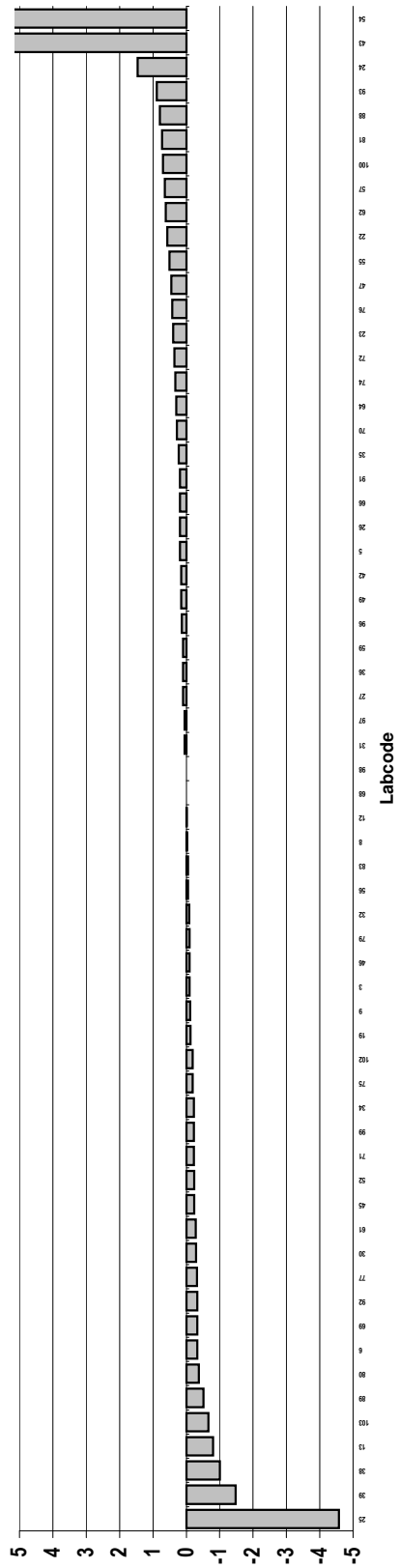
Consensus statistics

Consensus median, pg/g	106
Median all values pg/g	106
Consensus mean, pg/g	107
Standard deviation, pg/g	9.9
Relative standard deviation, %	9.2
No. of values reported	63
No. of values removed	3
No. of reported non-detects	0

CB 138



Z-score: CB 138



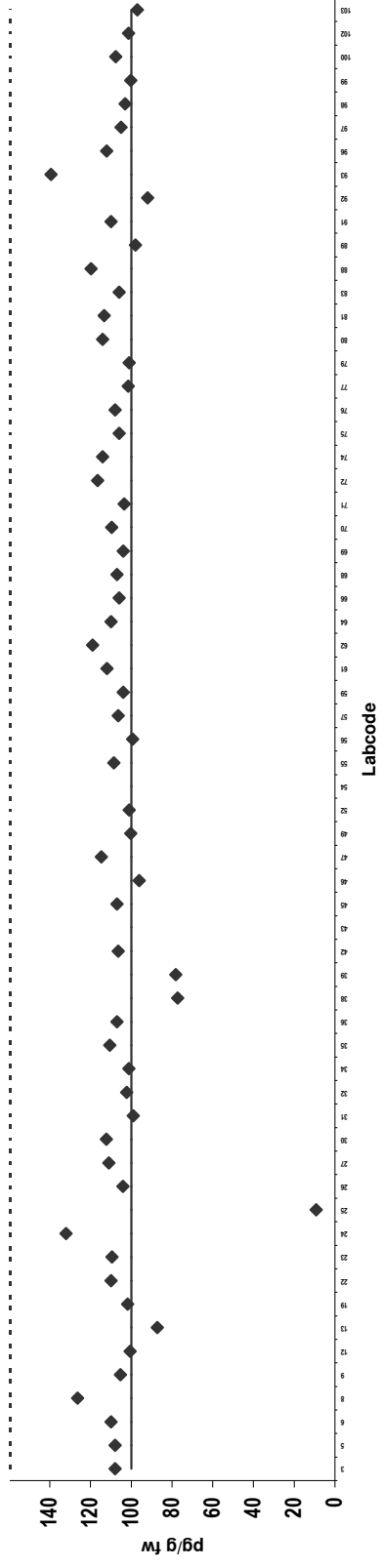
Analyte solution
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	108		76	108	
5	108		77	101	
6	110		79	101	
8	126		80	114	
9	105		81	113	
12	101		83	106	
13	87		88	120	
19	102		89	98	
22	110		91	110	
23	109		92	92	
24	132		93	139	
25	9.2	Outlier	96	112	
26	104		97	105	
27	111		98	103	
30	112		99	100	
31	99		100	108	
32	102		102	101	
34	101		103	97	
35	111				
36	107				
38	77				
39	78				
42	106				
43	3630	Outlier			
45	107				
46	96				
47	115				
49	100				
52	101				
54	67000	Outlier			
55	109				
56	99				
57	106				
59	104				
61	112				
62	119				
64	110				
66	106				
68	107				
69	104				
70	110				
71	104				
72	117				
74	114				
75	106				

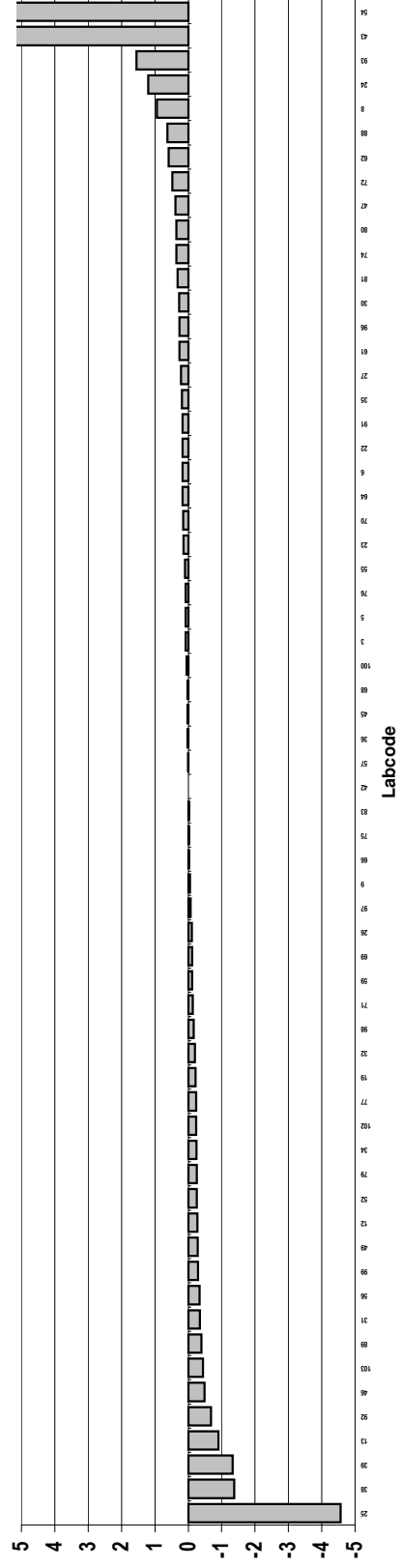
Consensus statistics

Consensus median, pg/g	106
Median all values pg/g	106
Consensus mean, pg/g	106
Standard deviation, pg/g	10
Relative standard deviation, %	9.4
No. of values reported	63
No. of values removed	3
No. of reported non-detects	0

CB 153



Z-score: CB 153



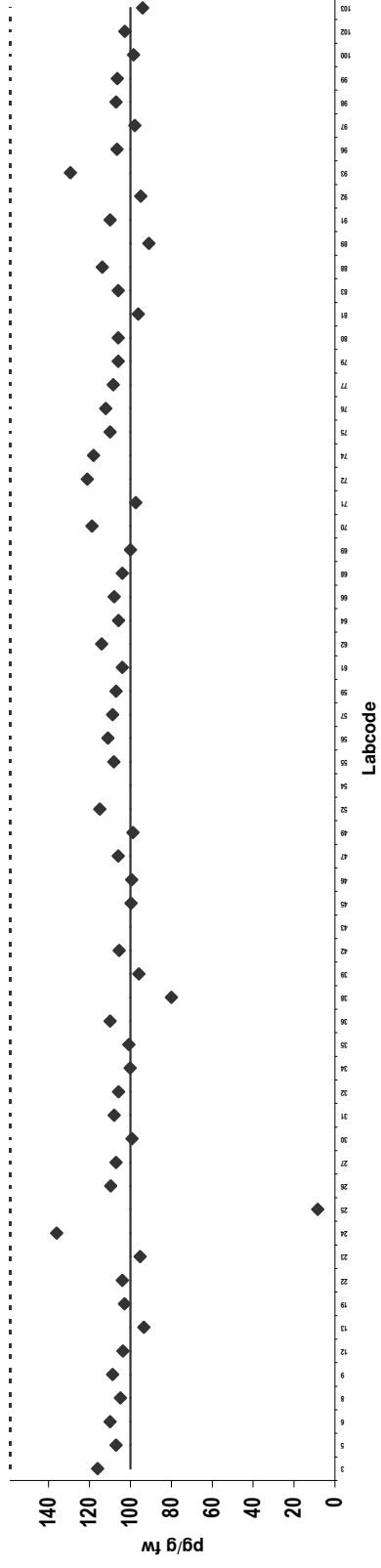
Analyte solution
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	116		76	112	
5	107		77	108	
6	110		79	106	
8	105		80	106	
9	109		81	96	
12	104		83	106	
13	93		88	114	
19	103		89	91	
22	104		91	110	
23	95		92	95	
24	136		93	129	
25	8.4	Outlier	96	107	
26	110		97	98	
27	107		98	107	
30	99		99	106	
31	108		100	98	
32	106		102	103	
34	100		103	94	
35	101				
36	110				
38	80				
39	96				
42	106				
43	4410	Outlier			
45	100				
46	99				
47	106				
49	99				
52	115				
54	96400	Outlier			
55	108				
56	111				
57	109				
59	107				
61	104				
62	114				
64	106				
66	108				
68	104				
69	100				
70	119				
71	97				
72	121				
74	118				
75	110				

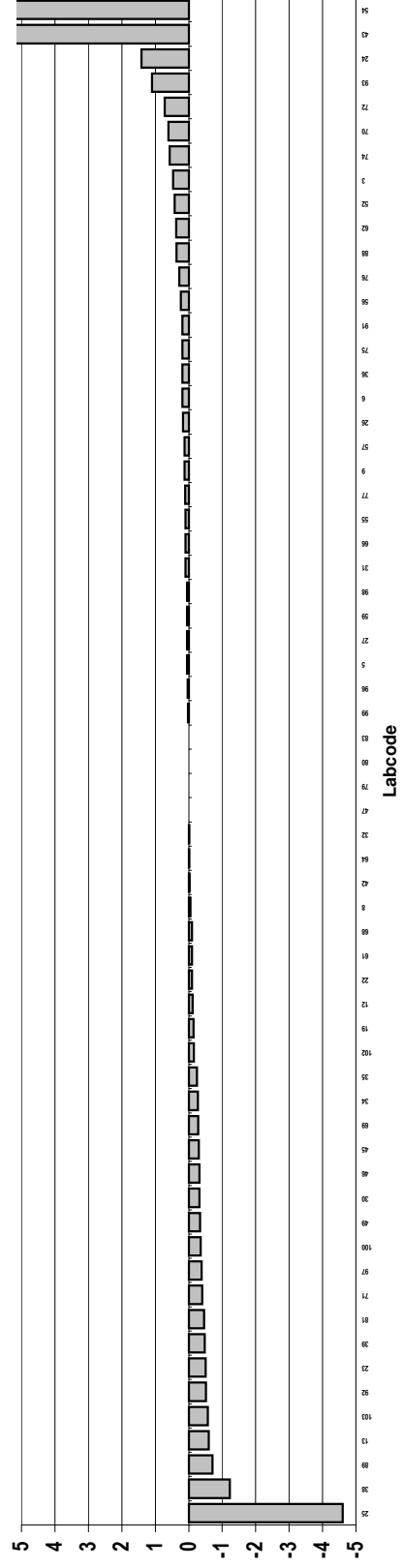
Consensus statistics

Consensus median, pg/g	106
Median all values pg/g	106
Consensus mean, pg/g	106
Standard deviation, pg/g	8.8
Relative standard deviation, %	8.4
No. of values reported	63
No. of values removed	3
No. of reported non-detects	0

CB 180



Z-score: CB 180



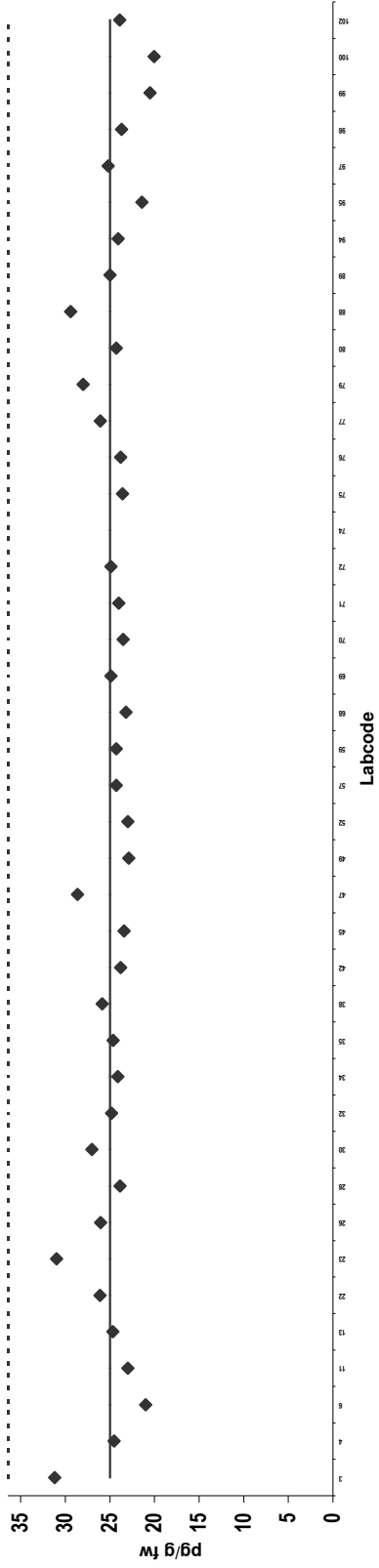
Analyte solution
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	31				
4	25				
6	21				
11	23				
13	25				
22	26				
23	31				
26	26				
28	24				
30	27				
32	25				
34	24				
35	25				
38	26				
42	24				
45	23				
47	29				
49	23				
52	23				
57	24				
59	24				
68	23				
69	25				
70	24				
71	24				
72	25				
74	38	Outlier			
75	24				
76	24				
77	26				
79	28				
80	24				
88	29				
89	25				
94	24				
95	21				
97	25				
98	24				
99	21				
100	20				
102	24				

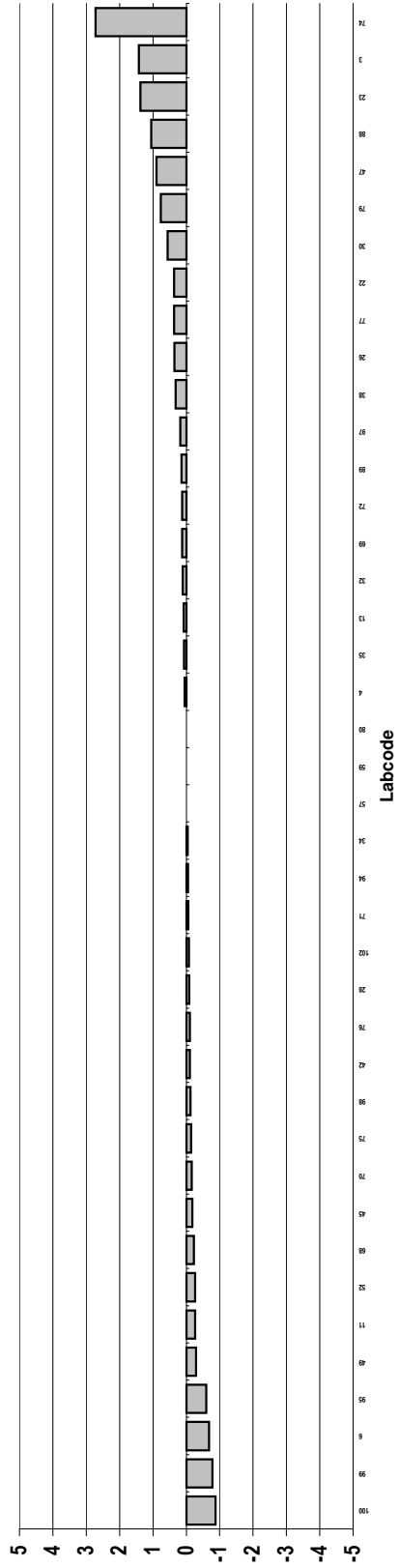
Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	25
Standard deviation, pg/g	2.4
Relative standard deviation, %	9.8
No. of values reported	41
No. of values removed	1
No. of reported non-detects	0

BDE 28



Z-score: BDE 28



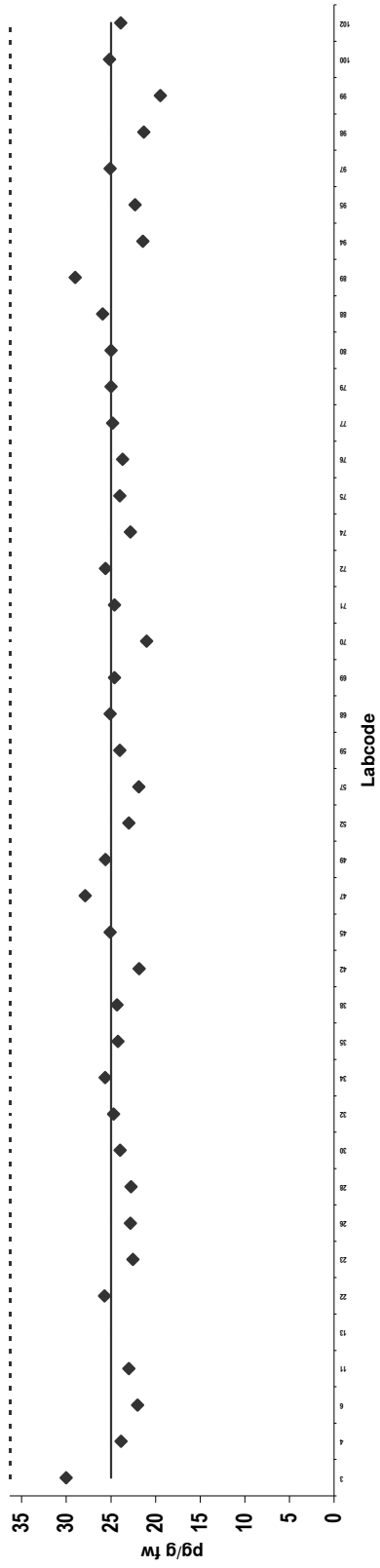
Analyte solution
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	30				
4	24				
6	22				
11	23				
13	37				
22	26				
23	23				
26	23				
28	23				
30	24				
32	25				
34	26				
35	24				
38	24				
42	22				
45	25				
47	28				
49	26				
52	23				
57	22				
59	24				
68	25				
69	25				
70	21				
71	25				
72	26				
74	23				
75	24				
76	24				
77	25				
79	25				
80	25				
88	26				
89	29				
94	21				
95	22				
97	25				
98	21				
99	19				
100	25				
102	24				
		Outlier			

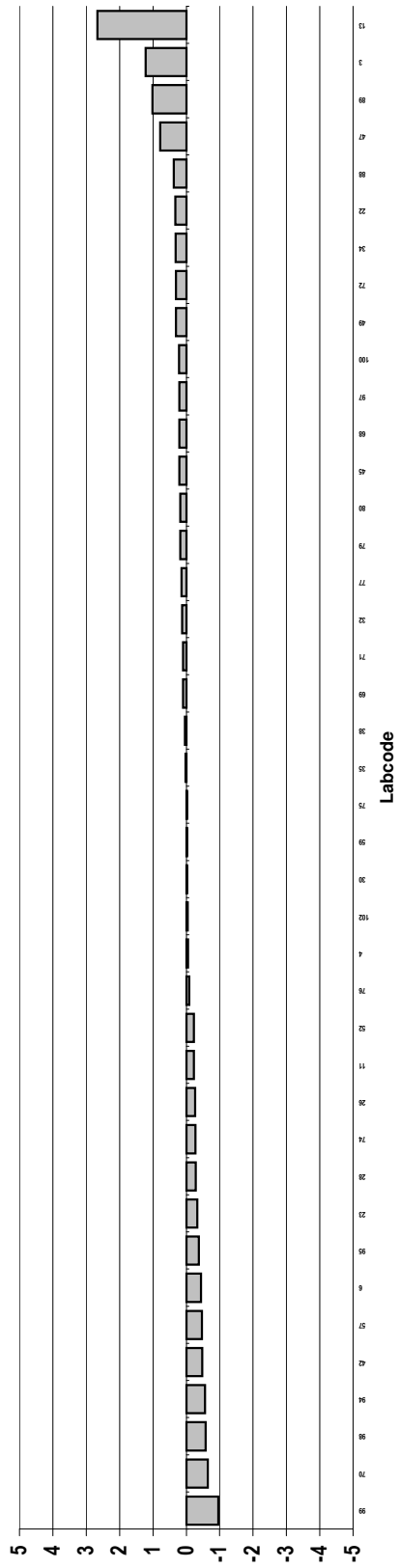
Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.1
Relative standard deviation, %	8.6
No. of values reported	41
No. of values removed	1
No. of reported non-detects	0

BDE 47



Z-score: BDE 47



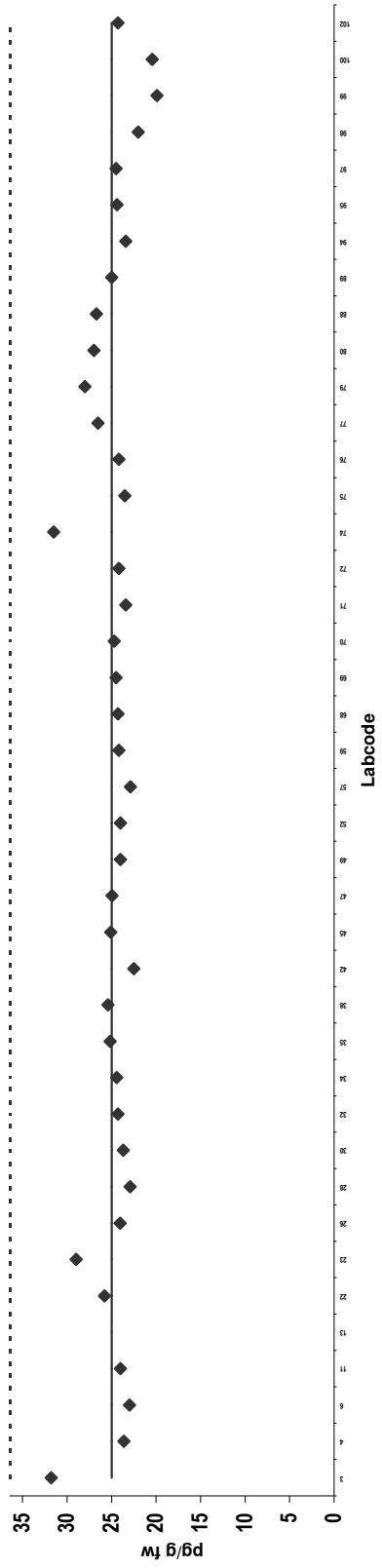
Analyte solution
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	32				
4	24				
6	23				
11	24				
13	42	Outlier			
22	26				
23	29				
26	24				
28	23				
30	24				
32	24				
34	24				
35	25				
38	25				
42	22				
45	25				
47	25				
49	24				
52	24				
57	23				
59	24				
68	24				
69	25				
70	25				
71	23				
72	24				
74	32				
75	24				
76	24				
77	27				
79	28				
80	27				
88	27				
89	25				
94	23				
95	24				
97	25				
98	22				
99	20				
100	20				
102	24				

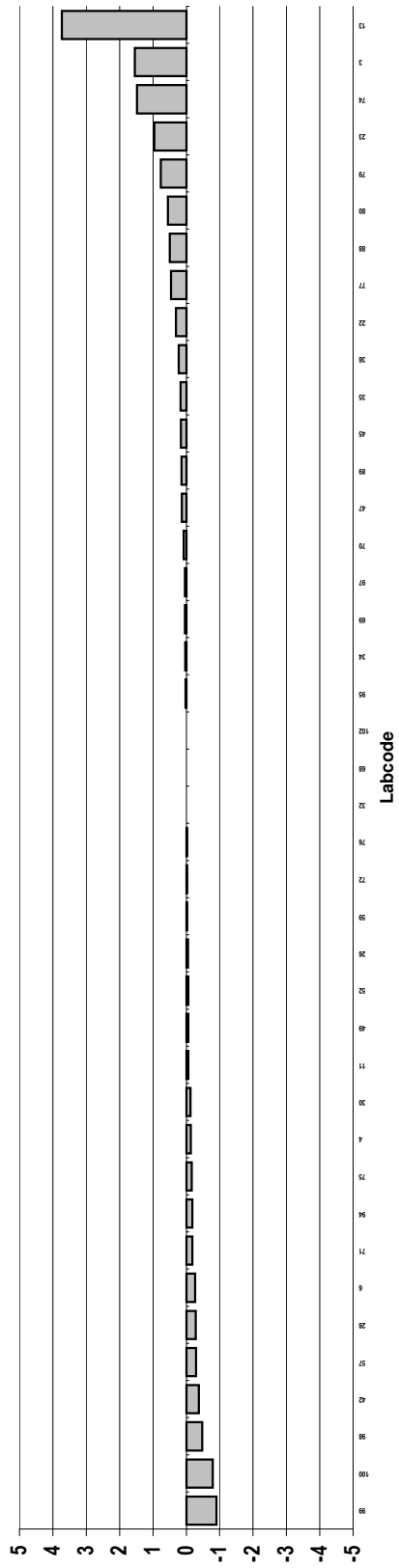
Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	25
Standard deviation, pg/g	2.3
Relative standard deviation, %	9.5
No. of values reported	41
No. of values removed	1
No. of reported non-detects	0

BDE 99



Z-score: BDE 99



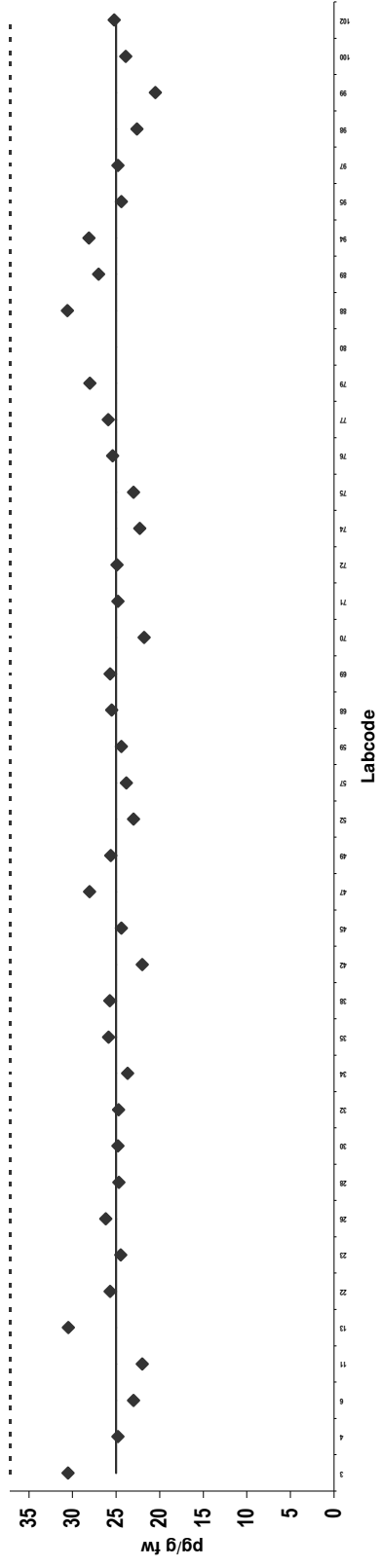
Analyte solution
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	31				
4	25				
6	23				
11	22				
13	30				
22	26				
23	24				
26	26				
28	25				
30	25				
32	25				
34	24				
35	26				
38	26				
42	22				
45	24				
47	28				
49	26				
52	23				
57	24				
59	24				
68	26				
69	26				
70	22				
71	25				
72	25				
74	22				
75	23				
76	25				
77	26				
79	28				
80	40				
88	31				
89	27				
94	28				
95	24				
97	25				
98	23				
99	20				
100	24				
102	25				
				Outlier	

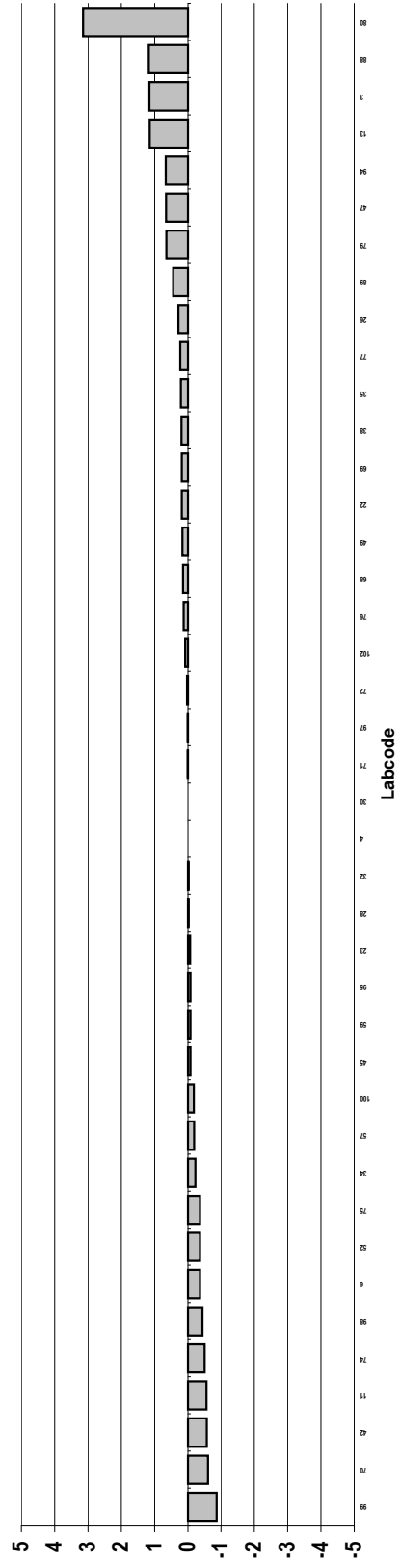
Consensus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.3
Relative standard deviation, %	9.2
No. of values reported	41
No. of values removed	1
No. of reported non-detects	0

BDE 100



Z-score: BDE 100



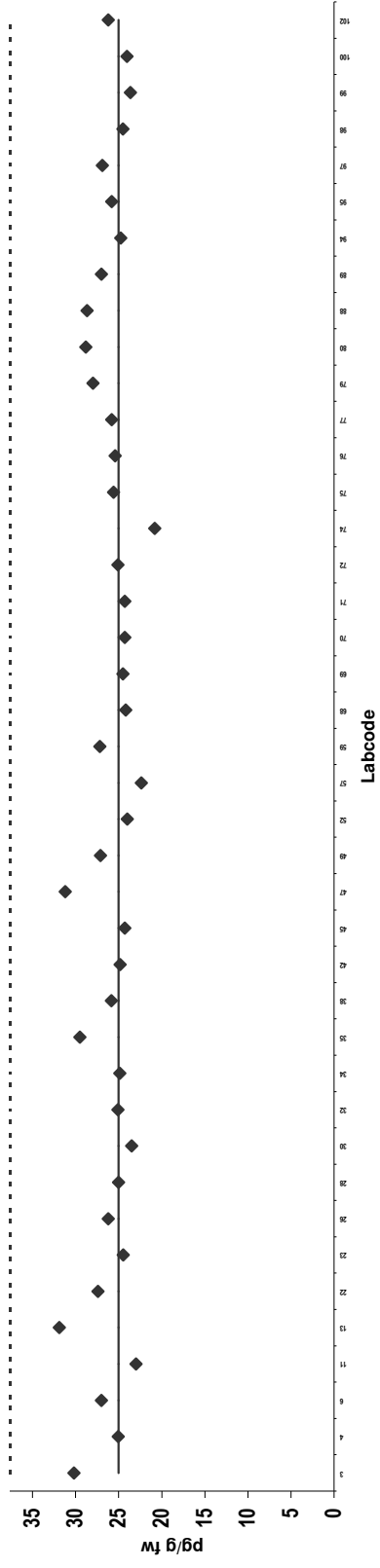
Analyte solution
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	30				
4	25				
6	27				
11	23				
13	32				
22	27				
23	24				
26	26				
28	25				
30	23				
32	25				
34	25				
35	30				
38	26				
42	25				
45	24				
47	31				
49	27				
52	24				
57	22				
59	27				
68	24				
69	25				
70	24				
71	24				
72	25				
74	21				
75	26				
76	25				
77	26				
79	28				
80	29				
88	29				
89	27				
94	25				
95	26				
97	27				
98	25				
99	24				
100	24				
102	26				

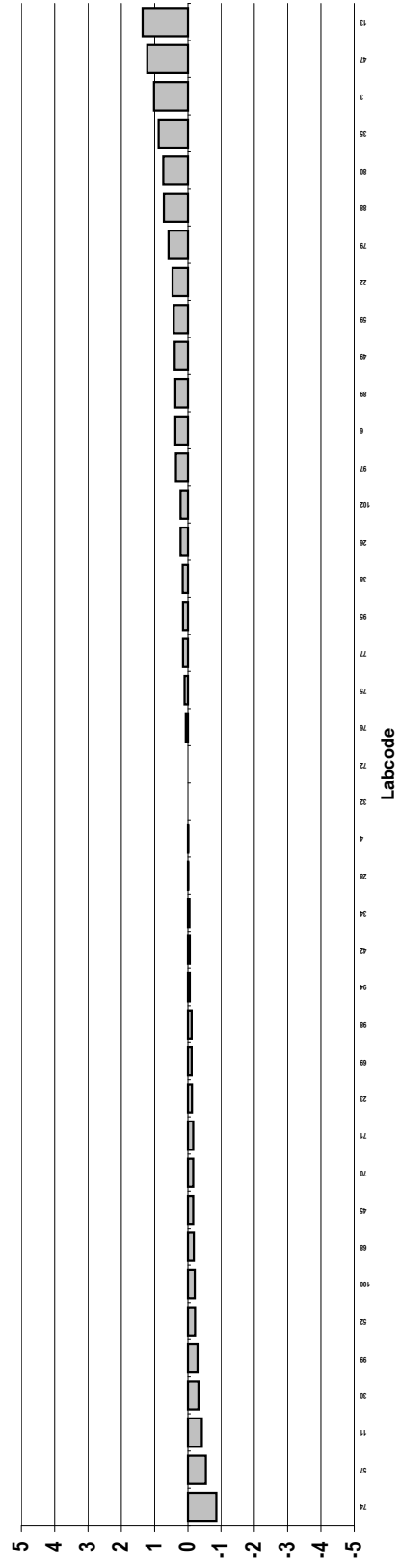
Consensus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	26
Standard deviation, pg/g	2.3
Relative standard deviation, %	8.9
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0

BDE 153



Z-score: BDE 153



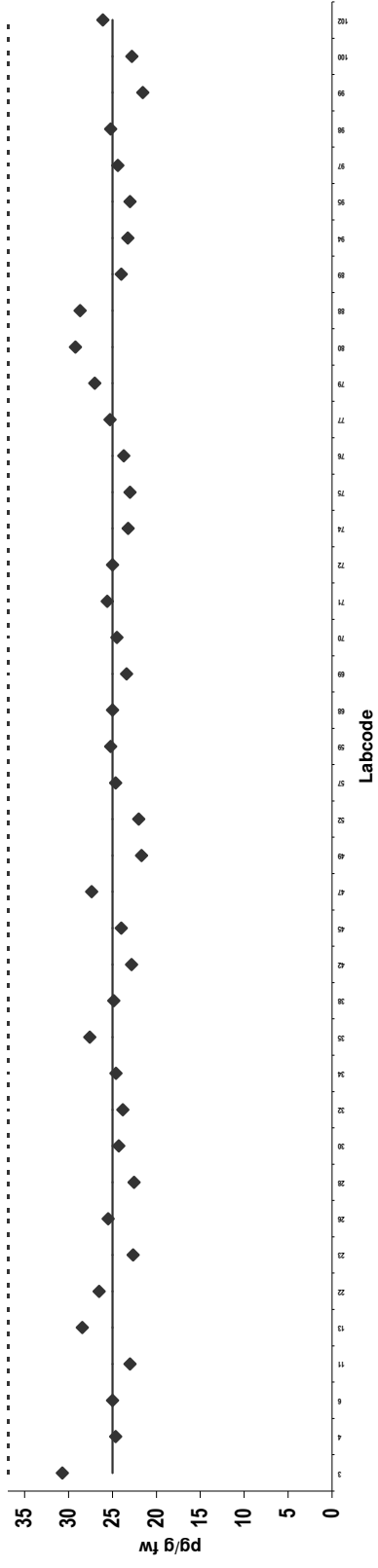
Analyte solution
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	31				
4	25				
6	25				
11	23				
13	28				
22	27				
23	23				
26	25				
28	23				
30	24				
32	24				
34	25				
35	28				
38	25				
42	23				
45	24				
47	27				
49	22				
52	22				
57	25				
59	25				
68	25				
69	23				
70	25				
71	26				
72	25				
74	23				
75	23				
76	24				
77	25				
79	27				
80	29				
88	29				
89	24				
94	23				
95	23				
97	24				
98	25				
99	22				
100	23				
102	26				

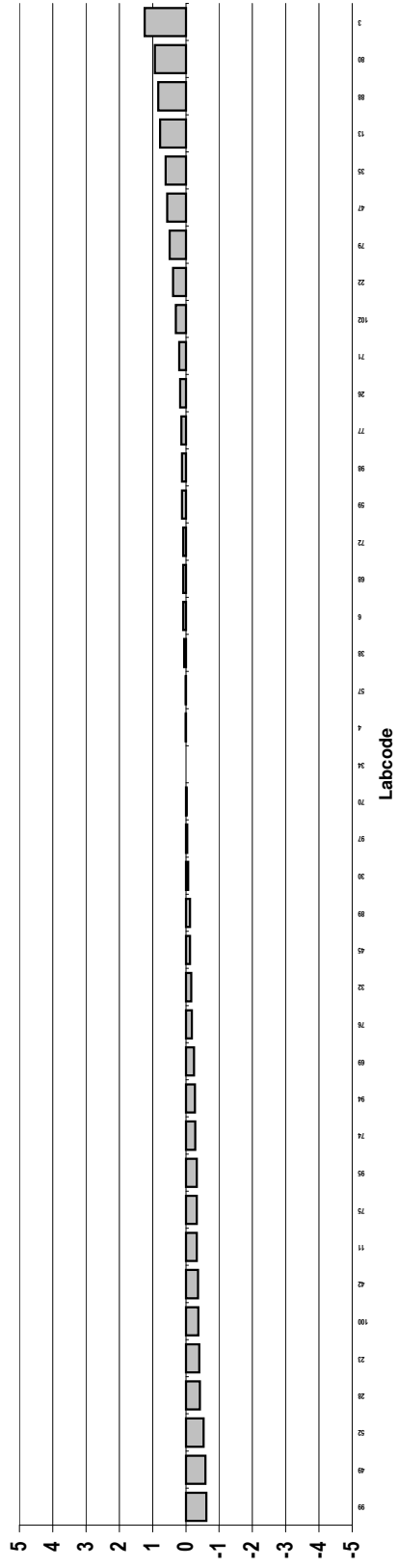
Consensus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.1
Relative standard deviation, %	8.4
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0

BDE 154



Z-score: BDE 154



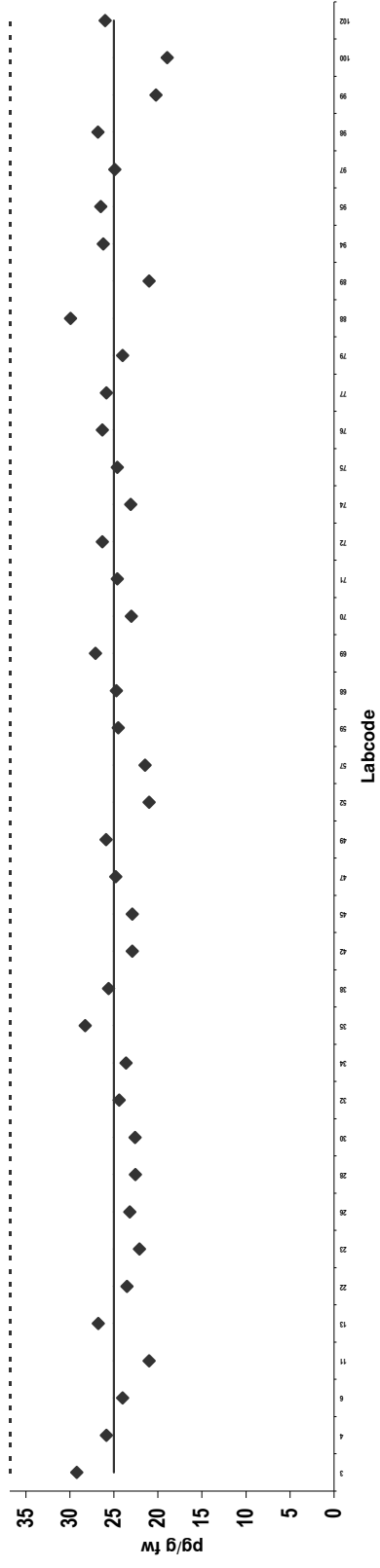
Analyte solution
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	29				
4	26				
6	24				
11	21				
13	27				
22	24				
23	22				
26	23				
28	23				
30	23				
32	24				
34	24				
35	28				
38	26				
42	23				
45	23				
47	25				
49	26				
52	21				
57	21				
59	25				
68	25				
69	27				
70	23				
71	25				
72	26				
74	23				
75	25				
76	26				
77	26				
79	24				
88	30				
89	21				
94	26				
95	27				
97	25				
98	27				
99	20				
100	19				
102	26				

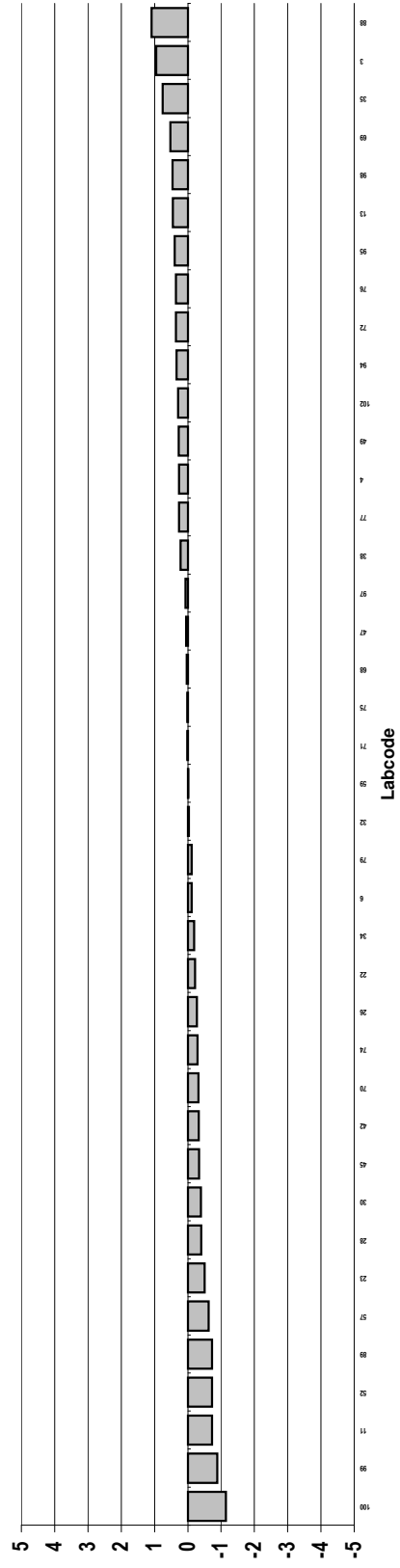
Consensus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	24
Standard deviation, pg/g	2.4
Relative standard deviation, %	9.9
No. of values reported	40
No. of values removed	0
No. of reported non-detects	0

BDE 183



Z-score: BDE 183

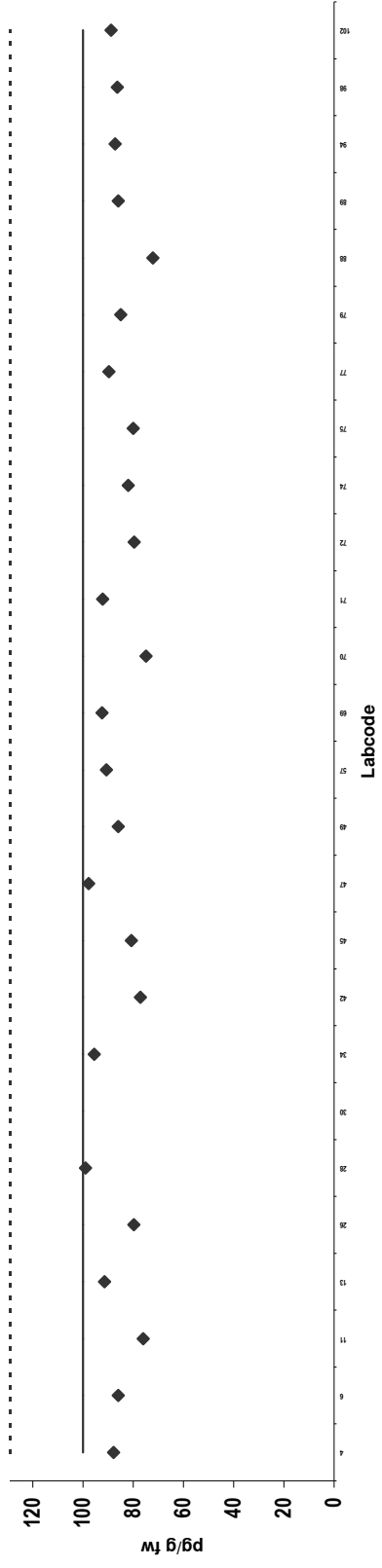


Analyte solution
Congener: BDE 209

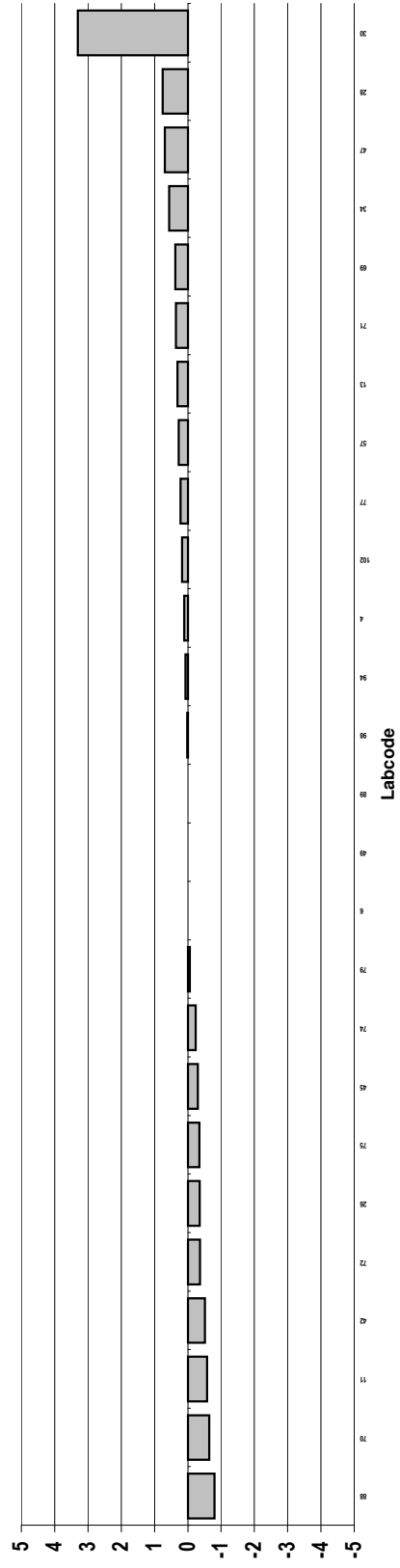
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	88				
6	86				
11	76				
13	91				
26	80				
28	99				
30	143				
34	96				
42	77				
45	81				
47	98				
49	86				
57	91				
69	93				
70	75				
71	92				
72	80				
74	82				
75	80				
77	90				
79	85				
88	72				
89	86				
94	87				
98	86				
102	89				
		Outlier			

Consensus statistics	
Consensus median, pg/g	86
Median all values pg/g	86
Consensus mean, pg/g	86
Standard deviation, pg/g	7.1
Relative standard deviation, %	8.3
No. of values reported	26
No. of values removed	1
No. of reported non-detects	0

BDE 209



Z-score: BDE 209

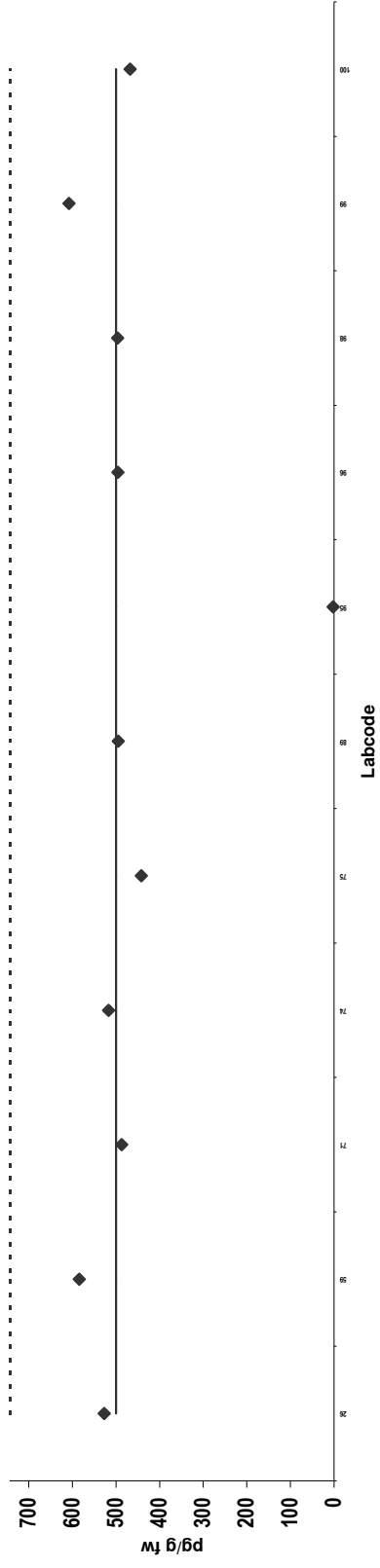


Analyte solution
Congener: α -HBCD

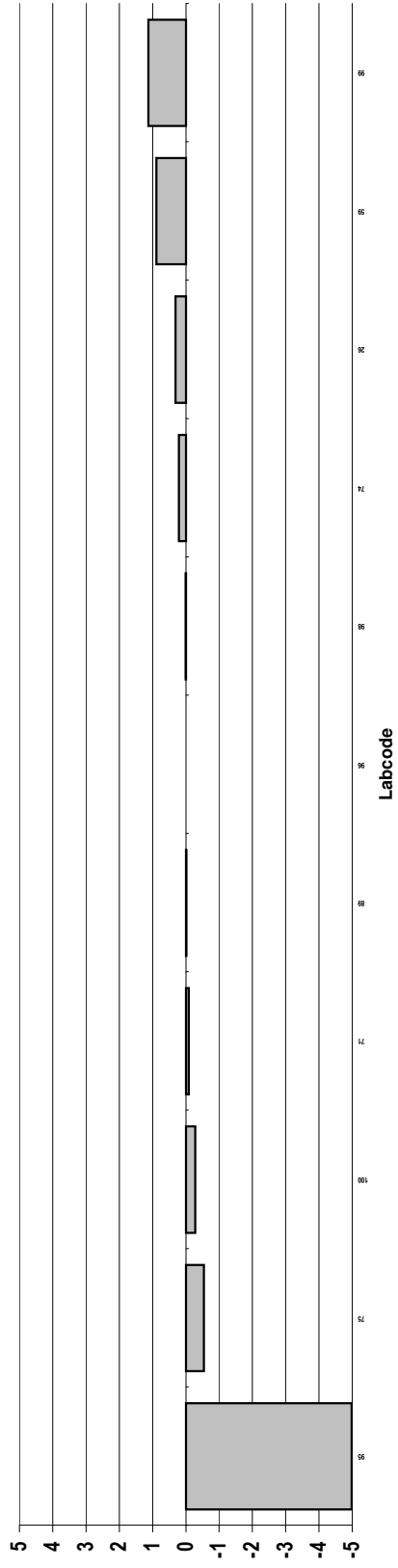
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	527				
59	584				
71	487				
74	517				
75	442				
89	495				
95	1.8	Outlier			
96	496				
98	496				
99	608				
100	468				

Consensus statistics	
Consensus median, pg/g	496
Median all values pg/g	496
Consensus mean, pg/g	512
Standard deviation, pg/g	50
Relative standard deviation, %	9.8
No. of values reported	11
No. of values removed	1
No. of reported non-detects	0

α -HBCD



Z-score: α -HBCD



Appendix 2:

Presentation of results
for beef

Appendix 2: Presentation of results: Beef

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:

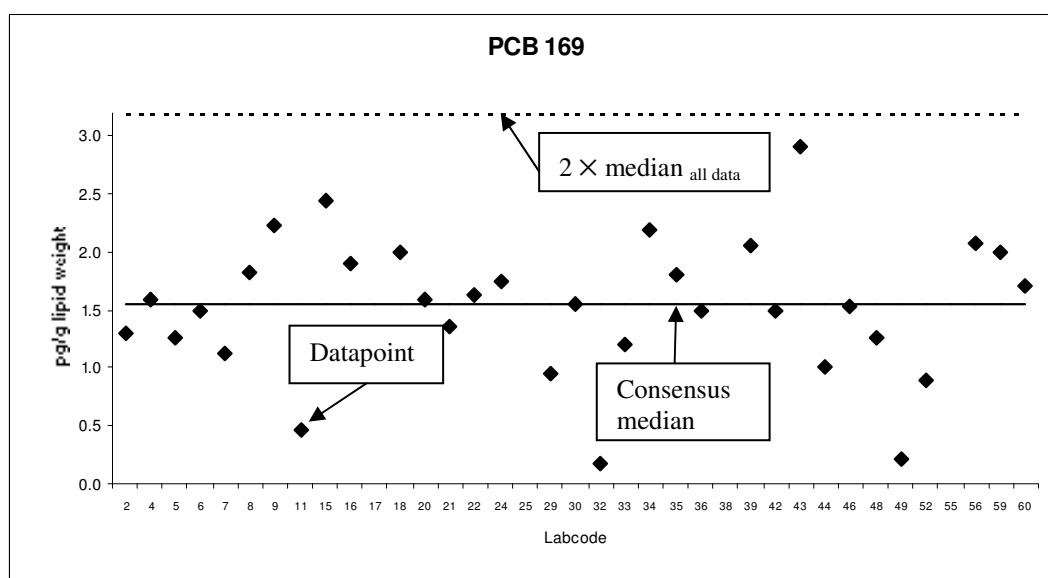
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding $2 \times$ this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

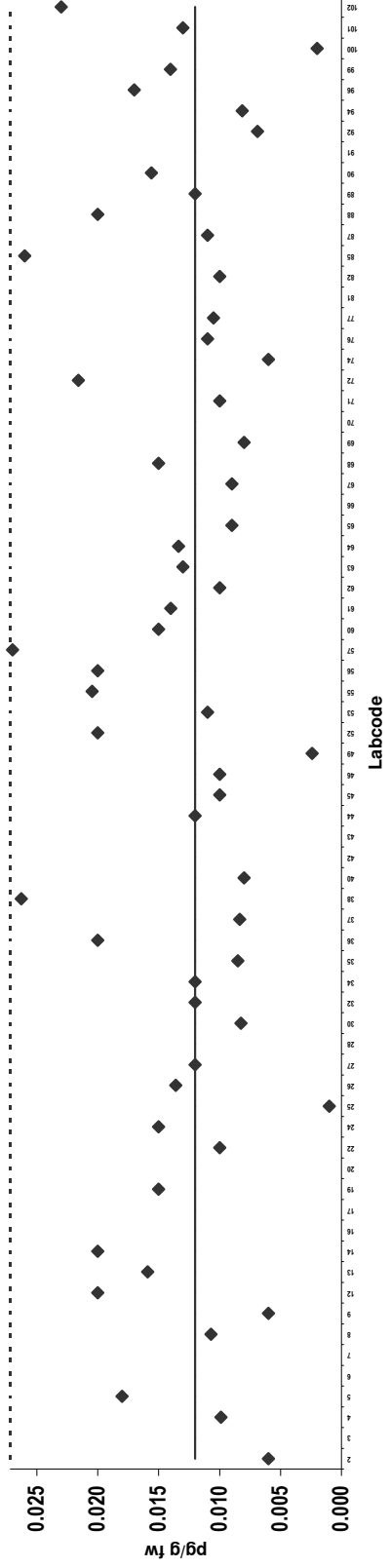
Beef
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.0060	ND	65	0.0090	
3	0.12	Outlier	66	0.050	Outlier,ND
4	0.0099		67	0.0090	
5	0.018	ND	68	0.015	
6	0.040	Outlier,ND	69	0.0080	
7	0.080	Outlier,ND	70	0.031	Outlier,ND
8	0.011		71	0.010	
9	0.0060		72	0.022	
12	0.020		74	0.0060	
13	0.016		76	0.011	
14	0.020		77	0.011	
16	0.054		81	0.14	Outlier
17	0.19	Outlier	82	0.010	
19	0.015	Outlier	85	0.026	ND
20	0.50	Outlier,ND	87	0.011	
22	0.010		88	0.020	
24	0.015	ND	89	0.012	
25	0.0010	ND	90	0.016	
26	0.014	ND	91	0.033	Outlier,ND
27	0.012	ND	92	0.0069	ND
28	0.30	Outlier	94	0.0081	
30	0.0083		96	0.017	ND
32	0.012		99	0.014	
34	0.012		100	0.020	ND
35	0.0085		101	0.013	
36	0.020	ND	102	0.023	
37	0.0083	ND			
38	0.026				
40	0.0080	ND			
42	0.038	Outlier,ND			
43	0.049	Outlier,ND			
44	0.012				
45	0.010	ND			
46	0.010	ND			
49	0.0024	ND			
52	0.020	ND			
53	0.011	ND			
55	0.020	ND			
56	0.020	ND			
57	0.027	ND			
60	0.015	ND			
61	0.014	ND			
62	0.010	ND			
63	0.013	ND			
64	0.013	ND			

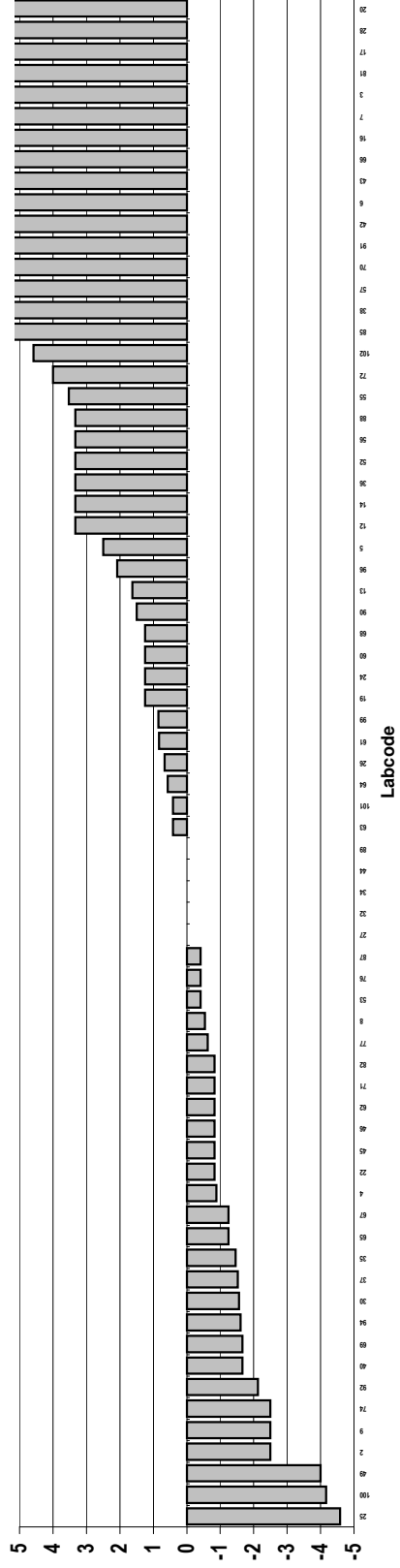
Consensus statistics

Consensus median, pg/g	0.012
Median all values pg/g	0.014
Consensus mean, pg/g	0.013
Standard deviation, pg/g	0.0059
Relative standard deviation, %	45
No. of values reported	71
No. of values removed	13
No. of reported non-detects	30

2,3,7,8 TCDD



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



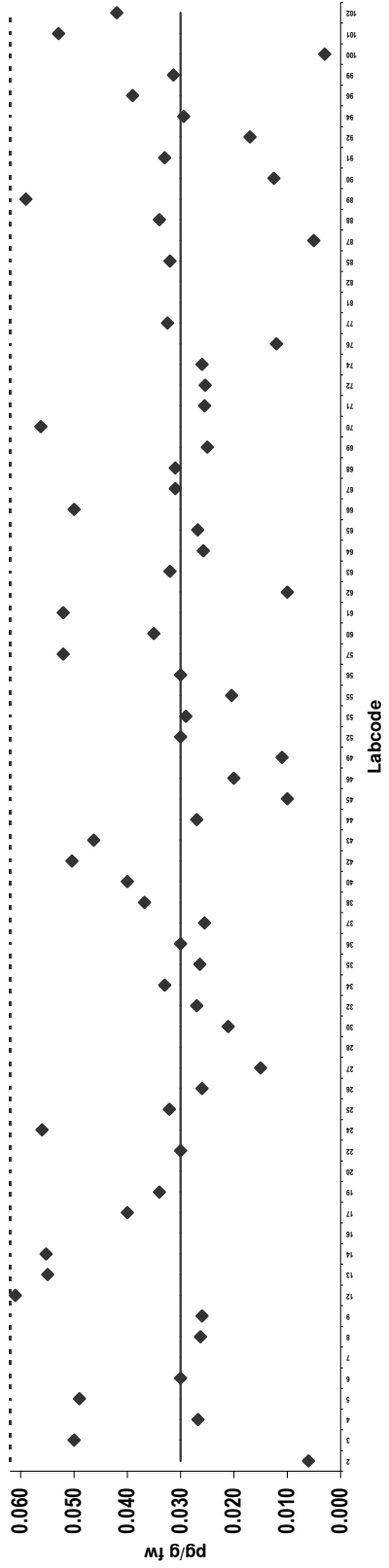
Beef
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.0060	ND	65	0.027	
3	0.050	ND	66	0.050	ND
4	0.027		67	0.031	
5	0.049	ND	68	0.031	
6	0.030	ND	69	0.025	
7	0.16	Outlier	70	0.056	ND
8	0.026		71	0.026	
9	0.026		72	0.025	
12	0.061		74	0.026	
13	0.055	ND	76	0.012	
14	0.055		77	0.032	
16	1.3	Outlier	81	0.26	Outlier
17	0.040		82	0.074	Outlier
19	0.034		85	0.032	ND
20	0.50	Outlier,ND	87	0.0050	ND
22	0.030		88	0.034	
24	0.056		89	0.059	
25	0.032		90	0.013	ND
26	0.026		91	0.033	
27	0.015	ND	92	0.017	ND
28	0.12	Outlier,ND	94	0.029	
30	0.021		96	0.039	
32	0.027		99	0.031	
34	0.033		100	0.030	
35	0.026		101	0.053	ND
36	0.030		102	0.042	
37	0.025				
38	0.037				
40	0.040	ND			
42	0.050	ND			
43	0.046	ND			
44	0.027				
45	0.010	ND			
46	0.020				
49	0.011	ND			
52	0.030				
53	0.029				
55	0.020	ND			
56	0.030				
57	0.052				
60	0.035				
61	0.052				
62	0.010	ND			
63	0.032	ND			
64	0.026				

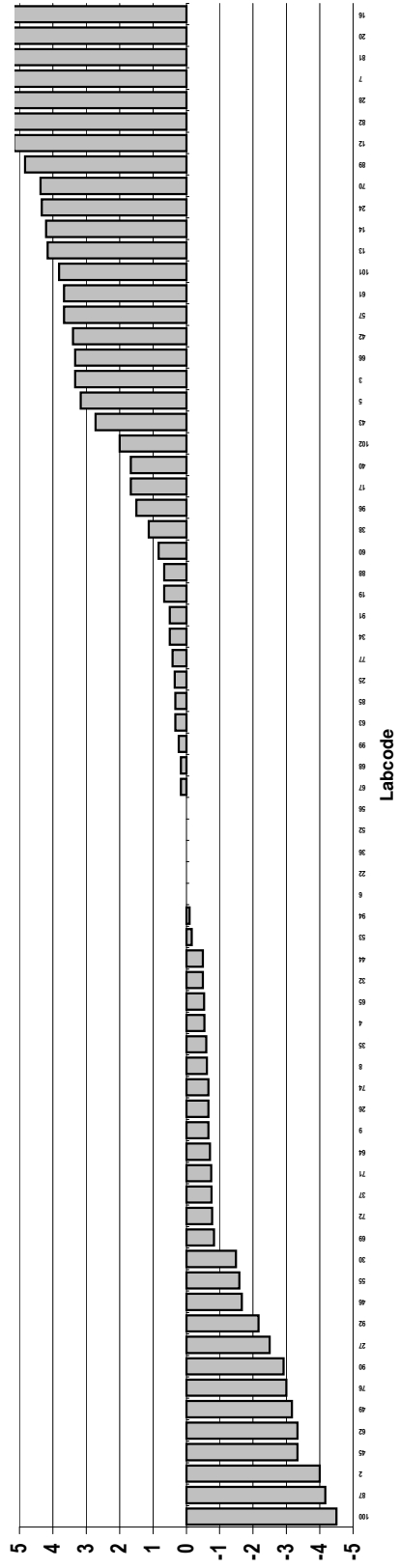
Consensus statistics

Consensus median, pg/g	0.030
Median all values pg/g	0.031
Consensus mean, pg/g	0.032
Standard deviation, pg/g	0.014
Relative standard deviation, %	44
No. of values reported	71
No. of values removed	6
No. of reported non-detects	23

1,2,3,7,8 PeCDD



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



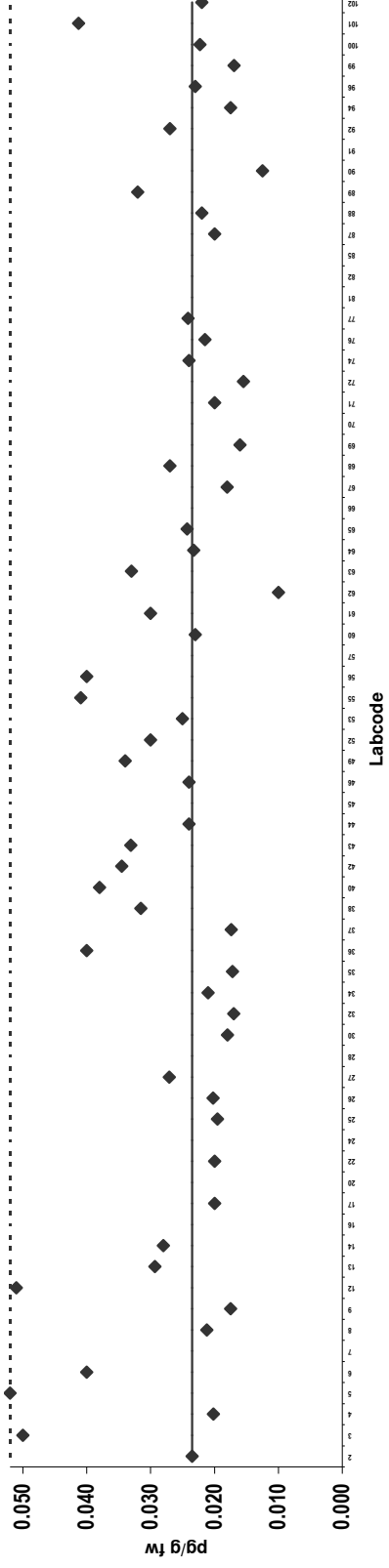
Beef
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.024		66	0.24	Outlier
3	0.050	ND	67	0.018	
4	0.020		68	0.027	
5	0.052	ND	69	0.016	
6	0.040	ND	70	0.070	Outlier,ND
7	0.080	Outlier,ND	71	0.020	
8	0.021		72	0.015	
9	0.018		74	0.024	
12	0.051		76	0.022	
13	0.029		77	0.024	
14	0.028		81	0.15	Outlier,ND
16	0.41	Outlier	82	0.068	Outlier
17	0.020		85	0.059	Outlier,ND
20	1.0	Outlier,ND	87	0.020	
22	0.020		88	0.022	
24	0.058	Outlier	89	0.032	
25	0.020		90	0.013	ND
26	0.020		91	0.098	Outlier
27	0.027		92	0.027	ND
28	0.071	Outlier,ND	94	0.017	
30	0.018		96	0.023	
32	0.017		99	0.017	
34	0.021		100	0.022	
35	0.017		101	0.041	
36	0.040		102	0.022	
37	0.017				
38	0.032				
40	0.038				
42	0.035				
43	0.033	ND			
44	0.024				
45	0.070	Outlier			
46	0.024				
49	0.034				
52	0.030				
53	0.025				
55	0.041	ND			
56	0.040				
57	0.091	Outlier,ND			
60	0.023				
61	0.030				
62	0.010	ND			
63	0.033	ND			
64	0.023				
65	0.024				

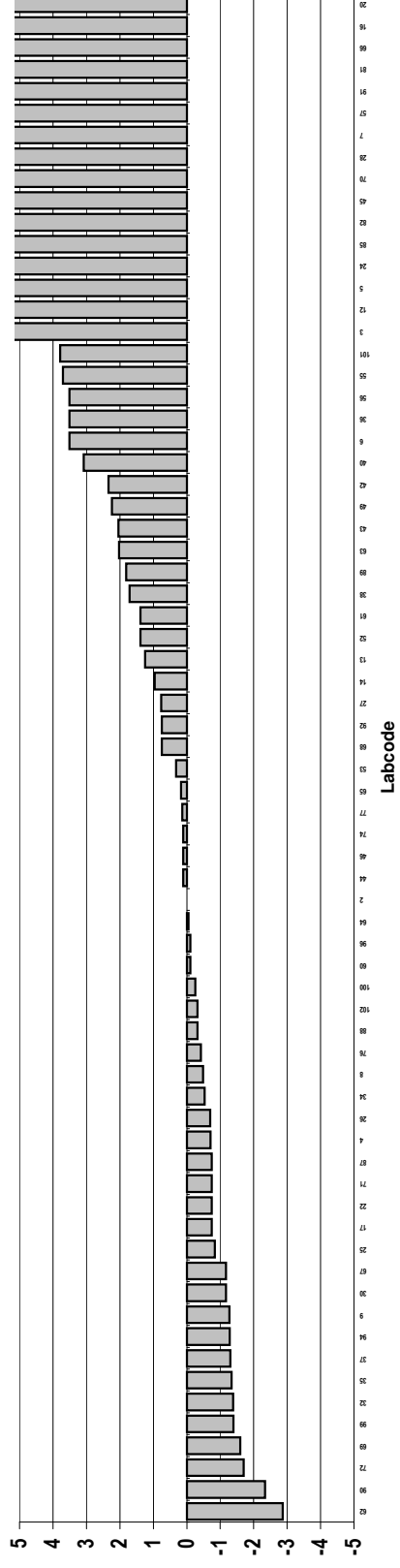
Consensus statistics

Consensus median, pg/g	0.024
Median all values pg/g	0.026
Consensus mean, pg/g	0.026
Standard deviation, pg/g	0.0095
Relative standard deviation, %	36
No. of values reported	70
No. of values removed	13
No. of reported non-detects	16

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



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



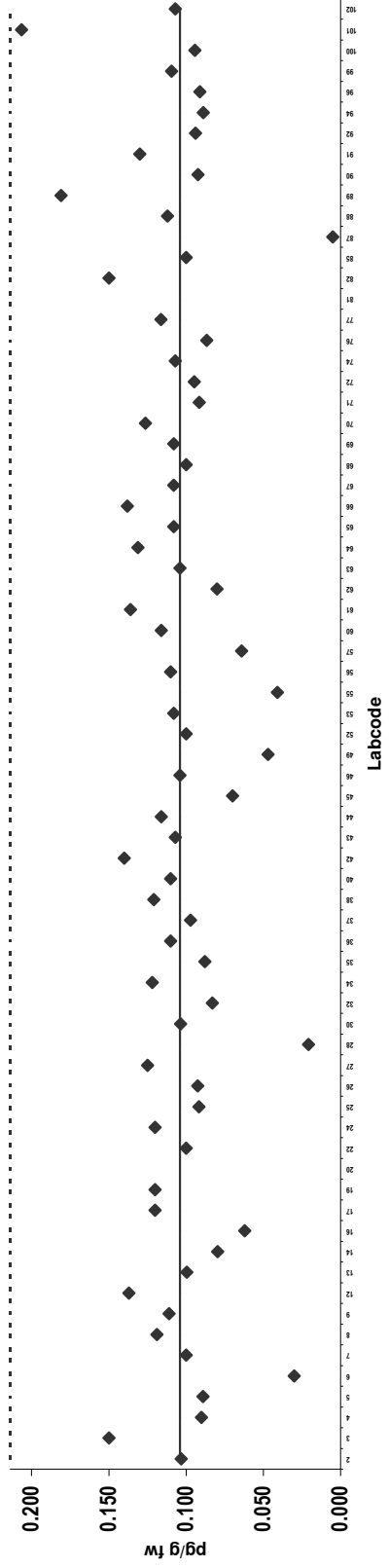
Beef
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.10		65	0.11	
3	0.15		66	0.14	
4	0.090		67	0.11	
5	0.089		68	0.10	
6	0.030	ND	69	0.11	
7	0.10		70	0.13	
8	0.12		71	0.092	
9	0.11		72	0.095	
12	0.14		74	0.11	
13	0.099		76	0.087	
14	0.080		77	0.12	
16	0.062		81	0.29	Outlier
17	0.12		82	0.15	
19	0.12		85	0.10	
20	1.0		87	0.0050	ND
22	0.10	Outlier,ND	88	0.11	
24	0.12		89	0.18	
25	0.092		90	0.092	
26	0.092		91	0.13	
27	0.13		92	0.094	
28	0.021		94	0.089	
30	0.10		96	0.091	
32	0.083		99	0.11	
34	0.12		100	0.094	
35	0.088		101	0.21	
36	0.11		102	0.11	
37	0.097				
38	0.12				
40	0.11				
42	0.14				
43	0.11				
44	0.12				
45	0.070				
46	0.10				
49	0.047				
52	0.10				
53	0.11				
55	0.041	ND			
56	0.11				
57	0.064				
60	0.12				
61	0.14				
62	0.080				
63	0.10				
64	0.13				

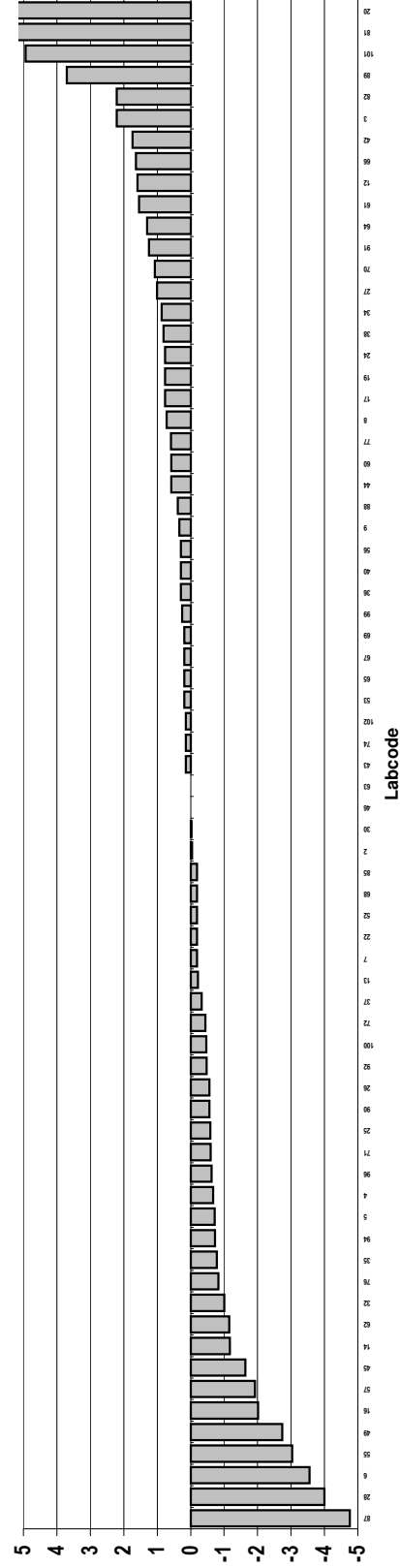
Consensus statistics

Consensus median, pg/g	0.10
Median all values pg/g	0.11
Consensus mean, pg/g	0.10
Standard deviation, pg/g	0.032
Relative standard deviation, %	31
No. of values reported	71
No. of values removed	2
No. of reported non-detects	4

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



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



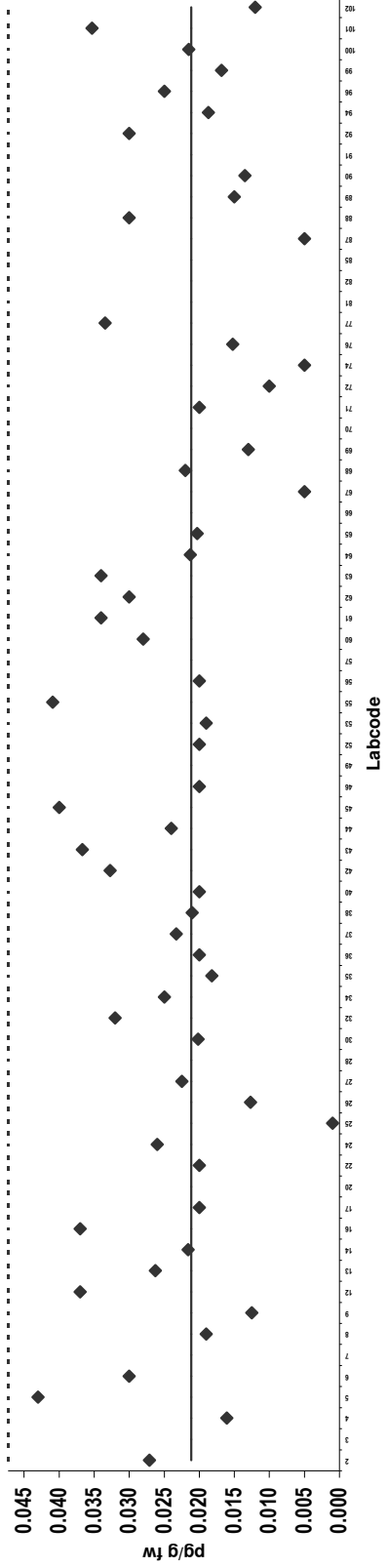
Beef
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.027		66	0.050	Outlier,ND
3	0.050	Outlier,ND	67	0.0050	ND
4	0.016		68	0.022	
5	0.043	ND	69	0.013	
6	0.030	ND	70	0.069	Outlier,ND
7	0.080	Outlier,ND	71	0.020	
8	0.019		72	0.010	
9	0.013		74	0.0050	ND
12	0.037		76	0.015	
13	0.026		77	0.033	
14	0.022		81	0.30	Outlier
16	0.037	ND	82	0.11	Outlier
17	0.020		85	0.10	Outlier
20	1.0	Outlier,ND	87	0.0050	ND
22	0.020		88	0.030	
24	0.026		89	0.015	
25	0.0010		90	0.014	
26	0.013	ND	91	0.12	
27	0.023		92	0.030	Outlier
28	0.078	Outlier,ND	94	0.019	ND
30	0.020		96	0.025	ND
32	0.032		99	0.017	
34	0.025		100	0.022	
35	0.018		101	0.035	
36	0.020	ND	102	0.012	
37	0.023				
38	0.021				
40	0.020	ND			
42	0.033	ND			
43	0.037	ND			
44	0.024				
45	0.040				
46	0.020				
49	0.054	Outlier			
52	0.020				
53	0.019				
55	0.041	ND			
56	0.020	ND			
57	0.049	Outlier			
60	0.028				
61	0.034				
62	0.030				
63	0.034	ND			
64	0.021				
65	0.020				

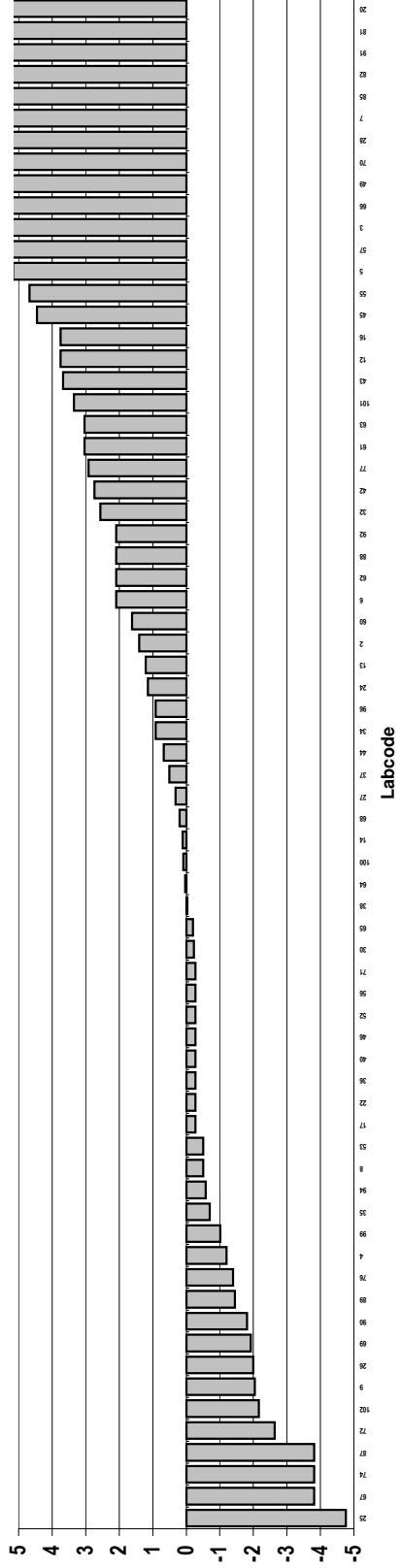
Consensus statistics

Consensus median, pg/g	0.021
Median all values pg/g	0.024
Consensus mean, pg/g	0.023
Standard deviation, pg/g	0.0094
Relative standard deviation, %	41
No. of values reported	70
No. of values removed	12
No. of reported non-detects	22

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



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



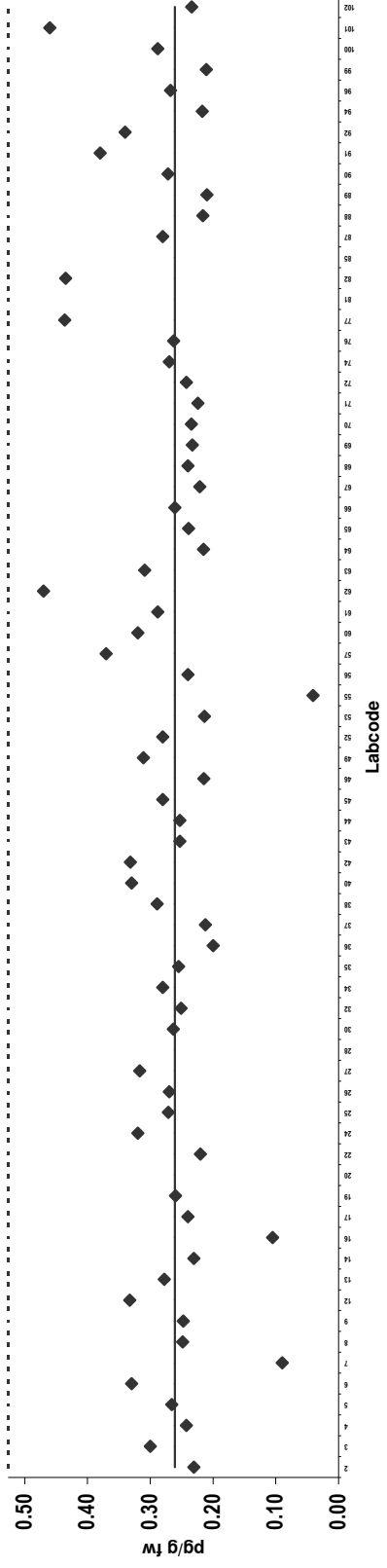
Beef
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.23		65	0.24	
3	0.30		66	0.26	
4	0.24		67	0.22	
5	0.27		68	0.24	
6	0.33		69	0.23	
7	0.090		70	0.23	
8	0.25		71	0.22	
9	0.25		72	0.24	
12	0.33		74	0.27	
13	0.28		76	0.26	
14	0.23		77	0.44	
16	0.11		81	0.62	Outlier
17	0.24		82	0.44	
19	0.26		85	1.6	Outlier
20	1.0		87	0.28	
22	0.22		88	0.22	
24	0.32		89	0.21	
25	0.27		90	0.27	
26	0.27		91	0.38	
27	0.32		92	0.34	
28	2.4		94	0.22	
30	0.26		96	0.27	
32	0.25		99	0.21	
34	0.28		100	0.29	
35	0.25		101	0.46	
36	0.20		102	0.23	
37	0.21				
38	0.29				
40	0.33				
42	0.33				
43	0.25				
44	0.25				
45	0.28				
46	0.22				
49	0.31				
52	0.28				
53	0.21				
55	0.041				
56	0.24				
57	0.37				
60	0.32				
61	0.29				
62	0.47				
63	0.31				
64	0.22				

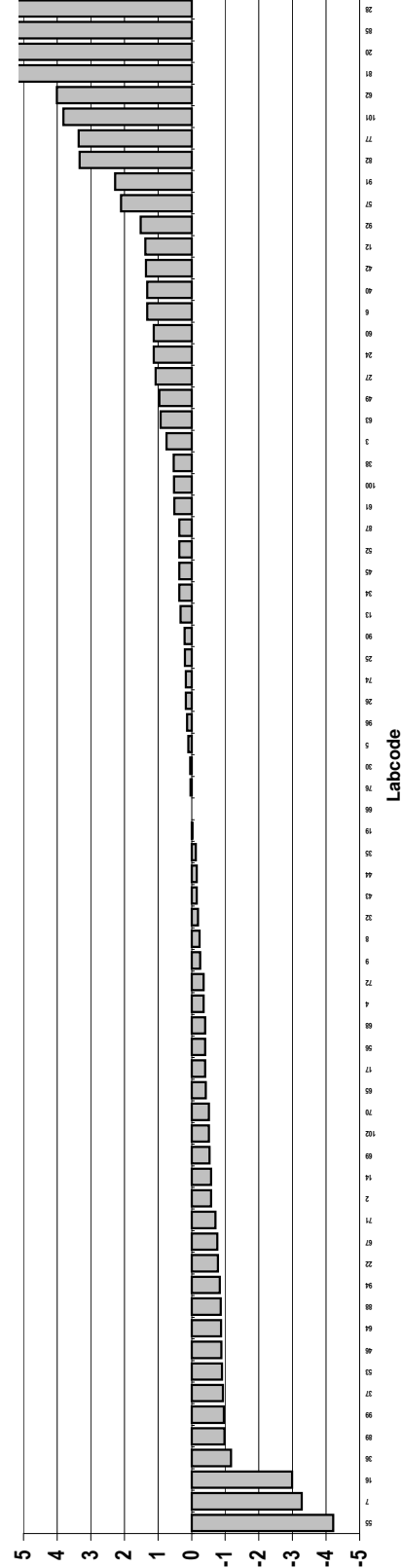
Consensus statistics

Consensus median, pg/g	0.26
Median all values pg/g	0.26
Consensus mean, pg/g	0.27
Standard deviation, pg/g	0.073
Relative standard deviation, %	27
No. of values reported	71
No. of values removed	4
No. of reported non-detects	2

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



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

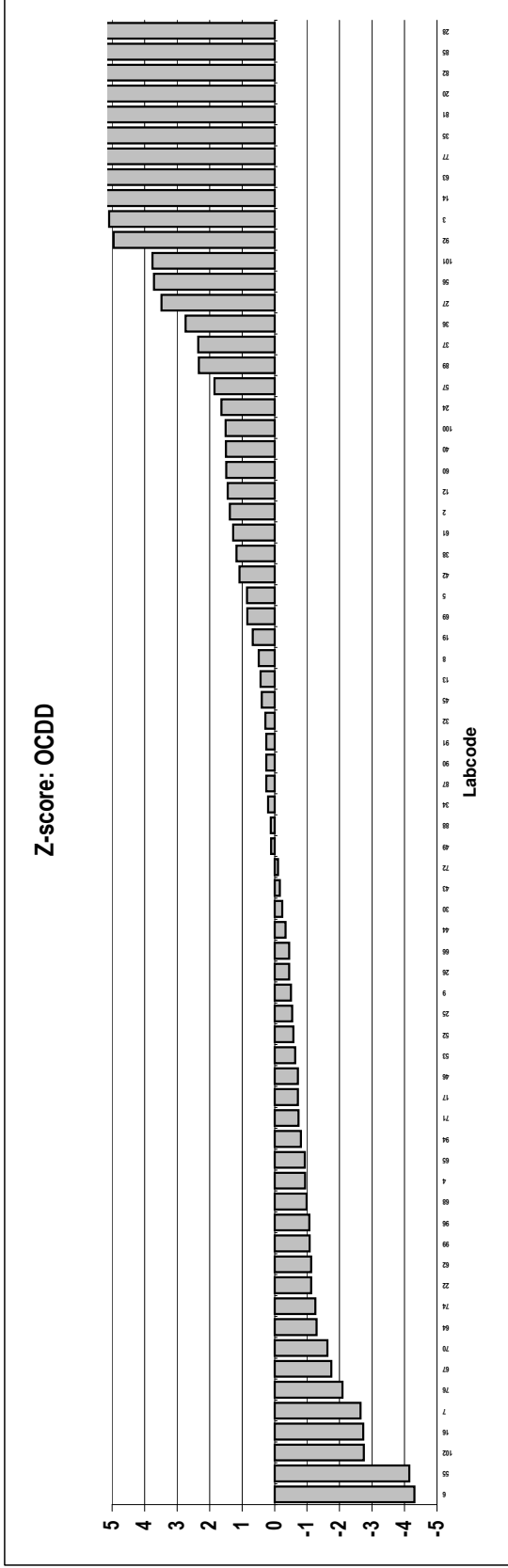
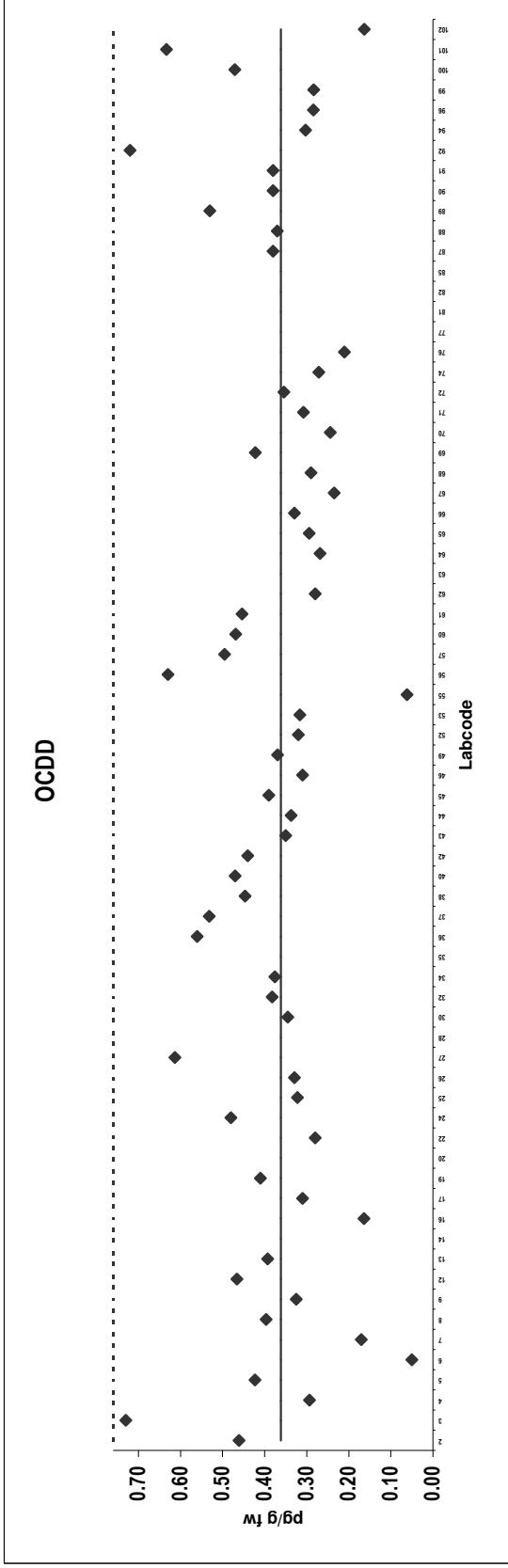


Beef
Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.46		65	0.29	
3	0.73		66	0.33	
4	0.29		67	0.24	
5	0.42		68	0.29	
6	0.050	ND	69	0.42	
7	0.17	ND	70	0.24	ND
8	0.40		71	0.31	
9	0.33		72	0.35	
12	0.47		74	0.27	
13	0.39		76	0.21	
14	0.85		77	0.95	
16	0.16	Outlier	81	1.5	Outlier
17	0.31		82	2.1	Outlier
19	0.41		85	3.4	Outlier
20	2.0	Outlier,ND	87	0.38	
22	0.28		88	0.37	
24	0.48		89	0.53	
25	0.32		90	0.38	
26	0.33		91	0.38	
27	0.61		92	0.72	
28	18	Outlier	94	0.30	
30	0.34		96	0.28	
32	0.38		99	0.28	
34	0.38		100	0.47	
35	1.2	Outlier	101	0.63	
36	0.56		102	0.16	
37	0.53	ND			
38	0.45				
40	0.47				
42	0.44				
43	0.35				
44	0.34				
45	0.39				
46	0.31				
49	0.37				
52	0.32				
53	0.32				
55	0.061	ND			
56	0.63				
57	0.50				
60	0.47				
61	0.45				
62	0.28				
63	0.88	Outlier			
64	0.27				

Consensus statistics

Consensus median, pg/g	0.36
Median all values pg/g	0.38
Consensus mean, pg/g	0.37
Standard deviation, pg/g	0.14
Relative standard deviation, %	36
No. of values reported	71
No. of values removed	9
No. of reported non-detects	6



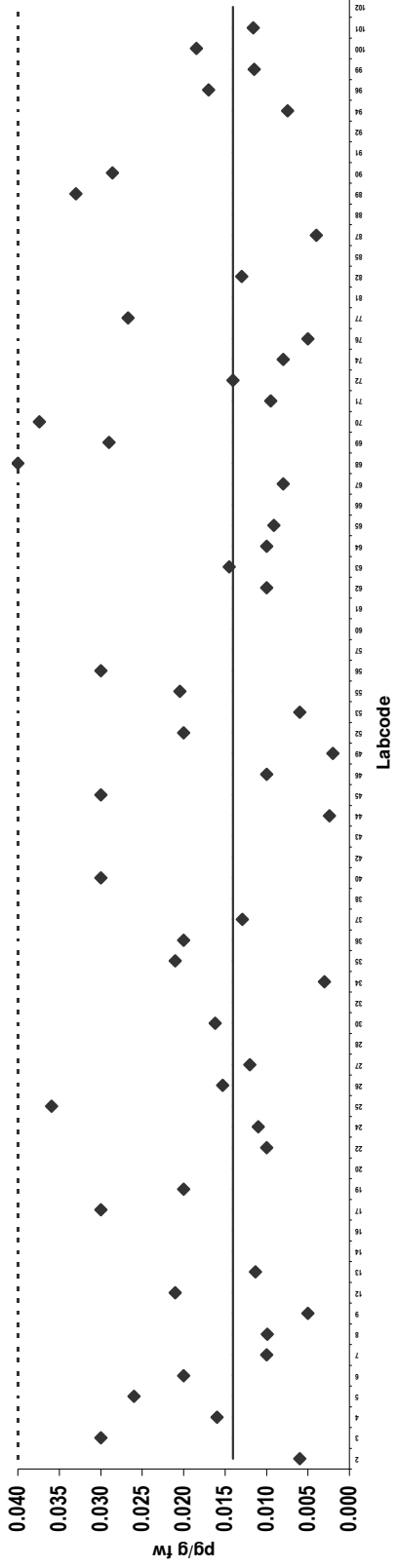
Beef
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.0060	ND	65	0.0091	
3	0.030	ND	66	0.057	Outlier
4	0.016		67	0.0080	
5	0.026		68	0.040	
6	0.020	ND	69	0.029	
7	0.010	ND	70	0.037	
8	0.0099		71	0.0095	
9	0.0050		72	0.014	
12	0.021		74	0.0080	ND
13	0.011		76	0.0050	ND
14	0.18		77	0.027	
16	0.043	Outlier	81	0.21	Outlier
17	0.030	Outlier	82	0.013	
19	0.020		85	0.049	
20	0.50	Outlier,ND	87	0.0040	Outlier,ND
22	0.010		88	0.056	Outlier
24	0.011	ND	89	0.033	
25	0.036		90	0.029	
26	0.015		91	0.10	Outlier
27	0.012	ND	92	0.048	Outlier
28	1.5	Outlier	94	0.0075	
30	0.016		96	0.017	ND
32	0.074	Outlier	99	0.011	
34	0.0030	ND	100	0.018	
35	0.021		101	0.012	
36	0.020		102	0.048	Outlier
37	0.013				
38	0.042	Outlier			
40	0.030				
42	0.080				
43	0.065	Outlier,ND			
44	0.0024	ND			
45	0.030				
46	0.010	ND			
49	0.0020	ND			
52	0.020	ND			
53	0.0060				
55	0.020	ND			
56	0.030				
57	0.060	Outlier			
60	0.076	Outlier			
61	0.045	Outlier			
62	0.010	ND			
63	0.015	ND			
64	0.010	ND			

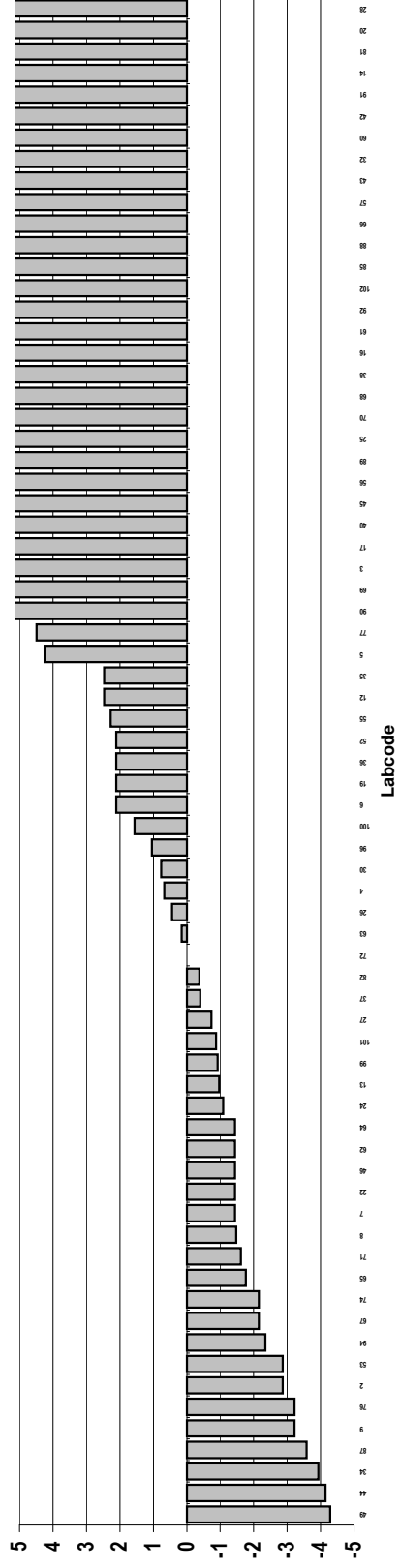
Consensus statistics

Consensus median, pg/g	0.014
Median all values pg/g	0.020
Consensus mean, pg/g	0.017
Standard deviation, pg/g	0.0099
Relative standard deviation, %	60
No. of values reported	71
No. of values removed	18
No. of reported non-detects	21

2,3,7,8 TCDF



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



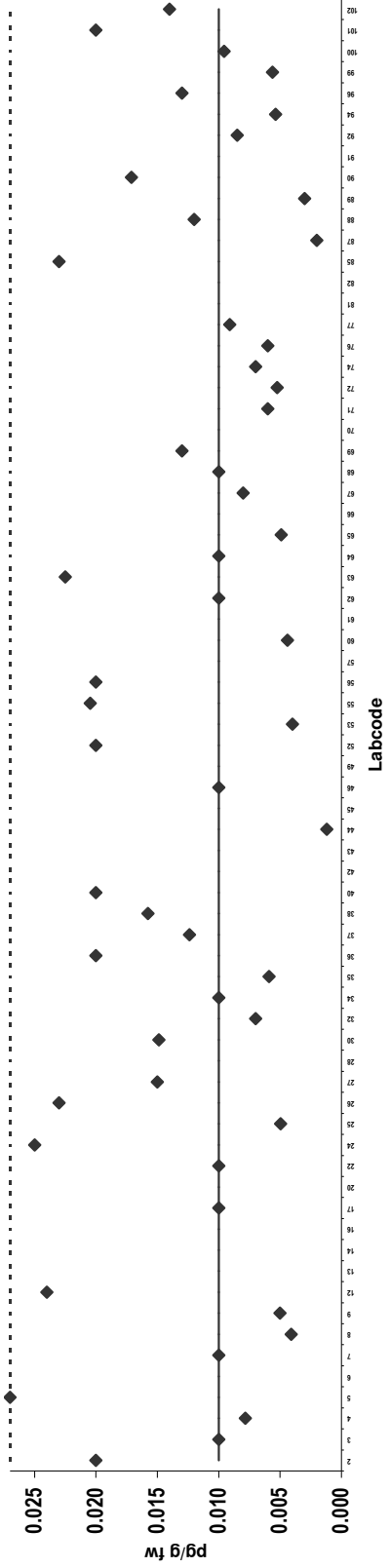
Beef
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.020		66	0.050	Outlier,ND
3	0.010	ND	67	0.0080	
4	0.0078		68	0.010	ND
5	0.027	ND	69	0.013	
6	0.030	Outlier,ND	70	0.037	Outlier
7	0.010	ND	71	0.0060	ND
8	0.0041		72	0.0052	
9	0.0050	ND	74	0.0070	ND
12	0.024		76	0.0060	
13	0.032	Outlier,ND	77	0.0091	
14	0.040	Outlier	81	0.19	Outlier
16	0.061	Outlier	82	0.038	Outlier
17	0.010		85	0.023	ND
20	0.50	Outlier,ND	87	0.0020	ND
22	0.010	ND	88	0.012	
24	0.025		89	0.0030	ND
25	0.0050		90	0.017	
26	0.023	ND	91	0.034	Outlier
27	0.015	ND	92	0.0085	ND
28	0.31	Outlier	94	0.0054	
30	0.015		96	0.013	ND
32	0.0070	ND	99	0.0056	ND
34	0.010		100	0.0096	
35	0.0059		101	0.020	
36	0.020	ND	102	0.014	
37	0.012	ND			
38	0.016				
40	0.020	ND			
42	0.035	Outlier,ND			
43	0.046	Outlier,ND			
44	0.0012	ND			
45	0.060	Outlier			
46	0.010	ND			
49	0.045	Outlier			
52	0.020	ND			
53	0.0040				
55	0.020	ND			
56	0.020	ND			
57	0.083	Outlier,ND			
60	0.0044	ND			
61	0.031	Outlier			
62	0.010	ND			
63	0.023	ND			
64	0.010	ND			
65	0.0049				

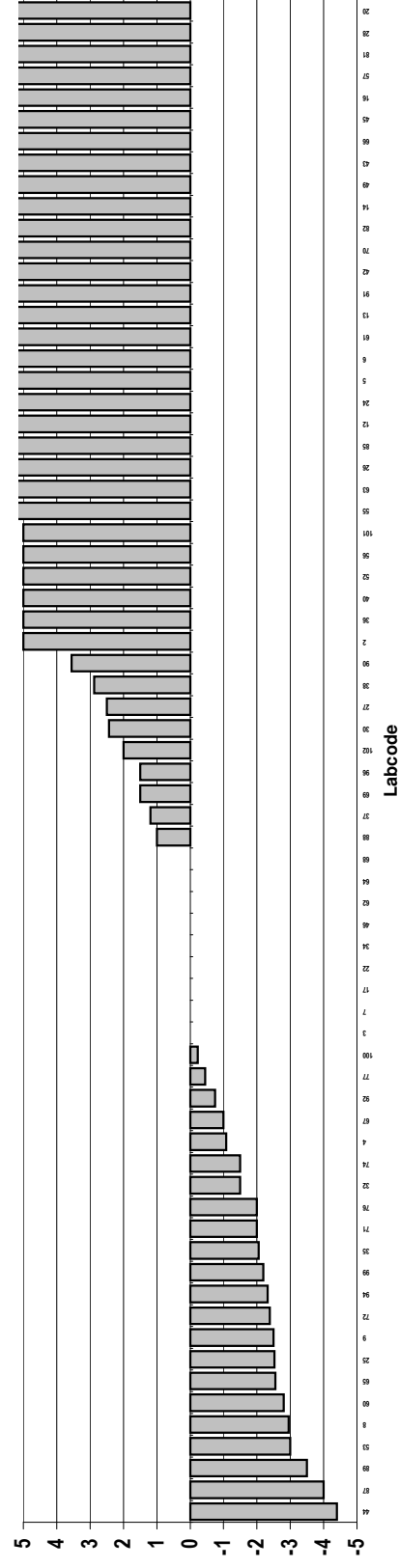
Consensus statistics

Consensus median, pg/g	0.010
Median all values pg/g	0.014
Consensus mean, pg/g	0.012
Standard deviation, pg/g	0.0068
Relative standard deviation, %	58
No. of values reported	70
No. of values removed	17
No. of reported non-detects	36

1,2,3,7,8 PeCDF



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



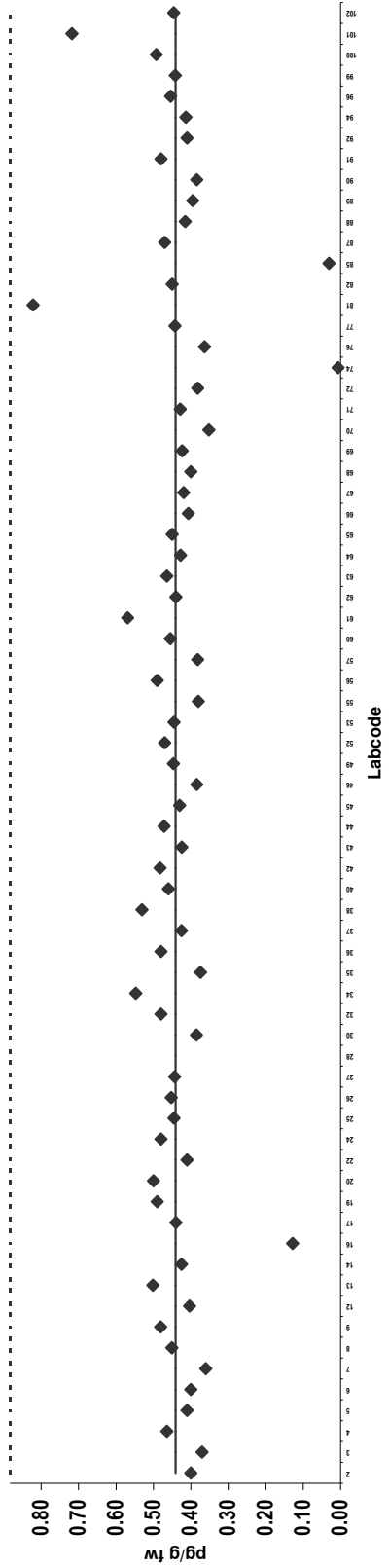
Beef
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.40		65	0.45	
3	0.37		66	0.41	
4	0.46		67	0.42	
5	0.41		68	0.40	
6	0.40		69	0.42	
7	0.36		70	0.35	
8	0.45		71	0.43	
9	0.48		72	0.38	
12	0.40		74	0.0070	ND
13	0.50		76	0.36	
14	0.42		77	0.44	
16	0.13		81	0.82	
17	0.44		82	0.45	
19	0.49		85	0.031	ND
20	0.50		87	0.47	
22	0.41	ND	88	0.42	
24	0.48		89	0.40	
25	0.44		90	0.38	
26	0.45		91	0.48	
27	0.44		92	0.41	
28	1.0	Outlier	94	0.41	
30	0.39		96	0.45	
32	0.48		99	0.44	
34	0.55		100	0.49	
35	0.37		101	0.72	
36	0.48		102	0.45	
37	0.43				
38	0.53				
40	0.46				
42	0.48				
43	0.42				
44	0.47				
45	0.43				
46	0.38				
49	0.45				
52	0.47				
53	0.45				
55	0.38				
56	0.49				
57	0.38				
60	0.46				
61	0.57				
62	0.44				
63	0.46				
64	0.43				

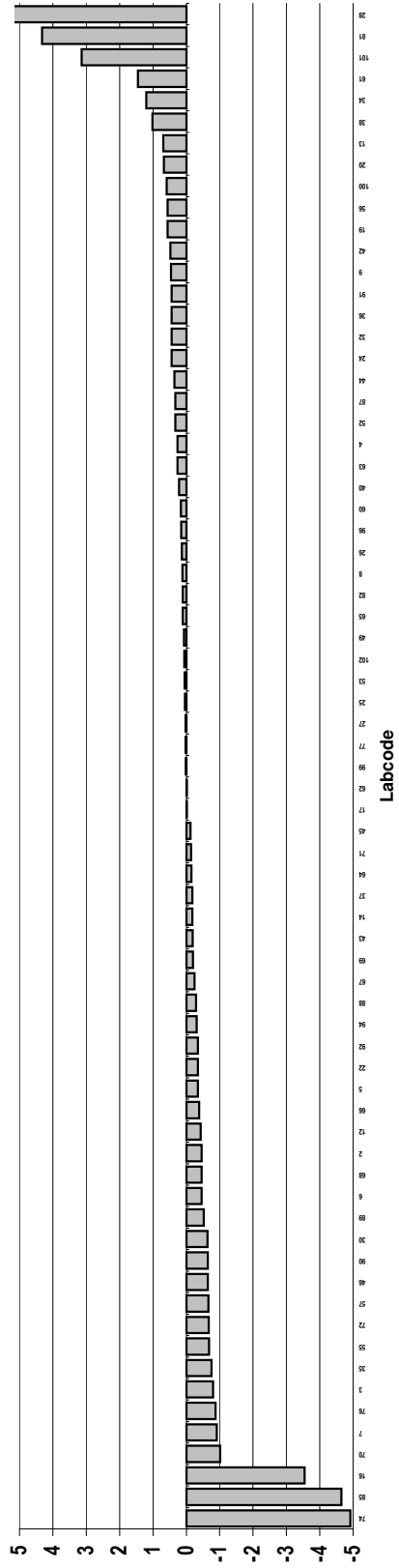
Consensus statistics

Consensus median, pg/g	0.44
Median all values pg/g	0.44
Consensus mean, pg/g	0.43
Standard deviation, pg/g	0.11
Relative standard deviation, %	25
No. of values reported	71
No. of values removed	1
No. of reported non-detects	3

2,3,4,7,8 PeCDF



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



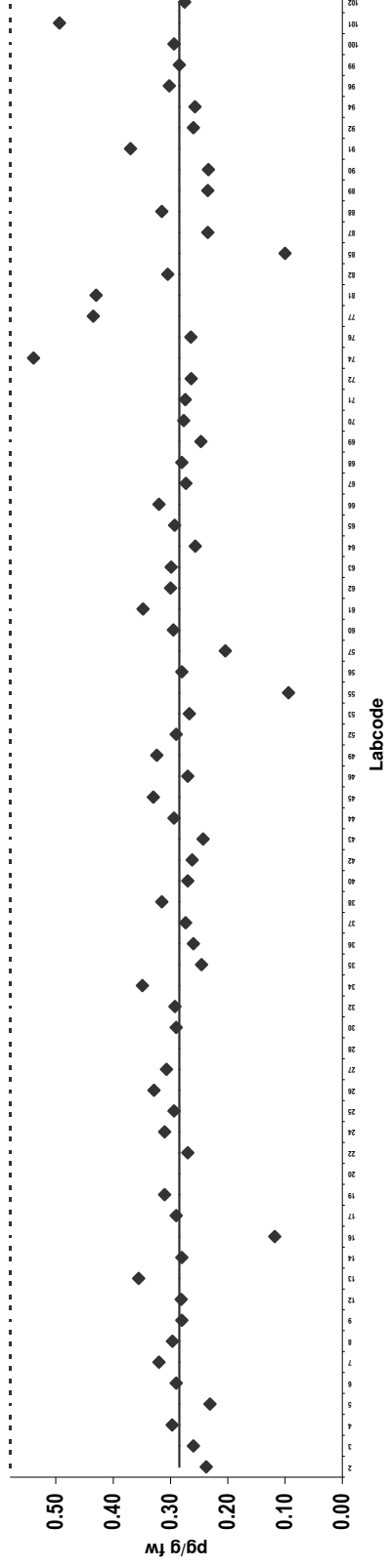
Beef
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.24		65	0.29	
3	0.26		66	0.32	
4	0.30		67	0.27	
5	0.23		68	0.28	
6	0.29		69	0.25	
7	0.32		70	0.28	
8	0.30		71	0.27	
9	0.28		72	0.26	
12	0.28		74	0.54	
13	0.36		76	0.26	
14	0.28		77	0.43	
16	0.12		81	0.43	
17	0.29		82	0.31	
19	0.31		85	0.10	
20	1.0	Outlier,ND	87	0.24	
22	0.27		88	0.32	
24	0.31		89	0.24	
25	0.29		90	0.23	
26	0.33		91	0.37	
27	0.31		92	0.26	
28	0.61	Outlier	94	0.26	
30	0.29		96	0.30	
32	0.29		99	0.28	
34	0.35		100	0.29	
35	0.25		101	0.49	
36	0.26		102	0.28	
37	0.27				
38	0.32				
40	0.27				
42	0.26				
43	0.24				
44	0.29				
45	0.33				
46	0.27				
49	0.32				
52	0.29				
53	0.27				
55	0.094				
56	0.28				
57	0.20				
60	0.30				
61	0.35				
62	0.30				
63	0.30				
64	0.26				

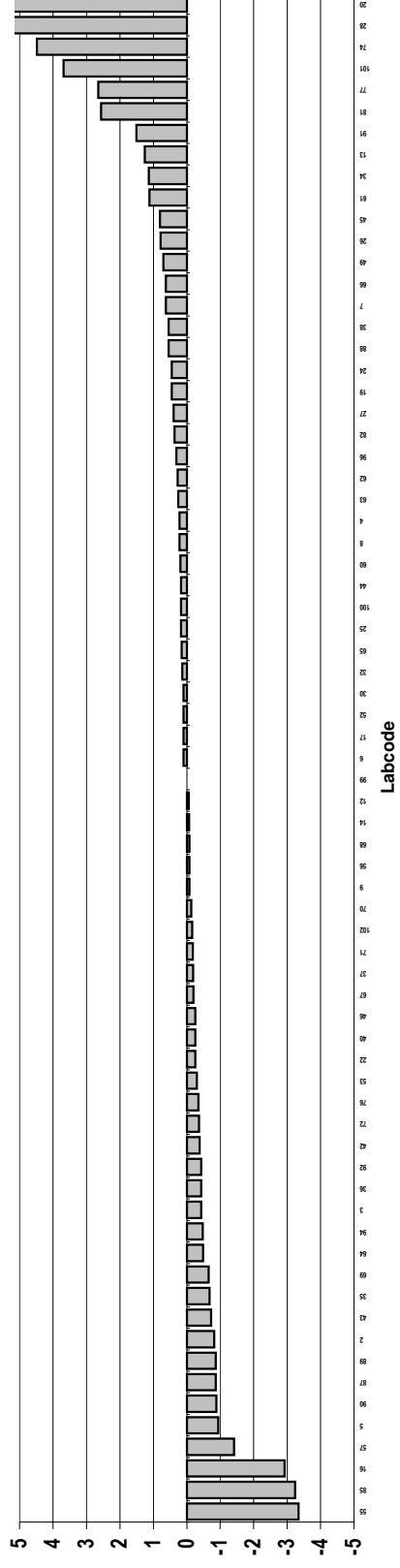
Consensus statistics

Consensus median, pg/g	0.28
Median all values pg/g	0.29
Consensus mean, pg/g	0.29
Standard deviation, pg/g	0.068
Relative standard deviation, %	24
No. of values reported	71
No. of values removed	2
No. of reported non-detects	1

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



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



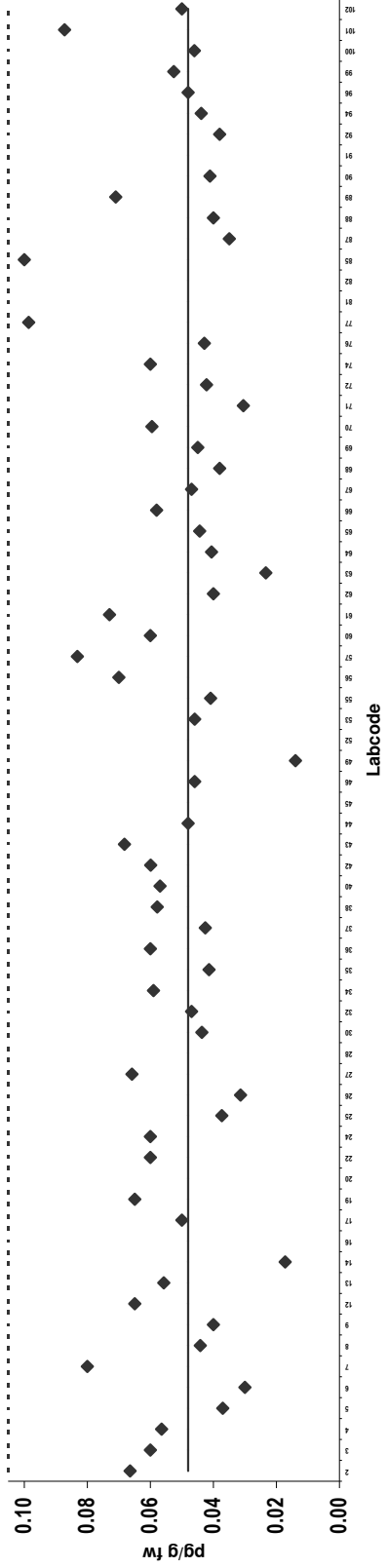
Beef
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.067		65	0.044	
3	0.060		66	0.058	
4	0.056		67	0.047	
5	0.037		68	0.038	
6	0.030	ND	69	0.045	
7	0.080		70	0.060	
8	0.044		71	0.031	
9	0.040		72	0.042	
12	0.065		74	0.060	
13	0.056		76	0.043	
14	0.017		77	0.099	
16	0.43	Outlier	81	0.22	Outlier
17	0.050		82	0.14	Outlier
19	0.065		85	0.10	
20	1.0	Outlier,ND	87	0.035	
22	0.060		88	0.040	
24	0.060		89	0.071	
25	0.037		90	0.041	
26	0.031		91	0.11	
27	0.066		92	0.038	
28	0.18		94	0.044	
30	0.044		96	0.048	
32	0.047		99	0.053	
34	0.059		100	0.046	
35	0.041		101	0.087	
36	0.060		102	0.050	
37	0.043				
38	0.058				
40	0.057				
42	0.060				
43	0.068				
44	0.048				
45	0.11	Outlier			
46	0.046				
49	0.014				
52	0.27	Outlier			
53	0.046				
55	0.041	ND			
56	0.070				
57	0.083				
60	0.060				
61	0.073				
62	0.040				
63	0.023	ND			
64	0.041				

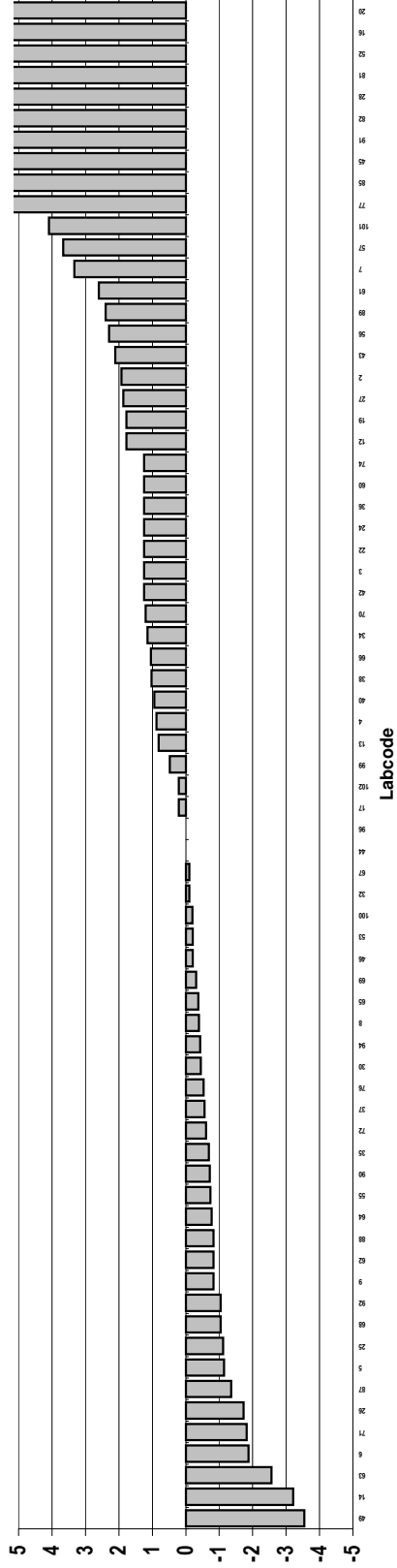
Consensus statistics

Consensus median, pg/g	0.048
Median all values pg/g	0.053
Consensus mean, pg/g	0.052
Standard deviation, pg/g	0.017
Relative standard deviation, %	33
No. of values reported	71
No. of values removed	8
No. of reported non-detects	4

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



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



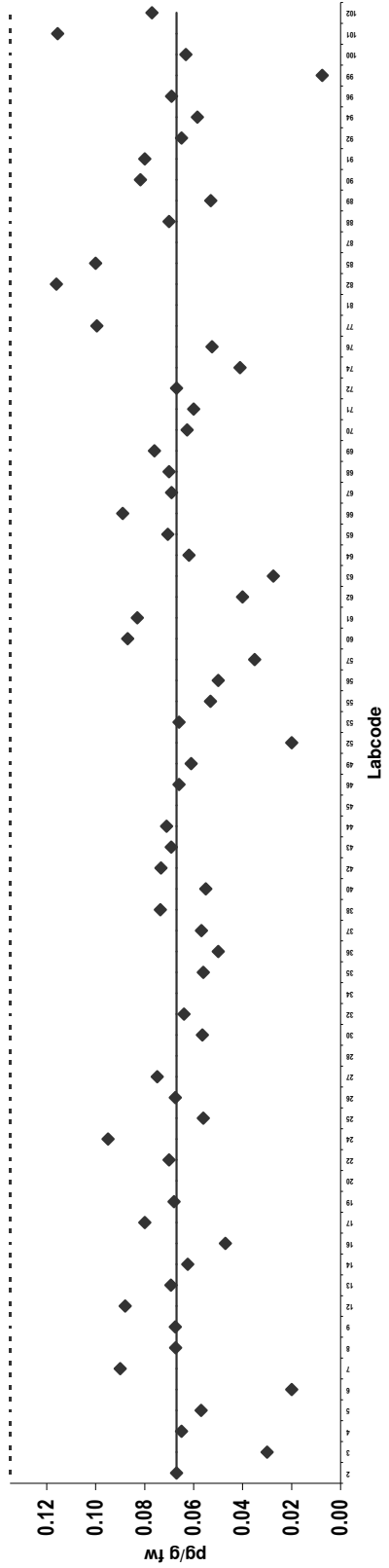
Beef
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.067		65	0.071	
3	0.030		66	0.089	
4	0.065		67	0.069	
5	0.057		68	0.070	
6	0.020	ND	69	0.076	
7	0.090		70	0.063	
8	0.067		71	0.060	
9	0.068		72	0.067	
12	0.088		74	0.041	
13	0.069		76	0.053	
14	0.062		77	0.099	
16	0.047		81	0.40	Outlier
17	0.080		82	0.12	
19	0.068		85	0.10	
20	1.0	Outlier,ND	87	1.1	Outlier
22	0.070		88	0.070	
24	0.095		89	0.053	
25	0.056		90	0.082	
26	0.068		91	0.080	
27	0.075		92	0.065	
28	0.28		94	0.058	
30	0.056		96	0.069	
32	0.064		99	0.0075	
34	0.20		100	0.063	ND
35	0.056		101	0.12	
36	0.050		102	0.077	
37	0.057				
38	0.074				
40	0.055				
42	0.073				
43	0.069				
44	0.071				
45	0.14	Outlier			
46	0.066				
49	0.061				
52	0.020	ND			
53	0.066				
55	0.053				
56	0.050				
57	0.035				
60	0.087				
61	0.083				
62	0.040				
63	0.028	ND			
64	0.062				

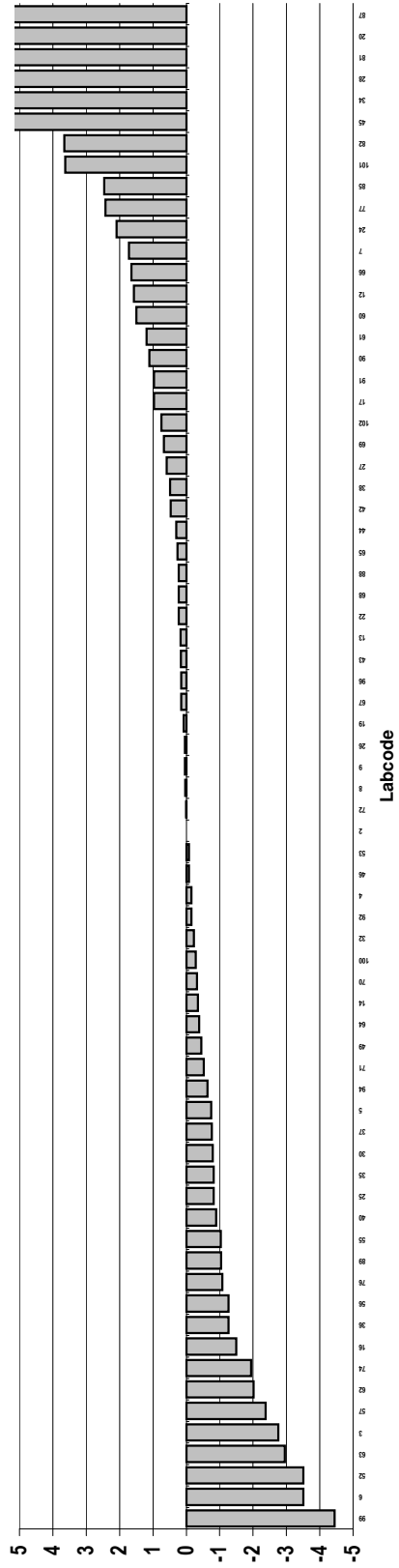
Consensus statistics

Consensus median, pg/g	0.067
Median all values pg/g	0.068
Consensus mean, pg/g	0.065
Standard deviation, pg/g	0.020
Relative standard deviation, %	31
No. of values reported	71
No. of values removed	6
No. of reported non-detects	5

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



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



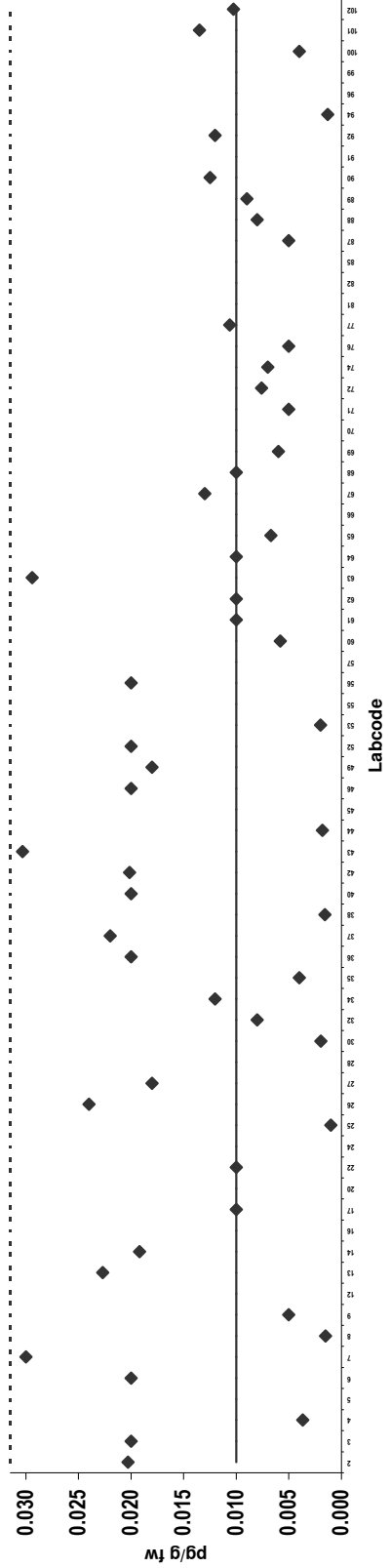
Beef
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.020		66	0.050	Outlier,ND
3	0.020	ND	67	0.013	
4	0.0037		68	0.010	ND
5	0.033	Outlier,ND	69	0.0060	
6	0.020	ND	70	0.11	Outlier,ND
7	0.030	ND	71	0.0050	ND
8	0.0015		72	0.0076	ND
9	0.0050		74	0.0070	ND
12	0.033	Outlier	76	0.0050	ND
13	0.023	ND	77	0.011	ND
14	0.019	ND	81	0.21	Outlier
16	0.056	Outlier	82	0.086	Outlier
17	0.010	ND	85	0.10	Outlier
20	1.0	Outlier,ND	87	0.0050	ND
22	0.010	ND	88	0.0080	ND
24	0.055	Outlier	89	0.0090	
25	0.0010	ND	90	0.013	ND
26	0.024	ND	91	0.046	Outlier
27	0.018	ND	92	0.012	ND
28	0.071	Outlier,ND	94	0.0013	
30	0.0020		96	0.20	Outlier,ND
32	0.0080	ND	99	0.061	Outlier
34	0.012		100	0.0040	ND
35	0.0040	ND	101	0.014	
36	0.020	ND	102	0.010	ND
37	0.022	ND			
38	0.0016	ND			
40	0.020	ND			
42	0.020	ND			
43	0.030	ND			
44	0.0018	ND			
45	0.11	Outlier			
46	0.020	ND			
49	0.018				
52	0.020	ND			
53	0.0020				
55	0.041	Outlier,ND			
56	0.020	ND			
57	0.042	Outlier,ND			
60	0.0058	ND			
61	0.010				
62	0.010	ND			
63	0.029	ND			
64	0.010	ND			
65	0.0067				

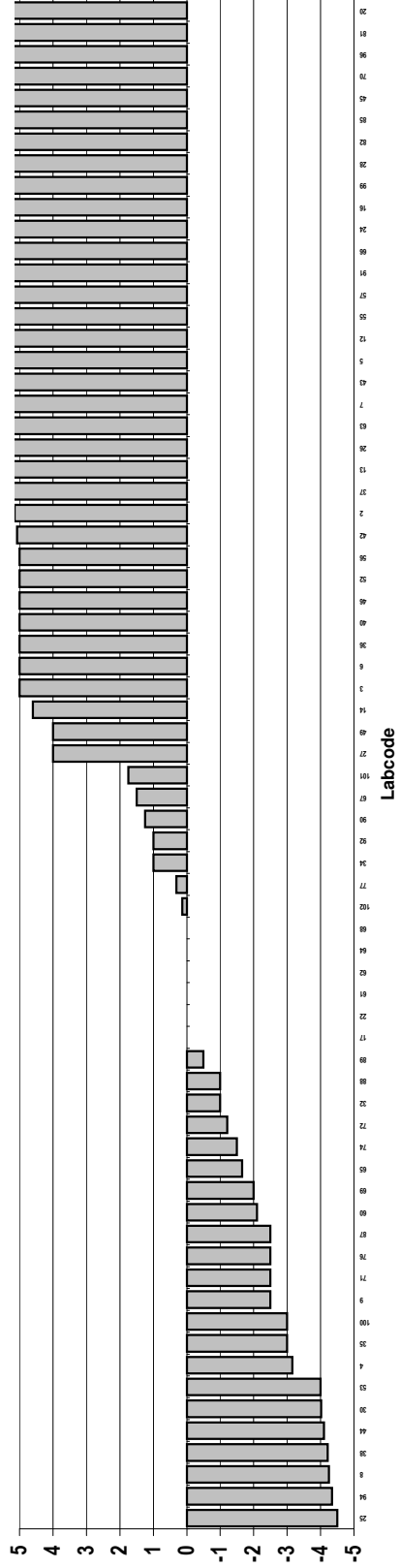
Consensus statistics

Consensus median, pg/g	0.010
Median all values pg/g	0.016
Consensus mean, pg/g	0.012
Standard deviation, pg/g	0.0081
Relative standard deviation, %	67
No. of values reported	70
No. of values removed	17
No. of reported non-detects	47

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



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



Beef

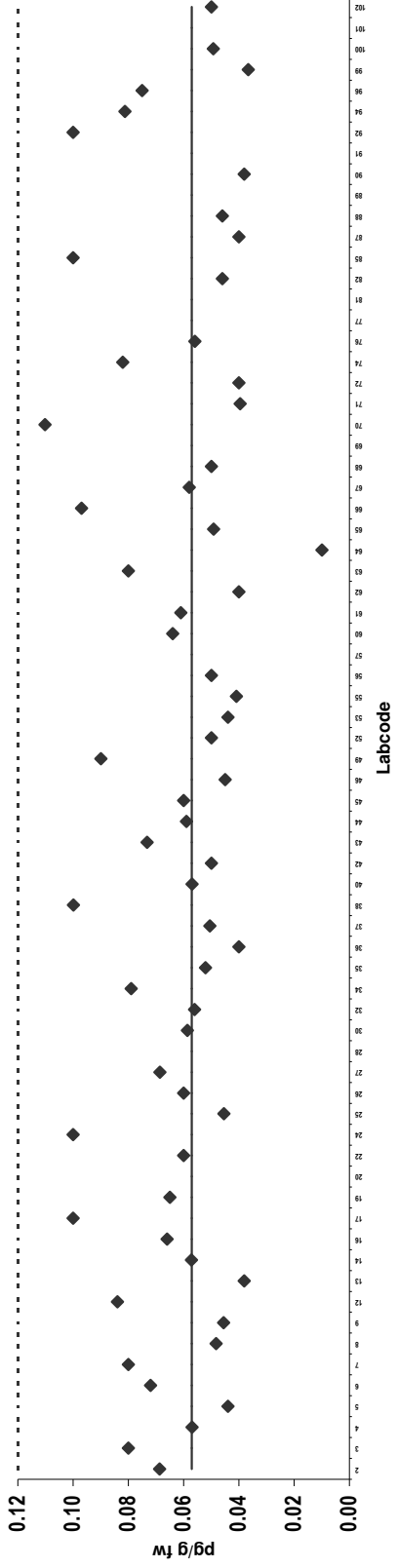
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.069		65	0.049	
3	0.080		66	0.097	
4	0.057		67	0.058	
5	0.044		68	0.050	Outlier
6	0.072		69	0.14	
7	0.080		70	0.11	
8	0.048		71	0.040	
9	0.046		72	0.040	
12	0.084		74	0.082	
13	0.038		76	0.056	
14	0.057		77	0.75	Outlier
16	0.066		81	0.24	Outlier
17	0.10		82	0.046	
19	0.065		85	0.10	
20	1.0		87	0.040	
22	0.060		88	0.046	
24	0.10		89	0.19	Outlier
25	0.045		90	0.038	
26	0.060		91	0.37	Outlier
27	0.069		92	0.10	
28	0.34		94	0.081	
30	0.059		96	0.075	
32	0.056		99	0.037	
34	0.079		100	0.049	
35	0.052		101	0.12	Outlier
36	0.040		102	0.050	
37	0.051				
38	0.10				
40	0.057				
42	0.050				
43	0.073				
44	0.059				
45	0.060				
46	0.045				
49	0.090				
52	0.050				
53	0.044				
55	0.041	ND			
56	0.050				
57	0.94	Outlier			
60	0.064				
61	0.061				
62	0.040				
63	0.080				
64	0.010	ND			

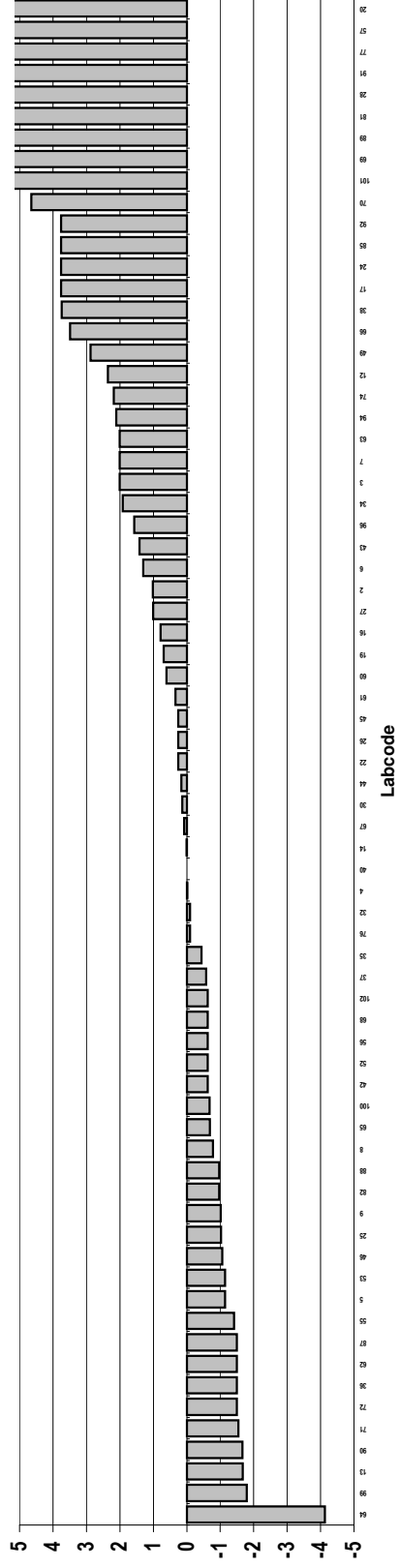
Consensus statistics

Consensus median, pg/g	0.057
Median all values pg/g	0.060
Consensus mean, pg/g	0.061
Standard deviation, pg/g	0.020
Relative standard deviation, %	33
No. of values reported	71
No. of values removed	9
No. of reported non-detects	4

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



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



Beef

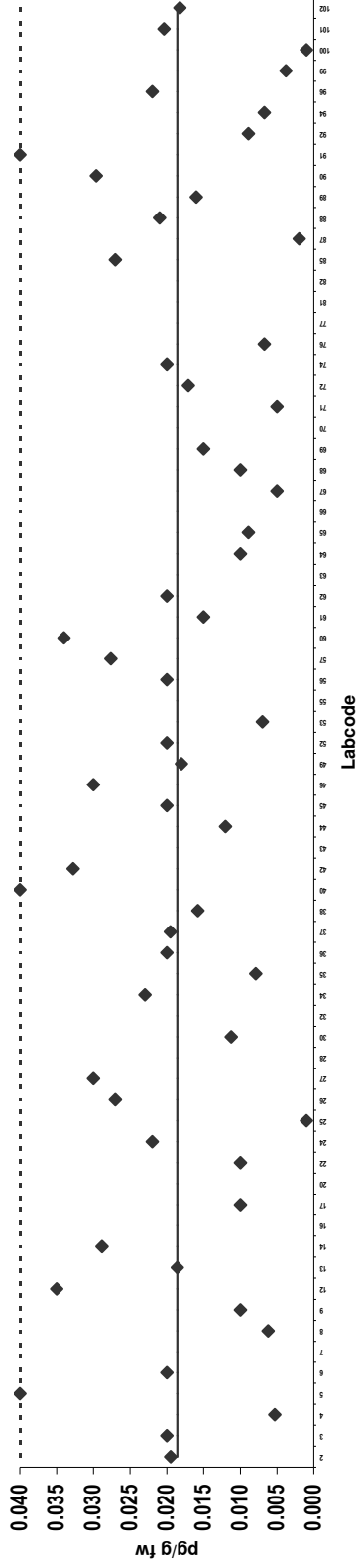
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.020		66	0.12	Outlier
3	0.020	ND	67	0.0050	ND
4	0.0053		68	0.010	ND
5	0.040	ND	69	0.015	
6	0.020	ND	70	0.18	Outlier,ND
7	0.080	Outlier,ND	71	0.0050	ND
8	0.0062		72	0.017	ND
9	0.010	ND	74	0.020	ND
12	0.035		76	0.0068	
13	0.019	ND	77	0.18	Outlier
14	0.029	ND	81	0.20	Outlier
16	0.10	Outlier	82	0.054	Outlier
17	0.010		85	0.027	ND
20	1.0	Outlier,ND	87	0.0020	ND
22	0.010	ND	88	0.021	ND
24	0.022	ND	89	0.016	ND
25	0.0010	ND	90	0.030	
26	0.027	ND	91	0.040	
27	0.030	ND	92	0.0089	ND
28	0.33	Outlier	94	0.0067	
30	0.011		96	0.022	ND
32	0.043	Outlier	99	0.0038	
34	0.023		100	0.0010	ND
35	0.0079		101	0.020	
36	0.020	ND	102	0.018	ND
37	0.020	ND			
38	0.016				
40	0.040	ND			
42	0.033	ND			
43	0.047	Outlier,ND			
44	0.012				
45	0.020				
46	0.030	ND			
49	0.018	ND			
52	0.020	ND			
53	0.0070				
55	0.041	Outlier,ND			
56	0.020	ND			
57	0.028				
60	0.034	ND			
61	0.015				
62	0.020	ND			
63	0.056	Outlier,ND			
64	0.010	ND			
65	0.0089				

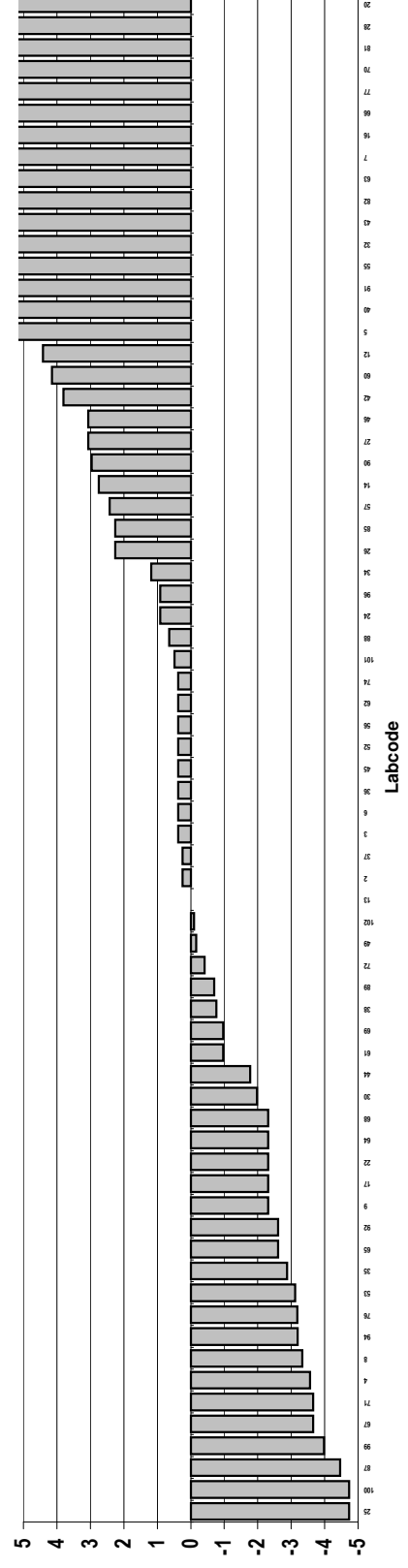
Consensus statistics

Consensus median, pg/g	0.019
Median all values pg/g	0.020
Consensus mean, pg/g	0.018
Standard deviation, pg/g	0.010
Relative standard deviation, %	58
No. of values reported	70
No. of values removed	13
No. of reported non-detects	40

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



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

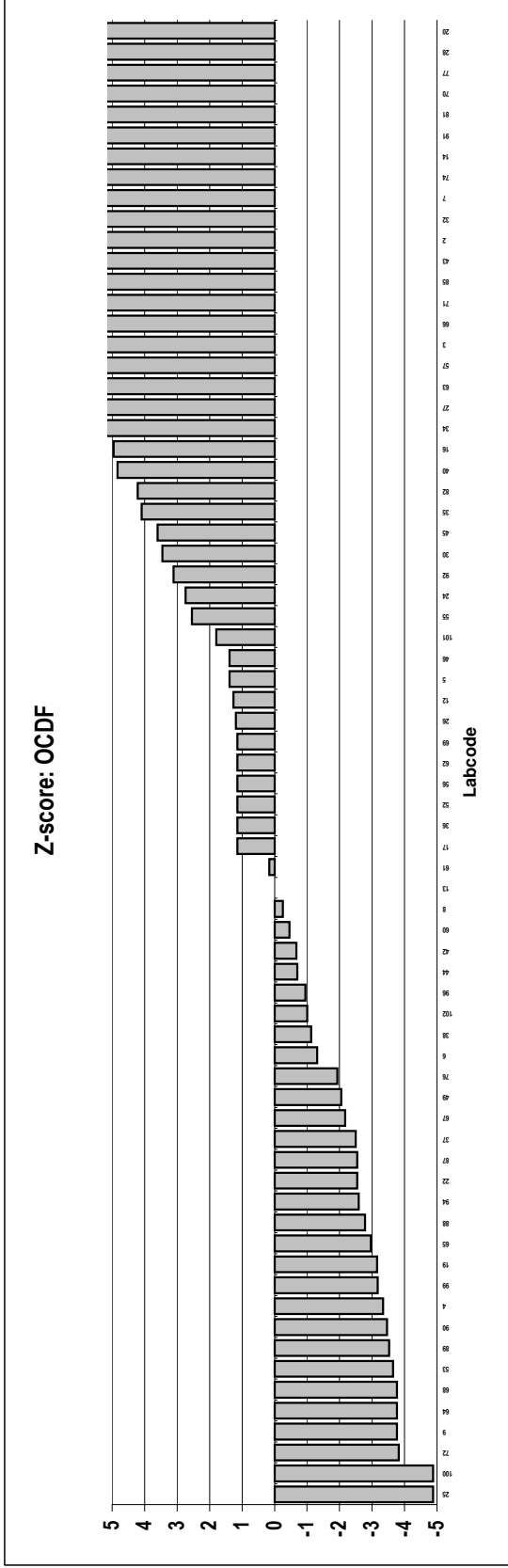
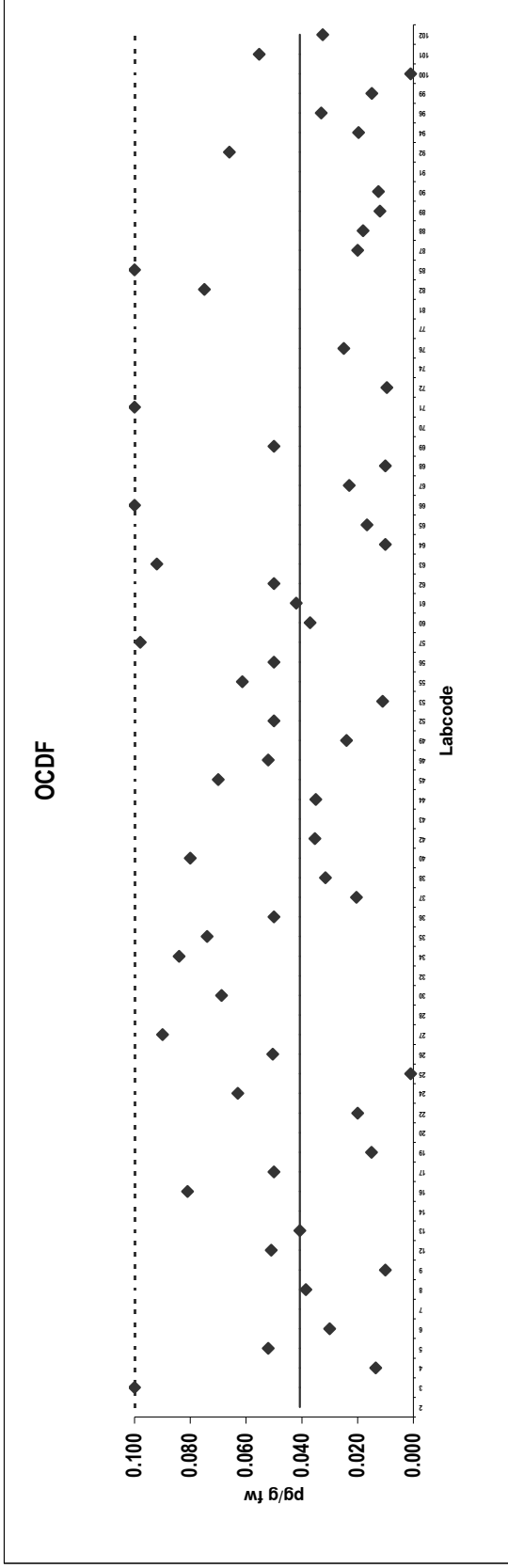


Beef
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.13		65	0.017	
3	0.10	Outlier	66	0.10	ND
4	0.013		67	0.023	
5	0.052	ND	68	0.010	ND
6	0.030	ND	69	0.050	
7	0.20	Outlier,ND	70	0.98	Outlier,ND
8	0.039		71	0.10	ND
9	0.010	ND	72	0.0095	ND
12	0.051	ND	74	0.21	Outlier
13	0.041		76	0.025	ND
14	0.23	Outlier	77	1.1	Outlier
16	0.081		81	0.43	Outlier
17	0.050		82	0.075	
19	0.015		85	0.10	
20	2.0	Outlier,ND	87	0.020	
22	0.020	ND	88	0.018	ND
24	0.063		89	0.012	ND
25	0.0010	ND	90	0.013	ND
26	0.050		91	0.33	Outlier,ND
27	0.090	ND	92	0.066	
28	1.4	Outlier	94	0.020	
30	0.069		96	0.033	ND
32	0.14		99	0.015	
34	0.084	Outlier	100	0.0010	ND
35	0.074		101	0.055	
36	0.050	ND	102	0.032	ND
37	0.020	ND			
38	0.032				
40	0.080	ND			
42	0.035	ND			
43	0.12	Outlier,ND			
44	0.035				
45	0.070				
46	0.052				
49	0.024				
52	0.050	ND			
53	0.011	ND			
55	0.061	ND			
56	0.050	ND			
57	0.098	ND			
60	0.037				
61	0.042				
62	0.050	ND			
63	0.092	ND			
64	0.010	ND			

Consensus statistics

Consensus median, pg/g	0.041
Median all values pg/g	0.050
Consensus mean, pg/g	0.045
Standard deviation, pg/g	0.029
Relative standard deviation, %	65
No. of values reported	71
No. of values removed	12
No. of reported non-detects	35



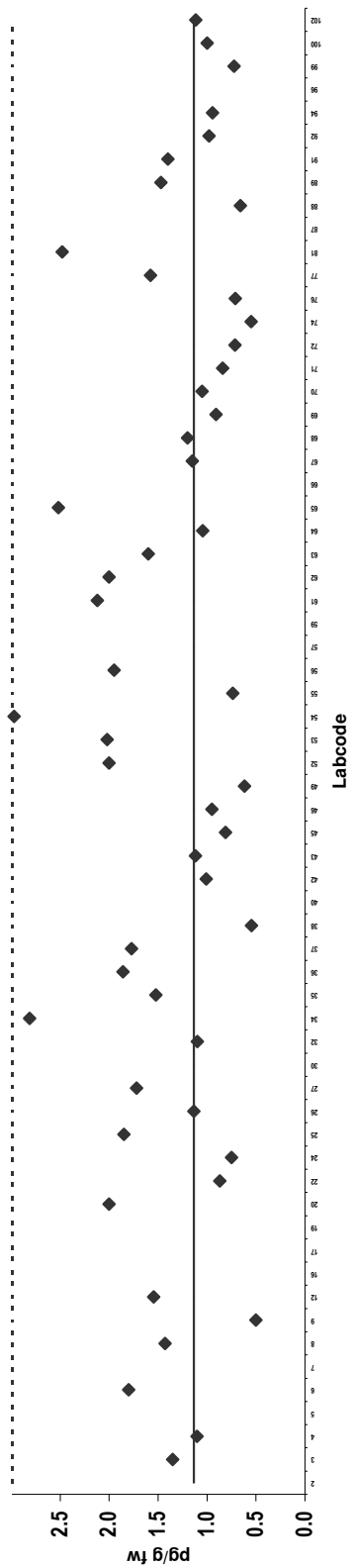
Beef
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4.9		68	1.2	
3	1.4	Outlier	69	0.91	
4	1.1		70	1.1	
5	3.7	Outlier	71	0.84	ND
6	1.8		72	0.71	
7	4.0	Outlier	74	0.55	
8	1.4		76	0.71	
9	0.50	ND	77	1.6	
12	1.5		81	2.5	
16	15	Outlier	87	3.9	Outlier
17	3.2	Outlier	88	0.66	
19	5.0	Outlier,ND	89	1.5	
20	2.0	ND	91	1.4	
22	0.87		92	0.98	
24	0.75		94	0.94	
25	1.9		96	15	
26	1.1		99	0.72	Outlier,ND
27	1.7		100	1.0	ND
30	3.2	Outlier	102	1.1	
32	1.1				
34	2.8				
35	1.5				
36	1.9				
37	1.8				
38	0.55	ND			
40	5.8				
42	1.0				
43	1.1				
45	0.81				
46	0.95				
49	0.62				
52	2.0				
53	2.0				
54	3.0				
55	0.74				
56	2.0				
57	6.5	Outlier			
59	3.1	Outlier,ND			
61	2.1				
62	2.0				
63	1.6				
64	1.0				
65	2.5				
66	3.4	Outlier			
67	1.2				

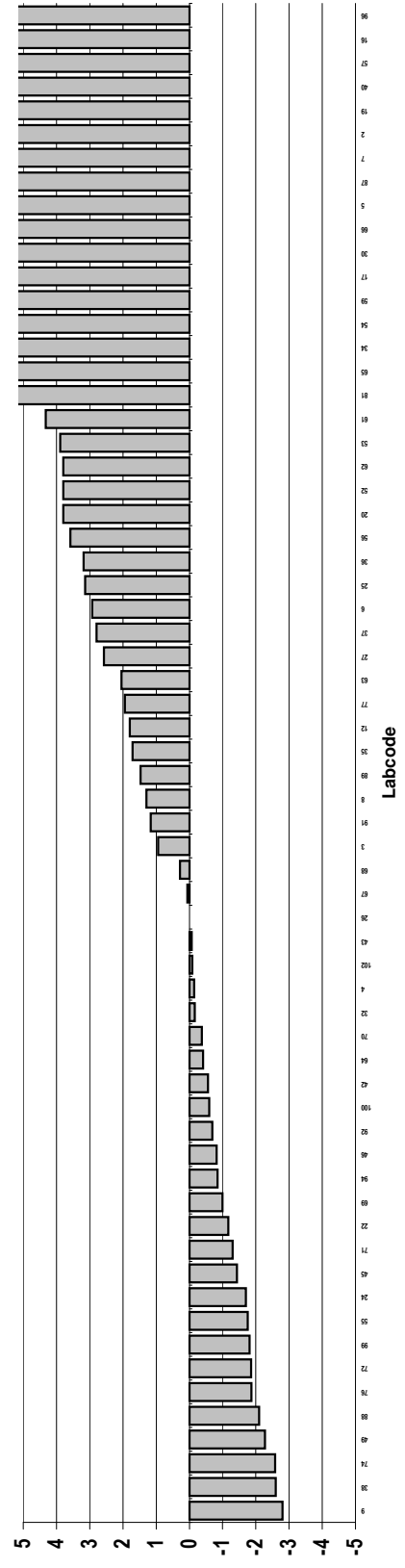
Consensus statistics

Consensus median, pg/g	1.1
Median all values pg/g	1.5
Consensus mean, pg/g	1.3
Standard deviation, pg/g	0.61
Relative standard deviation, %	45
No. of values reported	64
No. of values removed	13
No. of reported non-detects	8

PCB 77



Z-score: PCB 77



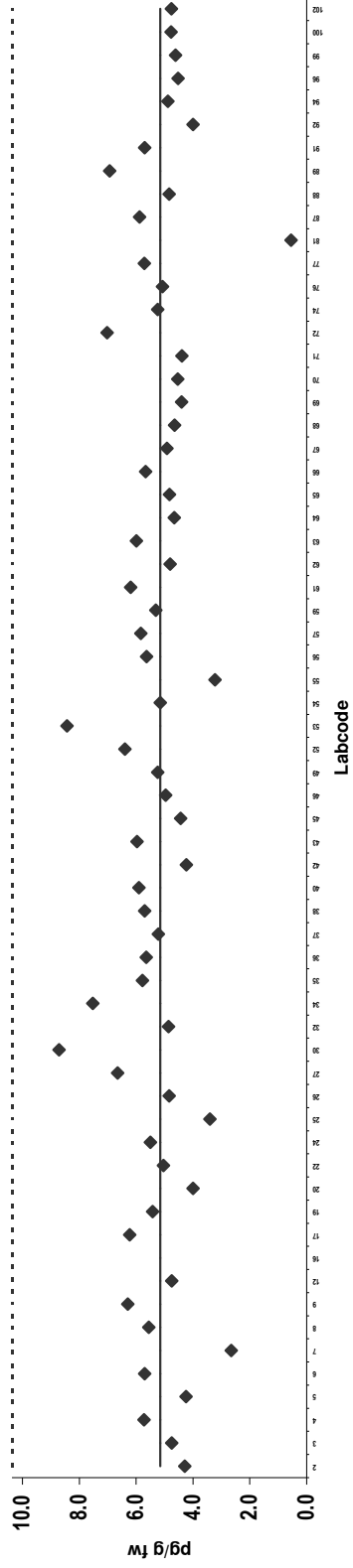
Beef
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4.3		68	4.7	
3	4.8		69	4.4	
4	5.7		70	4.5	
5	4.2		71	4.4	
6	5.7		72	7.0	
7	2.7		74	5.2	
8	5.6		76	5.1	
9	6.3		77	5.7	
12	4.7		81	0.55	ND
16	4.1		87	5.9	
17	6.2		88	4.8	
19	5.4		89	6.9	
20	4.0		91	5.7	
22	5.0		92	4.0	
24	5.5		94	4.9	
25	3.4		96	4.5	
26	4.8		99	4.6	
27	6.7		100	4.8	
30	8.7		102	4.8	
32	4.9				
34	7.5				
35	5.8				
36	5.6				
37	5.2				
38	5.7				
40	5.9				
42	4.2				
43	6.0				
45	4.4				
46	5.0				
49	5.2				
52	6.4				
53	8.4				
54	5.2				
55	3.2				
56	5.6				
57	5.8				
59	5.3				
61	6.2				
62	4.8				
63	6.0				
64	4.7				
65	4.8				
66	5.7				
67	4.9				

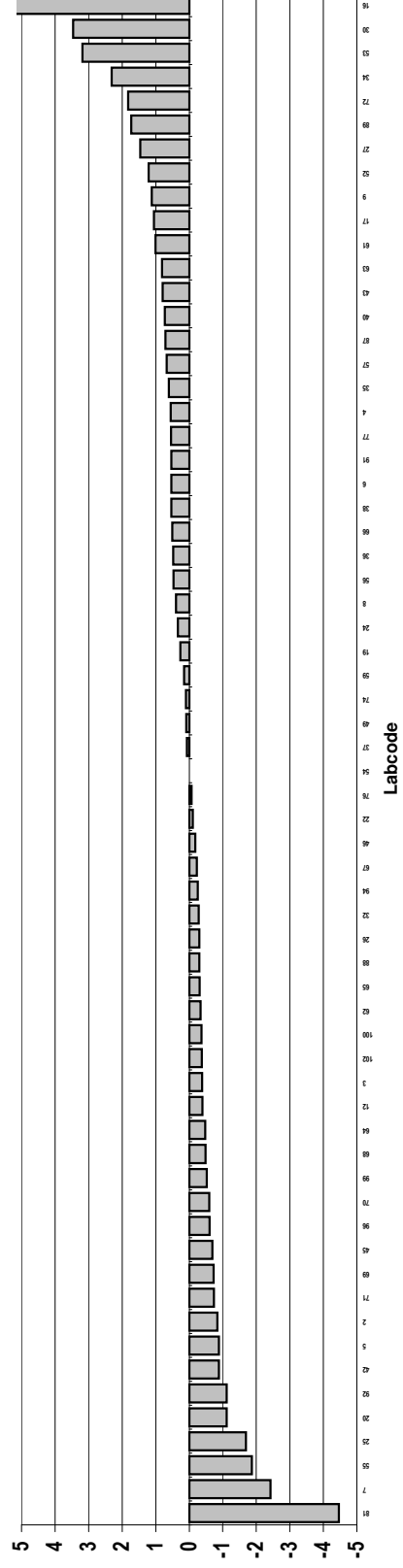
Consensus statistics

Consensus median, pg/g	5.2
Median all values pg/g	5.2
Consensus mean, pg/g	5.2
Standard deviation, pg/g	1.2
Relative standard deviation, %	23
No. of values reported	64
No. of values removed	1
No. of reported non-detects	1

PCB 126



Z-score: PCB 126



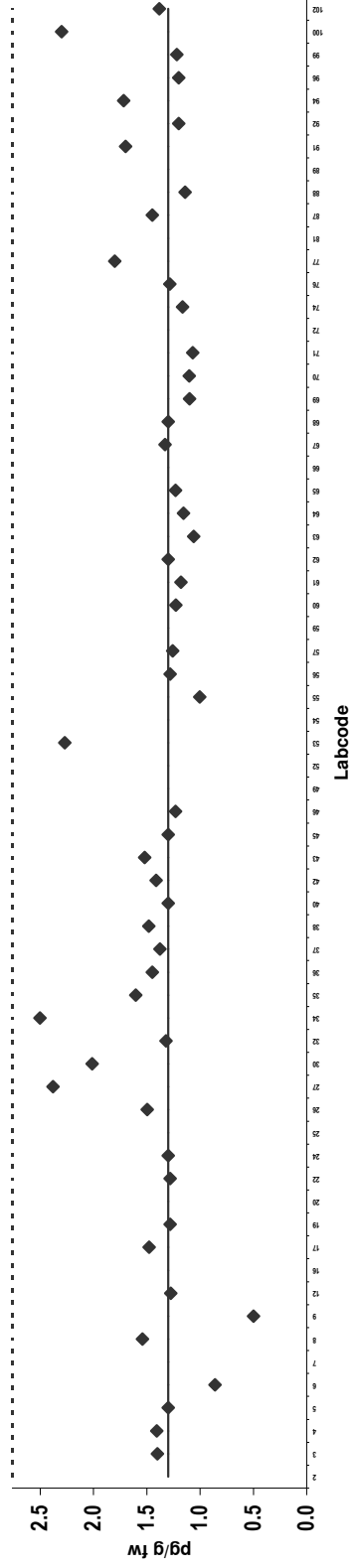
Beef
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	3.0		67	1.3	
3	1.4	Outlier	68	1.3	
4	1.4		69	1.1	
5	1.3		70	1.1	
6	0.86	ND	71	1.1	
7	3.2	Outlier	72	6.2	Outlier,ND
8	1.5		74	1.2	
9	0.50	ND	76	1.3	
12	1.3		77	1.8	
16	4.5	Outlier	81	7.7	Outlier
17	1.5		87	1.5	
19	1.3		88	1.1	
20	4.0	Outlier	89	3.1	Outlier
22	1.3		91	1.7	
24	1.3		92	1.2	
25	9.0	Outlier	94	1.7	
26	1.5		96	1.2	
27	2.4		99	1.2	
30	2.0		100	2.3	ND
32	1.3		102	1.4	
34	2.5				
35	1.6				
36	1.5				
37	1.4				
38	1.5				
40	1.3				
42	1.4				
43	1.5				
45	1.3				
46	1.2				
49	4.7	Outlier			
52	3.2	Outlier			
53	2.3				
54	2.1	Outlier			
55	1.0				
56	1.3				
57	1.3				
59	3.1	Outlier,ND			
60	1.2				
61	1.2				
62	1.3				
63	1.1	ND			
64	1.2				
65	1.2				
66	9.9	Outlier			

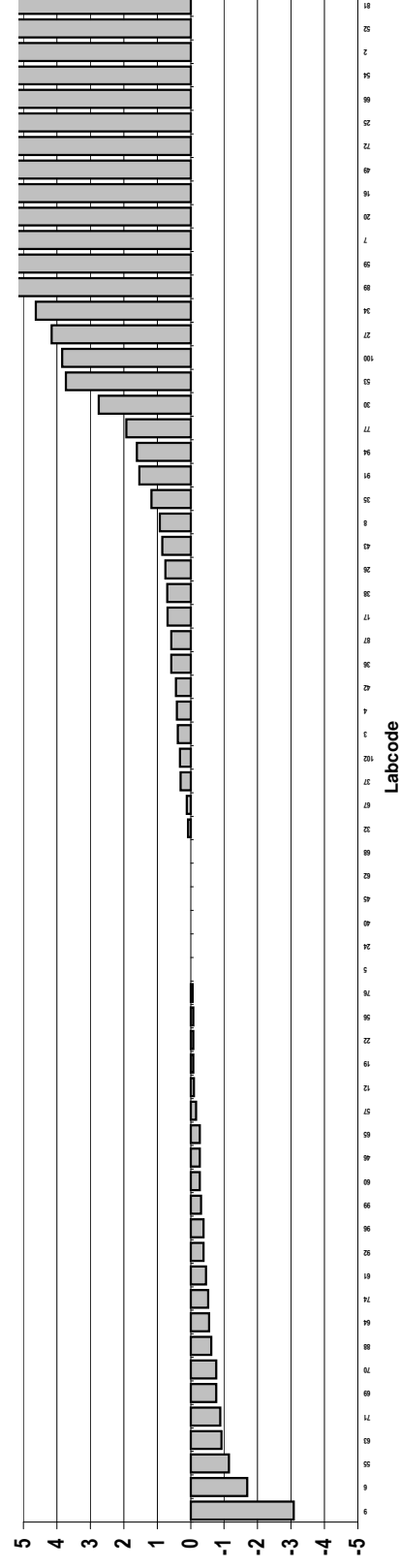
Consensus statistics

Consensus median, pg/g	1.3
Median all values pg/g	1.4
Consensus mean, pg/g	1.4
Standard deviation, pg/g	0.37
Relative standard deviation, %	26
No. of values reported	65
No. of values removed	13
No. of reported non-detects	6

PCB 169



Z-score: PCB 169



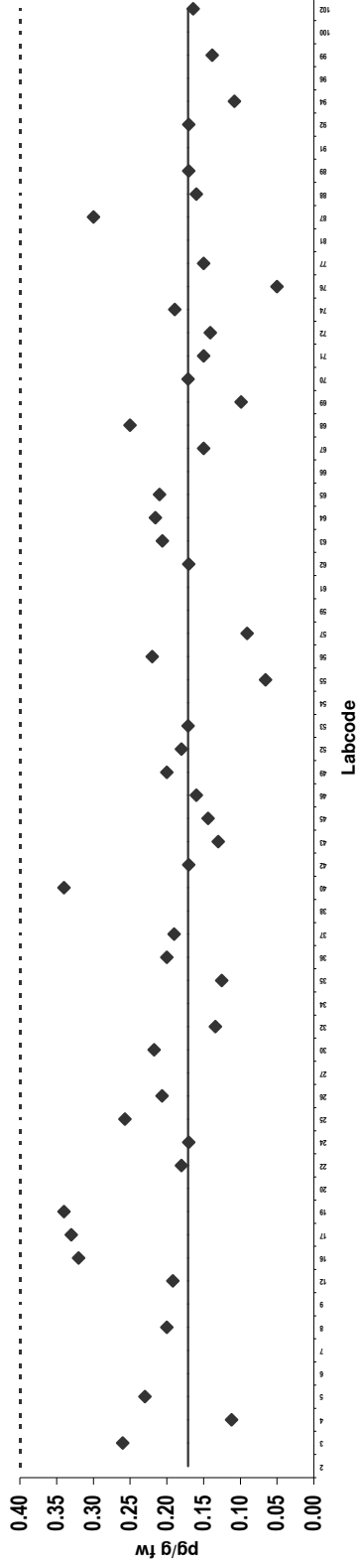
Beef
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	1.7	Outlier	68	0.25	
3	0.26		69	0.099	
4	0.11		70	0.17	
5	0.23		71	0.15	ND
6	0.71	Outlier,ND	72	0.14	ND
7	1.0	Outlier,ND	74	0.19	
8	0.20		76	0.050	ND
9	0.50	Outlier,ND	77	0.15	
12	0.19		81	0.42	Outlier,ND
16	0.32		87	0.30	
17	0.33		88	0.16	
19	0.34		89	0.17	
20	2.0	Outlier,ND	91	0.66	Outlier
22	0.18		92	0.17	
24	0.17		94	0.11	
25	0.26		96	0.55	Outlier
26	0.21		99	0.14	
27	0.50	Outlier,ND	100	1.0	Outlier,ND
30	0.22		102	0.16	
32	0.13				
34	1.0	Outlier			
35	0.13				
36	0.20				
37	0.19				
38	2.4	Outlier			
40	0.34				
42	0.17				
43	0.13				
45	0.14				
46	0.16				
49	0.20	ND			
52	0.18				
53	0.17				
54	1.2	Outlier			
55	0.065				
56	0.22				
57	0.091				
59	3.1	Outlier,ND			
61	0.54	Outlier			
62	0.17				
63	0.21	ND			
64	0.22				
65	0.21				
66	1.0	Outlier,ND			
67	0.15				

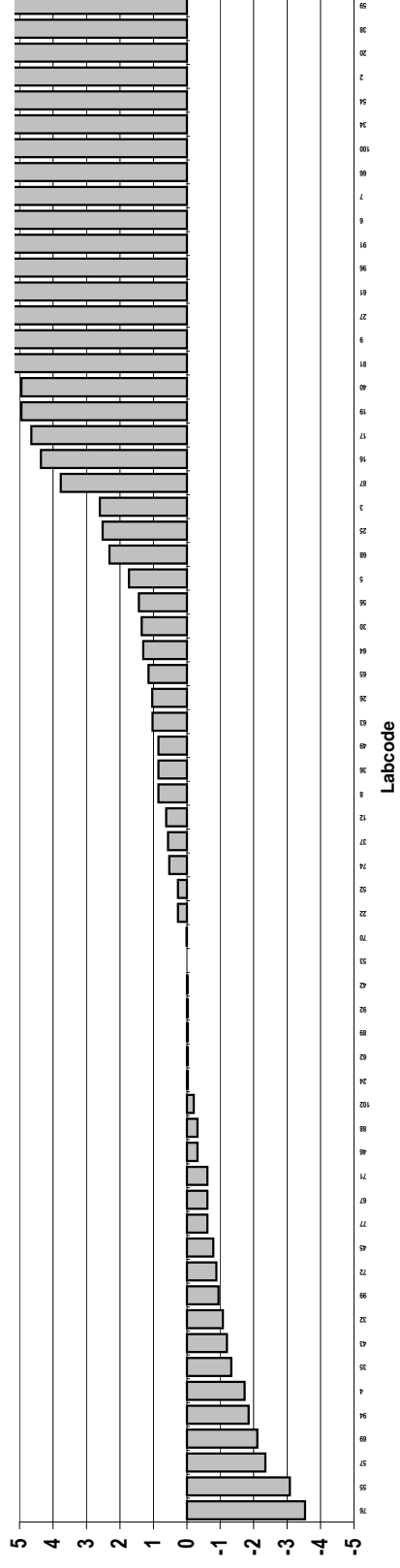
Consensus statistics

Consensus median, pg/g	0.17
Median all values pg/g	0.20
Consensus mean, pg/g	0.19
Standard deviation, pg/g	0.066
Relative standard deviation, %	36
No. of values reported	64
No. of values removed	16
No. of reported non-detects	14

PCB 81



Z-score: PCB 81



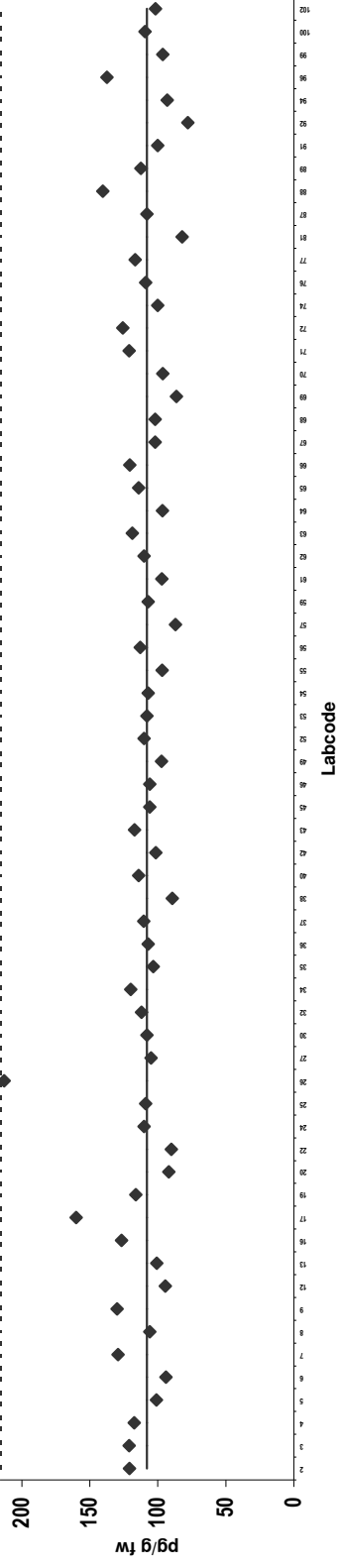
Beef
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	121		67	102	
3	121		68	102	
4	117		69	86	
5	101		70	96	
6	94		71	121	
7	129		72	126	
8	106		74	100	
9	130		76	109	
12	95		77	117	
13	101		81	82	
16	127		87	108	
17	160		88	140	
19	116		89	113	
20	92		91	100	
22	90		92	78	
24	110		94	93	
25	109		96	137	
26	213		99	96	
27	105		100	109	
30	108		102	102	
32	112				
34	120				
35	103				
36	107				
37	110				
38	89				
40	114				
42	102				
43	117				
45	106				
46	106				
49	97				
52	110				
53	108				
54	107				
55	97				
56	113				
57	87				
59	107				
61	97				
62	110				
63	119				
64	97				
65	114				
66	121				

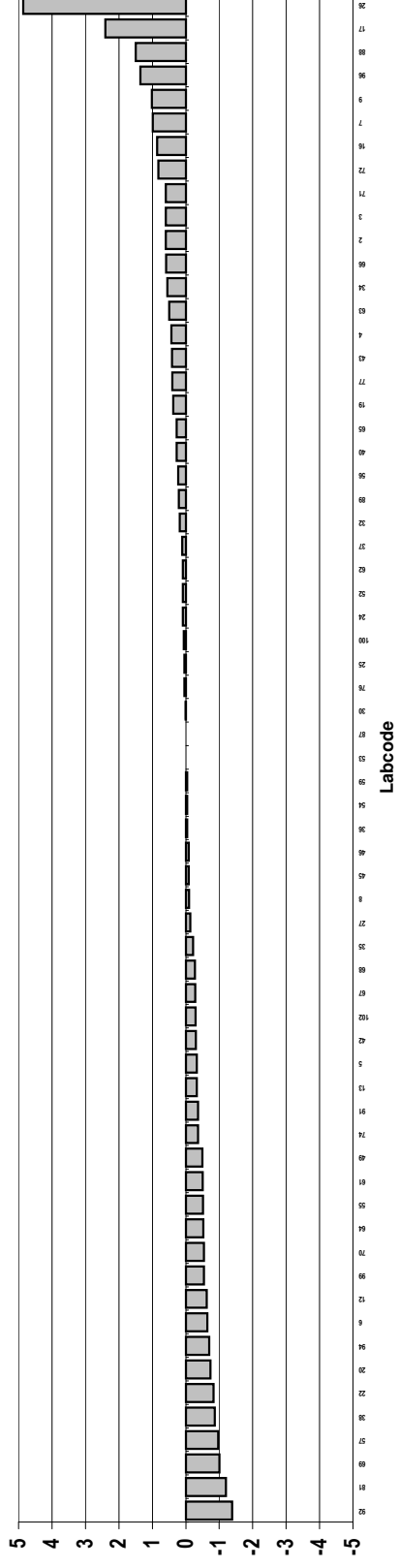
Consensus statistics

Consensus median, pg/g	108
Median all values pg/g	108
Consensus mean, pg/g	110
Standard deviation, pg/g	19
Relative standard deviation, %	18
No. of values reported	65
No. of values removed	0
No. of reported non-detects	0

PCB 105



Z-score: PCB 105



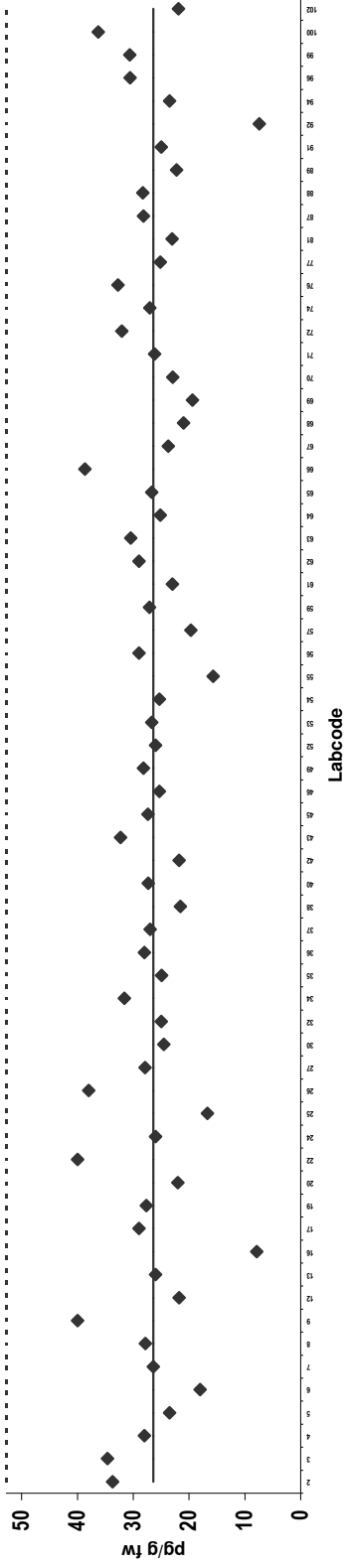
Beef
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	34		67	24	
3	35		68	21	
4	28		69	19	
5	24		70	23	
6	18		71	26	
7	26		72	32	
8	28		74	27	
9	40		76	33	
12	22		77	25	
13	26		81	23	
16	7.9		87	28	
17	29		88	28	
19	28		89	22	
20	22		91	25	
22	40		92	7.4	ND
24	26		94	24	
25	17		96	31	
26	38		99	31	
27	28		100	36	
30	25		102	22	
32	25				
34	32				
35	25				
36	28				
37	27				
38	22				
40	27				
42	22				
43	32				
45	27				
46	25				
49	28				
52	26				
53	27				
54	25				
55	16				
56	29				
57	20				
59	27				
61	23				
62	29				
63	30				
64	25				
65	27				
66	39				

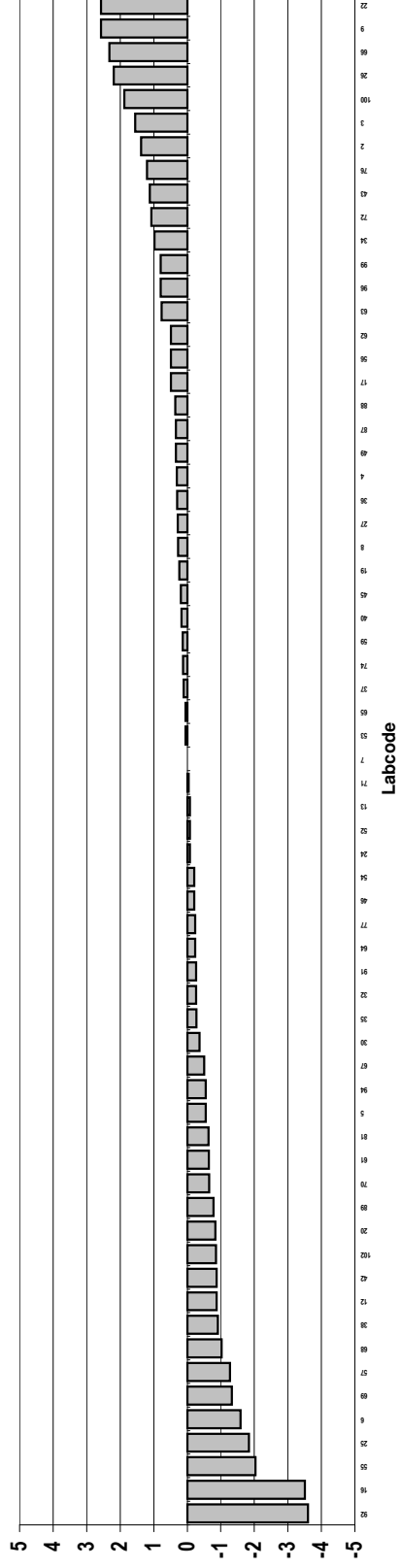
Consensus statistics

Consensus median, pg/g	26
Median all values pg/g	26
Consensus mean, pg/g	26
Standard deviation, pg/g	6.1
Relative standard deviation, %	23
No. of values reported	65
No. of values removed	0
No. of reported non-detects	1

PCB 114



Z-score: PCB 114



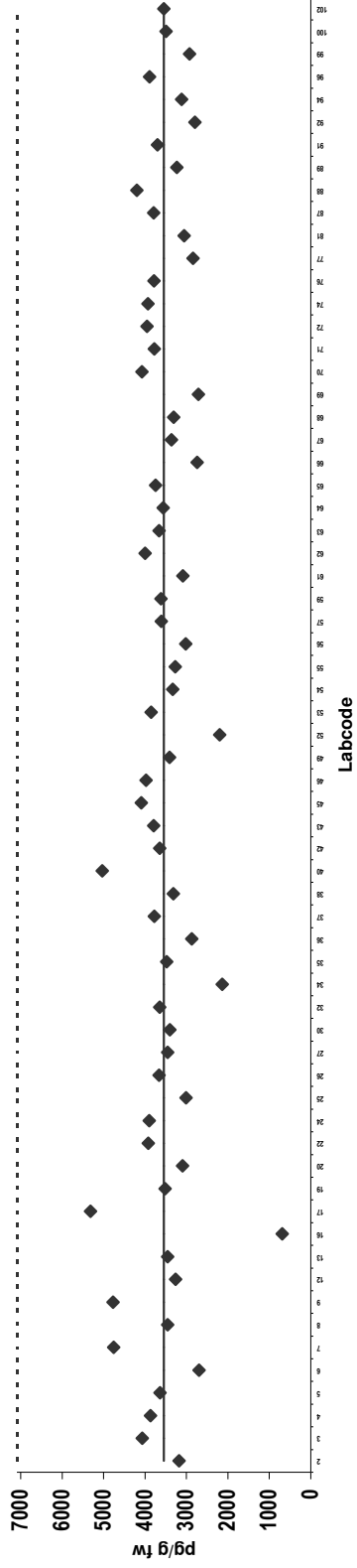
Beef
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	3182		67	3361	
3	4072		68	3310	
4	3871		69	2710	
5	3638		70	4074	
6	2700		71	3780	
7	4760		72	3955	
8	3458		74	3934	
9	4775		76	3783	
12	3264		77	2842	
13	3452		81	3057	
16	687		87	3790	
17	5316		88	4201	
19	3515		89	3230	
20	3097		91	3700	
22	3920		92	2800	
24	3900		94	3116	
25	3010		96	3894	
26	3665		99	2924	
27	3456		100	3495	
30	3400		102	3547	
32	3648				
34	2135				
35	3477				
36	2870				
37	3780				
38	3317				
40	5032				
42	3647				
43	3790				
45	4090				
46	3980				
49	3410				
52	2200				
53	3857				
54	3330				
55	3270				
56	3020				
57	3605				
59	3615				
61	3089				
62	4000				
63	3659				
64	3564				
65	3750				
66	2745				

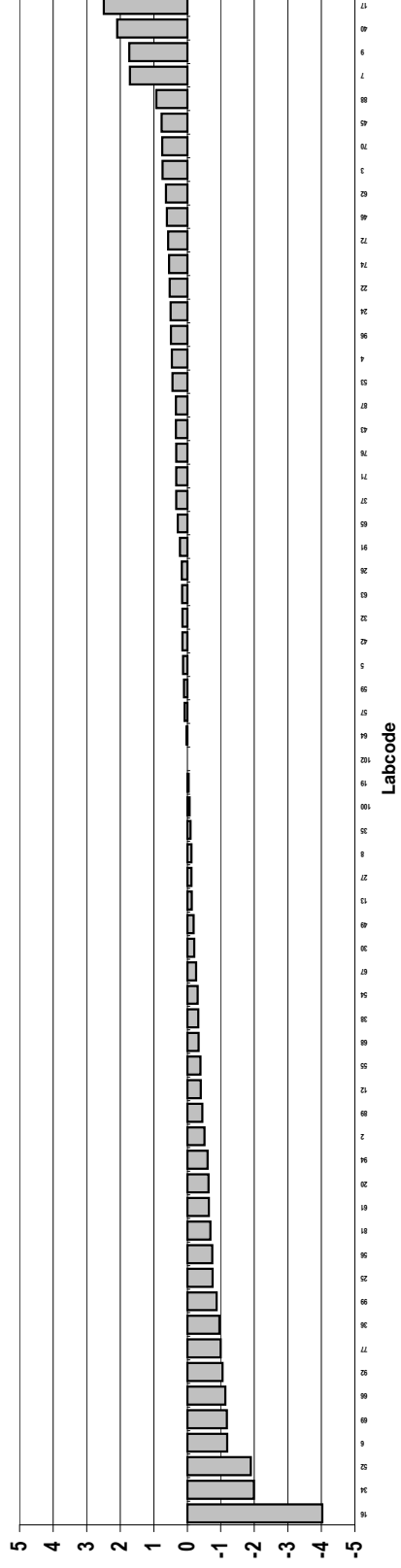
Consensus statistics

Consensus median, pg/g	3547
Median all values pg/g	3547
Consensus mean, pg/g	3500
Standard deviation, pg/g	675
Relative standard deviation, %	19
No. of values reported	65
No. of values removed	0
No. of reported non-detects	0

PCB 118



Z-score: PCB 118



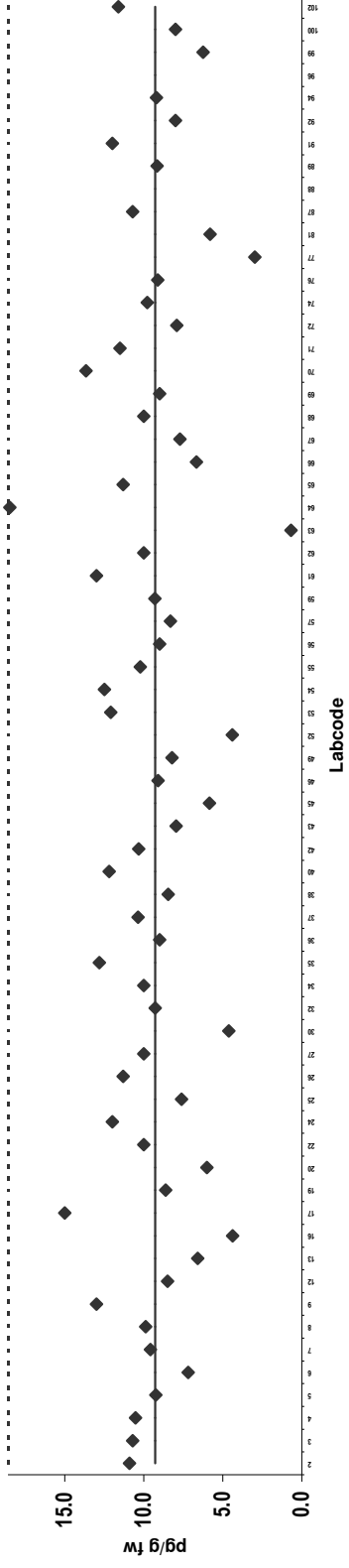
Beef
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	11		67	7.7	
3	11		68	10	
4	11		69	9.0	
5	9.2		70	14	
6	7.2		71	12	
7	9.6		72	7.9	
8	9.9		74	9.8	
9	13		76	9.1	
12	8.5		77	3.0	ND
13	6.6		81	5.8	
16	4.4		87	11	Outlier
17	15		88	20	
19	8.6		89	9.2	
20	6.0		91	12	
22	10		92	8.0	ND
24	12		94	9.2	
25	7.6		96	20	Outlier
26	11		99	6.3	
27	10		100	8.0	ND
30	4.6		102	12	
32	9.3				
34	10				
35	13				
36	9.0				
37	10				
38	8.4				
40	12				
42	10				
43	8.0				
45	5.9				
46	9.1				
49	8.2				
52	4.4				
53	12				
54	13				
55	10				
56	9.0				
57	8.3				
59	9.3				
61	13				
62	10				
63	0.69				
64	18	ND			
65	11				
66	6.7				

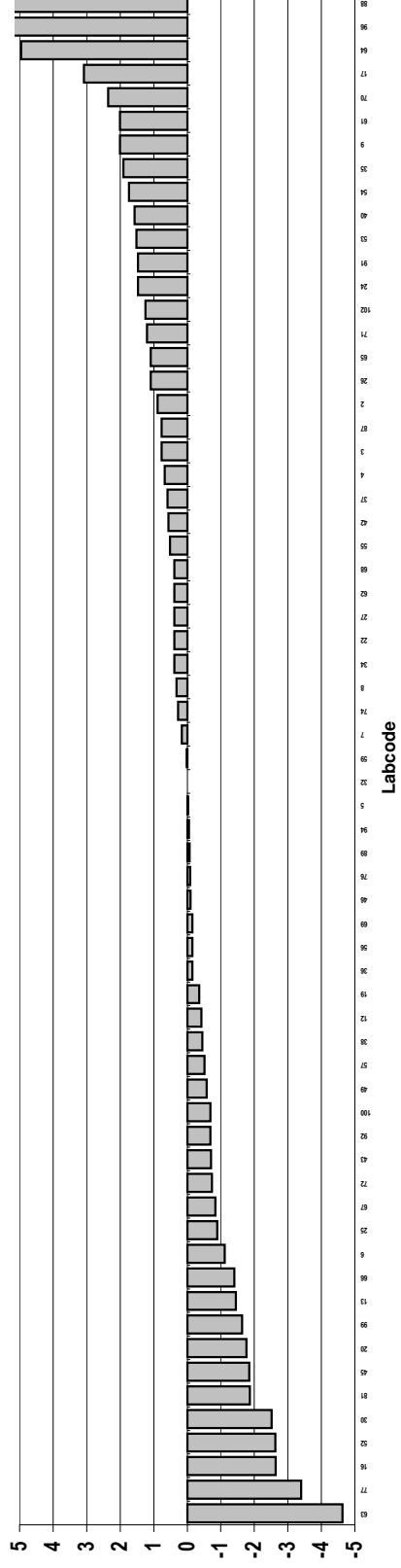
Consensus statistics

Consensus median, pg/g	9.3
Median all values pg/g	9.3
Consensus mean, pg/g	9.3
Standard deviation, pg/g	2.9
Relative standard deviation, %	31
No. of values reported	65
No. of values removed	2
No. of reported non-detects	4

PCB 123



Z-score: PCB 123



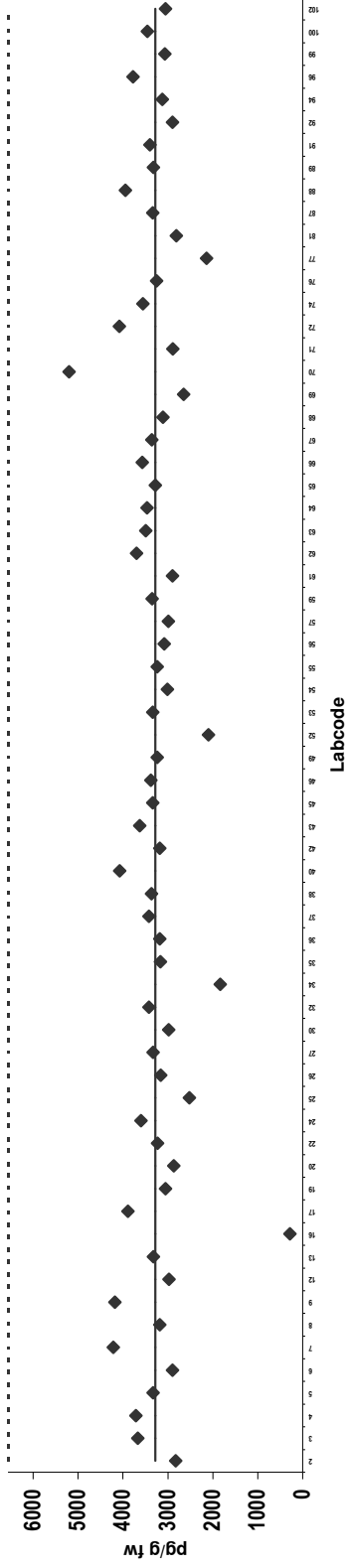
Beef
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	2828		67	3361	
3	3669		68	3110	
4	3711		69	2652	
5	3333		70	5199	
6	2900		71	2890	
7	4216		72	4079	
8	3180		74	3555	
9	4177		76	3251	
12	2973		77	2139	
13	3323		81	2813	
16	282		87	3340	
17	3888		88	3943	
19	3051		89	3326	
20	2868		91	3400	
22	3230		92	2900	
24	3600		94	3127	
25	2520		96	3775	
26	3161		99	3066	
27	3327		100	3459	
30	2985		102	3050	
32	3421				
34	1837				
35	3165				
36	3180				
37	3420				
38	3366				
40	4070				
42	3182				
43	3630				
45	3340				
46	3380				
49	3240				
52	2100				
53	3339				
54	3010				
55	3235				
56	3080				
57	2992				
59	3350				
61	2895				
62	3700				
63	3489				
64	3465				
65	3280				
66	3569				

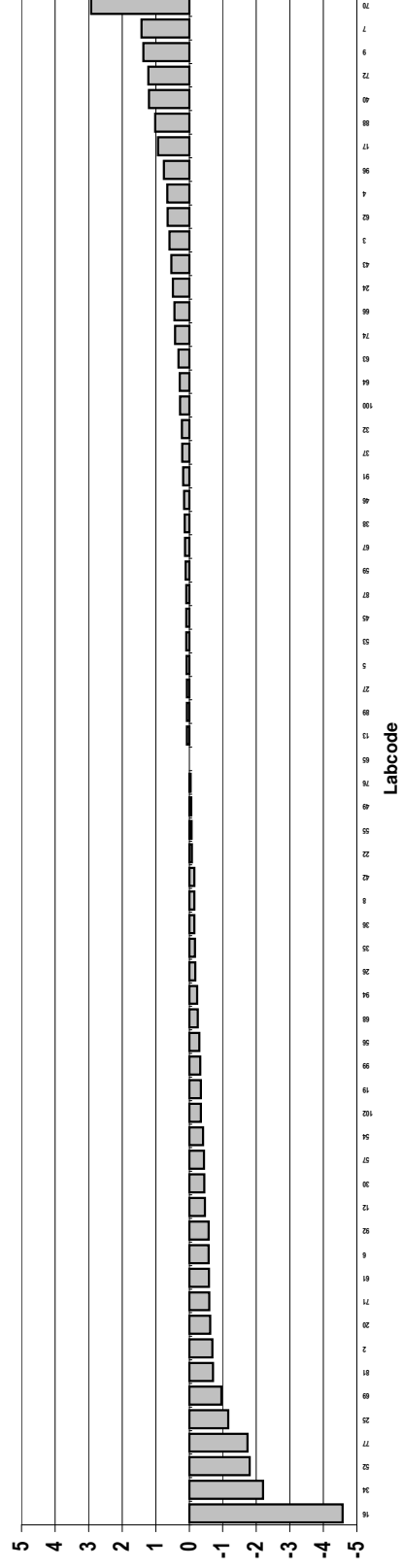
Consensus statistics

Consensus median, pg/g	3280
Median all values pg/g	3280
Consensus mean, pg/g	3237
Standard deviation, pg/g	628
Relative standard deviation, %	19
No. of values reported	65
No. of values removed	0
No. of reported non-detects	0

PCB 156



Z-score: PCB 156



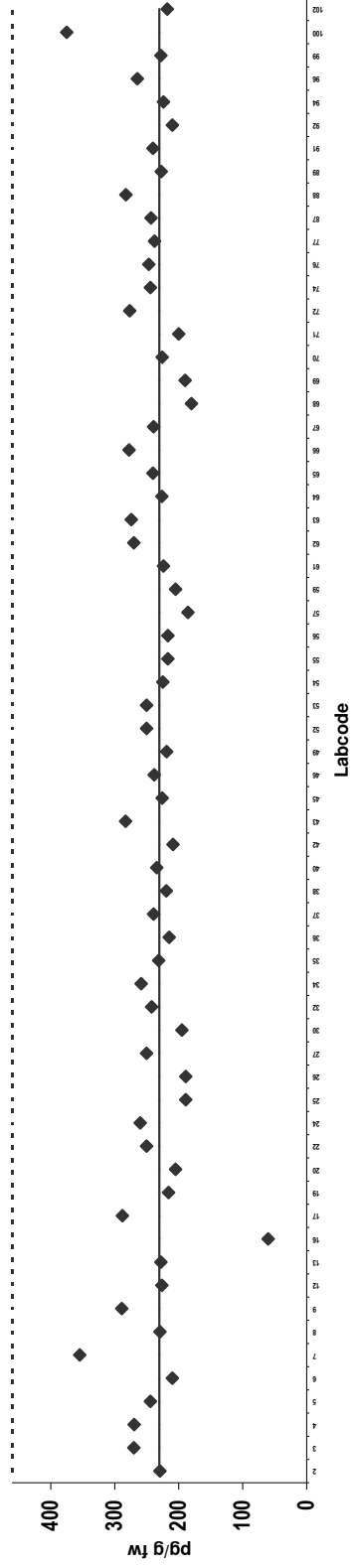
Beef
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	229		67	239	
3	270		68	180	
4	269		69	190	
5	244		70	226	
6	210		71	200	
7	354		72	277	
8	229		74	244	
9	289		76	247	
12	226		77	238	
13	228		87	243	
16	60		88	282	
17	288		89	227	
19	216		91	240	
20	205		92	210	
22	250		94	224	
24	260		96	265	
25	189		99	228	
26	189		100	375	
27	250		102	218	
30	195				
32	242				
34	259				
35	231				
36	215				
37	239				
38	219				
40	234				
42	209				
43	283				
45	226				
46	238				
49	219				
52	250				
53	250				
54	225				
55	217				
56	217				
57	185				
59	205				
61	224				
62	270				
63	274				
64	226				
65	240				
66	277				

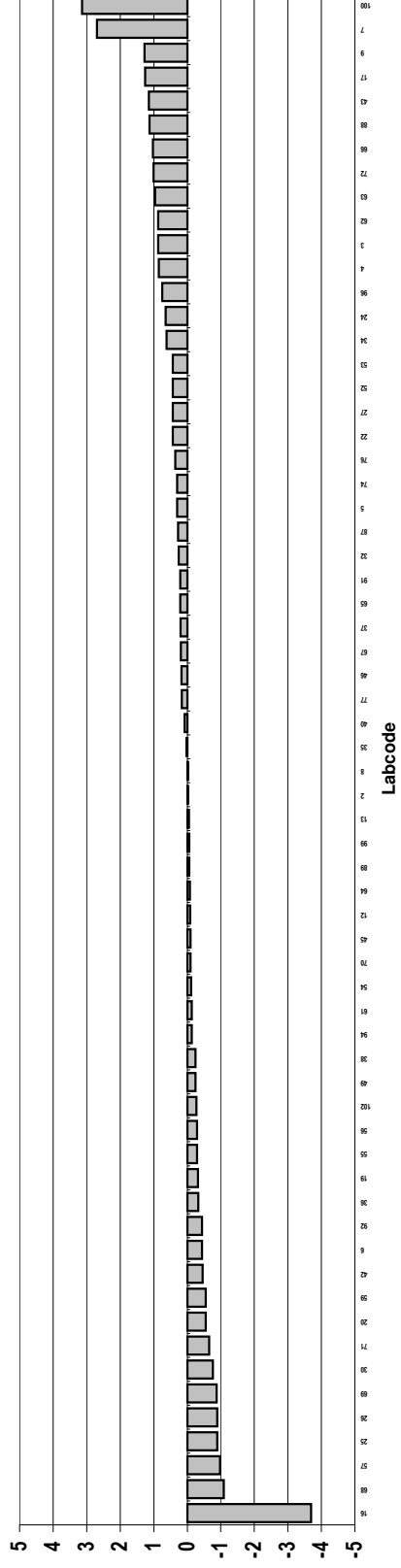
Consensus statistics

Consensus median, pg/g	230
Median all values pg/g	230
Consensus mean, pg/g	236
Standard deviation, pg/g	41
Relative standard deviation, %	18
No. of values reported	64
No. of values removed	0
No. of reported non-detects	0

PCB 157



Z-score: PCB 157



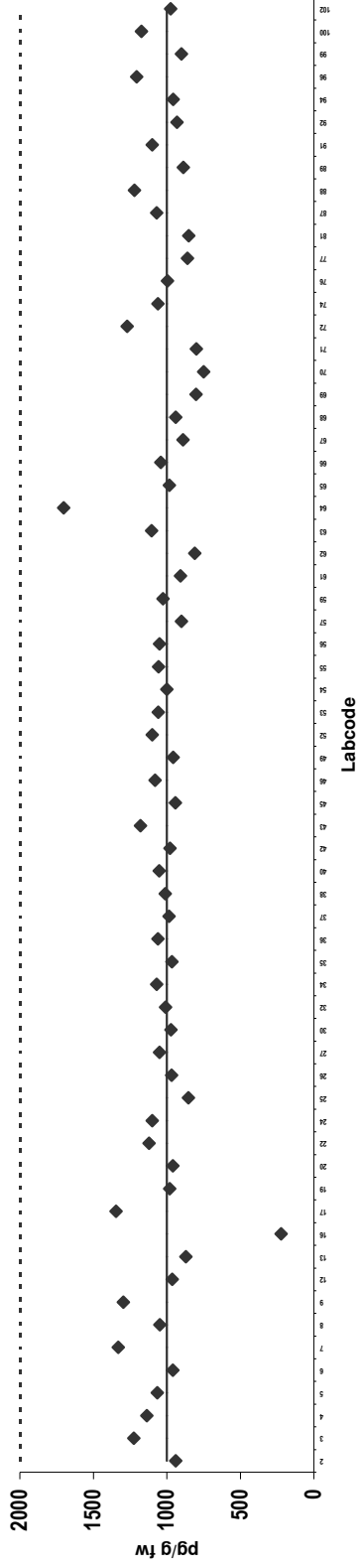
Beef
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	939		67	889	
3	1225		68	940	
4	1136		69	801	
5	1065		70	750	
6	960		71	800	
7	1331		72	1271	
8	1048		74	1060	
9	1296		76	997	
12	964		77	859	
13	871		81	852	
16	224		87	1070	
17	1346		88	1221	
19	980		89	887	
20	958		91	1100	
22	1120		92	930	
24	1100		94	956	
25	853		96	1205	
26	967		99	900	
27	1049		100	1173	
30	972		102	974	
32	1008				
34	1069				
35	966				
36	1060				
37	985				
38	1010				
40	1051				
42	978				
43	1180				
45	941				
46	1080				
49	956				
52	1100				
53	1059				
54	1000				
55	1055				
56	1050				
57	900				
59	1025				
61	907				
62	810				
63	1104				
64	1702				
65	983				
66	1041				

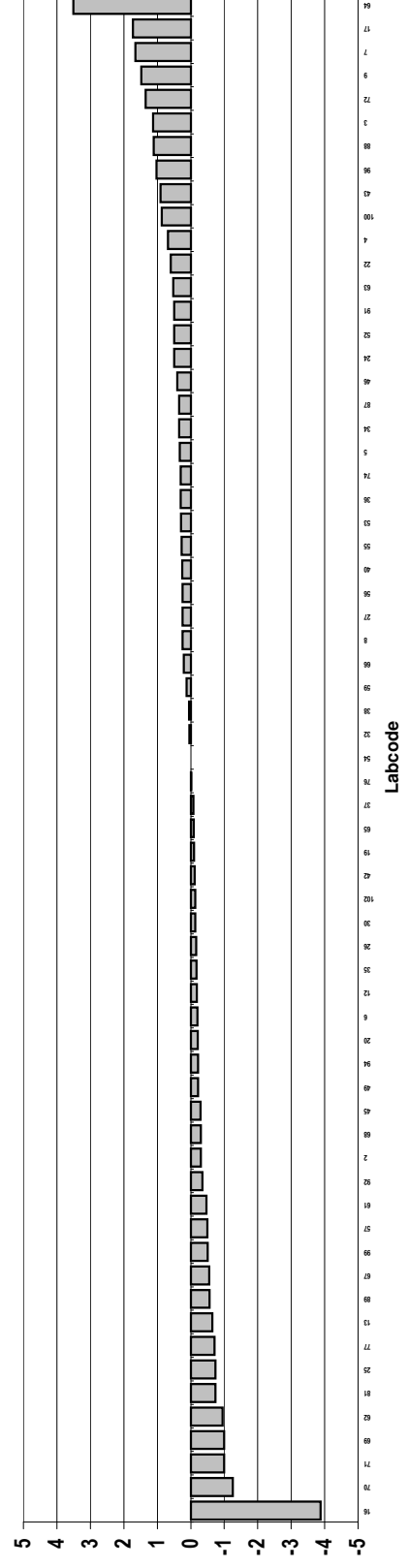
Consensus statistics

Consensus median, pg/g	1000
Median all values pg/g	1000
Consensus mean, pg/g	1016
Standard deviation, pg/g	183
Relative standard deviation, %	18
No. of values reported	65
No. of values removed	0
No. of reported non-detects	0

PCB 167



Z-score: PCB 167



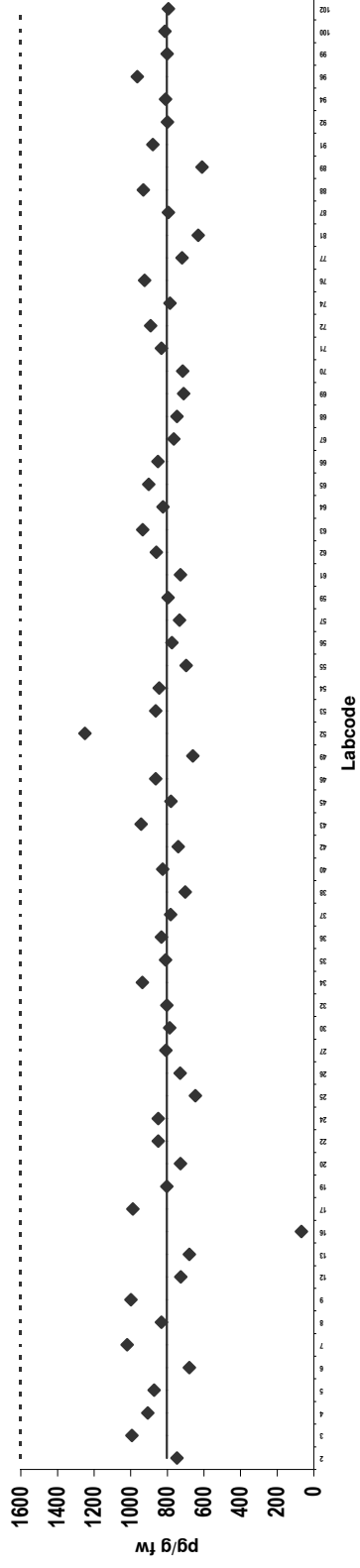
Beef
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	747		67	765	
3	993		68	748	
4	907		69	711	
5	872		70	716	
6	680		71	833	
7	1019		72	891	
8	832		74	786	
9	999		76	924	
12	727		77	719	
13	679		81	632	
16	68		87	794	
17	989		88	931	
19	803		89	610	
20	729		91	880	
22	850		92	800	
24	850		94	809	
25	647		96	964	
26	731		99	800	
27	808		100	814	
30	788		102	794	
32	803				
34	937				
35	810				
36	832				
37	783				
38	702				
40	825				
42	740				
43	944				
45	781				
46	864				
49	660				
52	1250				
53	863				
54	845				
55	697				
56	775				
57	734				
59	796				
61	729				
62	860				
63	935				
64	824				
65	901				
66	851				

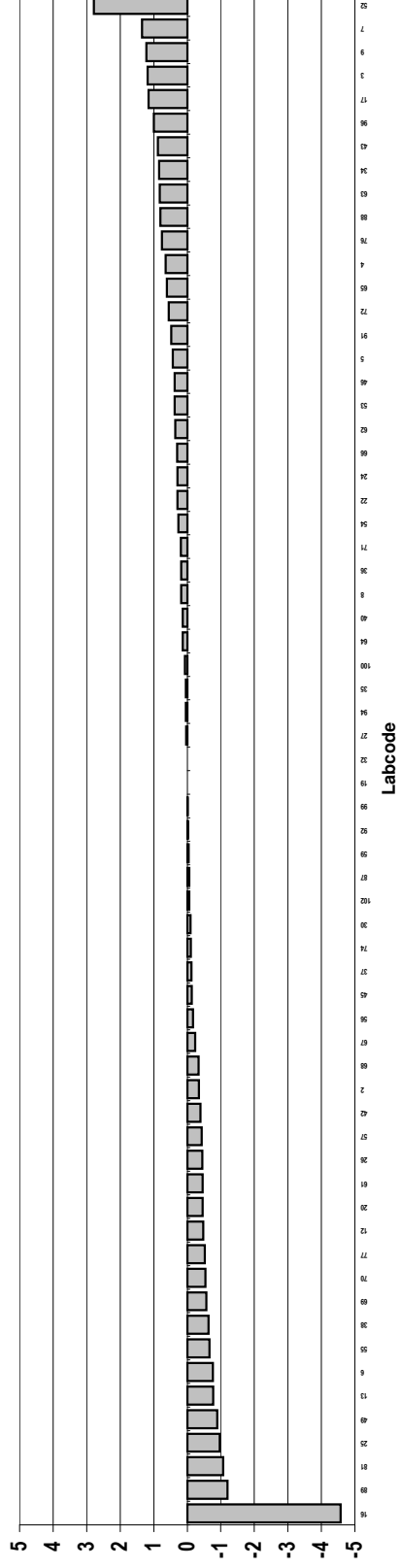
Consensus statistics

Consensus median, pg/g	803
Median all values pg/g	803
Consensus mean, pg/g	806
Standard deviation, pg/g	142
Relative standard deviation, %	18
No. of values reported	65
No. of values removed	0
No. of reported non-detects	0

PCB 189



Z-score: PCB 189



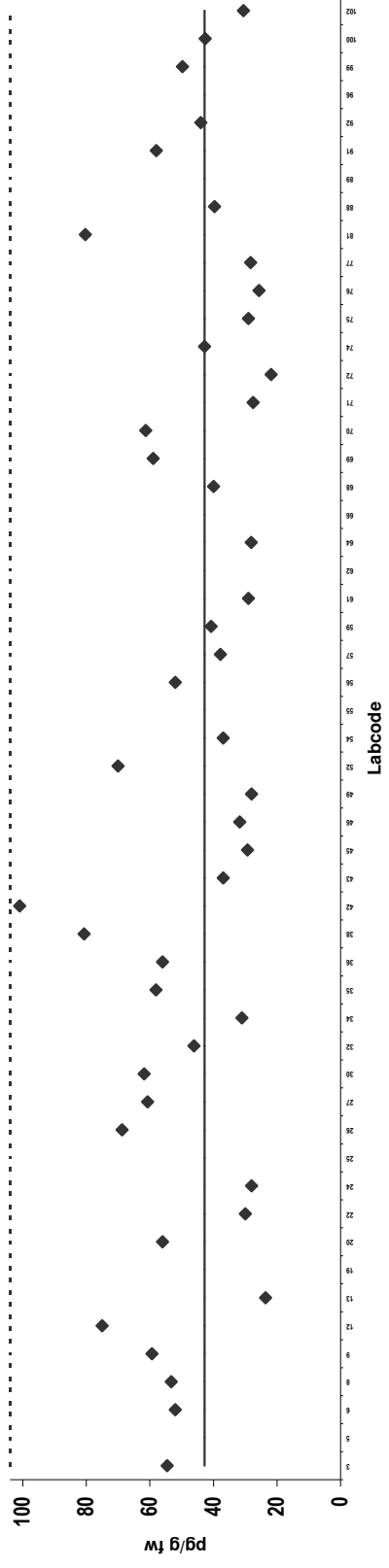
Beef
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	55		88	40	
5	484	Outlier	89	938	Outlier
6	52		91	58	
8	53		92	44	
9	59		96	600	Outlier,ND
12	75		99	50	
13	24		100	43	
19	189	Outlier	102	31	
20	56				
22	30				
24	28				
25	500	Outlier,ND			
26	69				
27	61				
30	62				
32	46				
34	31				
35	58				
36	56				
38	81				
42	101				
43	37				
45	29				
46	32				
49	28				
52	70				
54	37	Outlier			
55	122				
56	52				
57	38				
59	41				
61	29				
62	124	Outlier			
64	28				
66	114	Outlier			
68	40				
69	59				
70	61				
71	28				
72	22				
74	43				
75	29				
76	26				
77	28				
81	80				

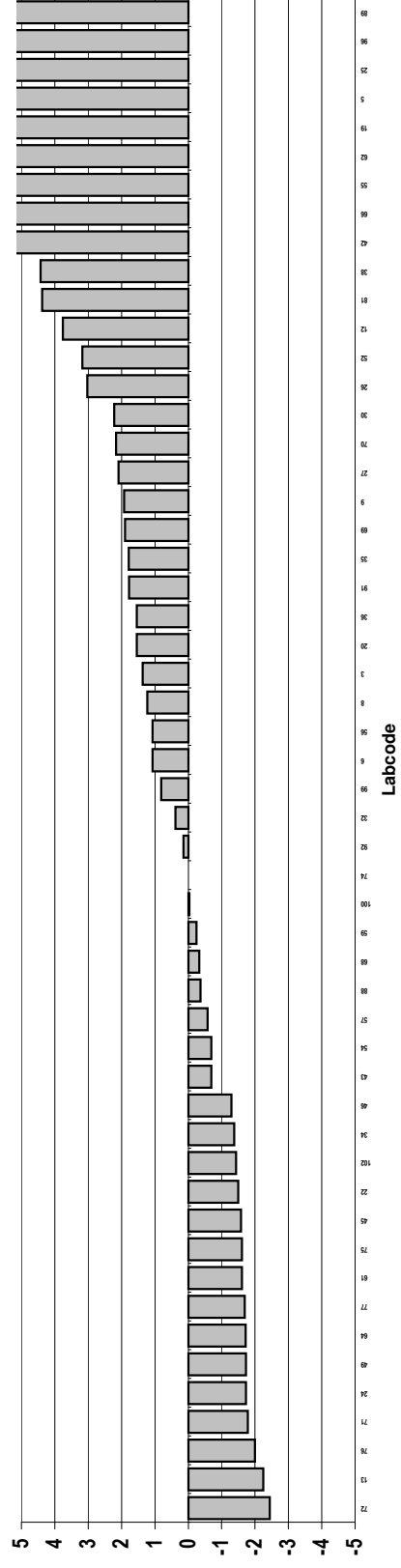
Consensus statistics

Consensus median, pg/g	43
Median all values pg/g	52
Consensus mean, pg/g	47
Standard deviation, pg/g	18
Relative standard deviation, %	39
No. of values reported	53
No. of values removed	8
No. of reported non-detects	2

CB 28



Z-score: CB 28



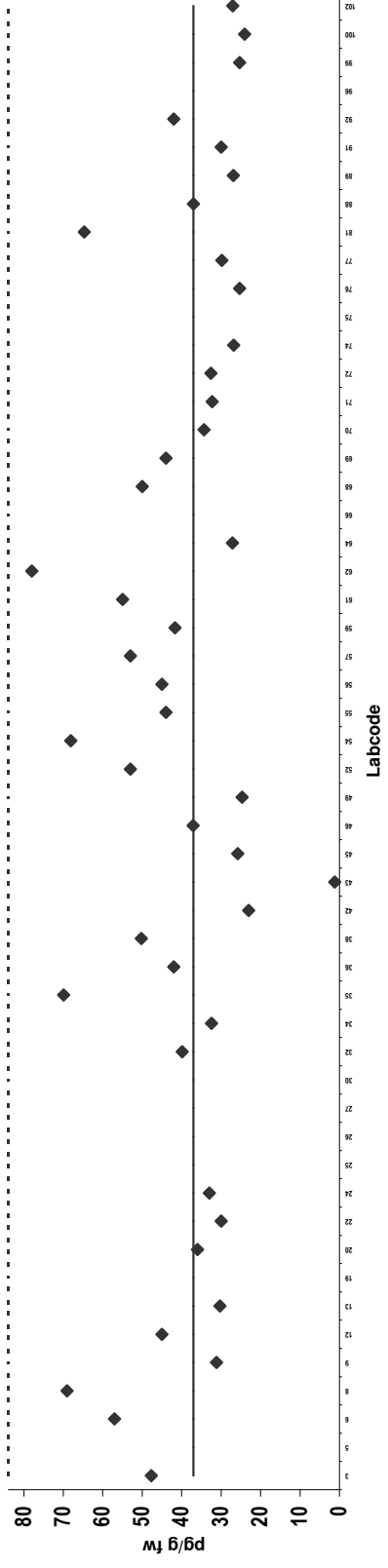
Beef
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	48		88	37	
5	1222	Outlier	89	27	
6	57		91	30	
8	69		92	42	
9	31		96	600	Outlier,ND
12	45		99	25	
13	30		100	24	
19	585	Outlier	102	27	
20	36				
22	30				
24	33				
25	500	Outlier,ND			
26	138	Outlier			
27	110	Outlier			
30	111	Outlier			
32	40				
34	32				
35	70				
36	42				
38	50				
42	23				
43	1.2	ND			
45	26				
46	37				
49	25				
52	53				
54	68				
55	44				
56	45				
57	53				
59	42				
61	55				
62	78				
64	27				
66	224	Outlier			
68	50				
69	44				
70	34				
71	32				
72	33				
74	27				
75	88	Outlier			
76	25				
77	30				
81	65				

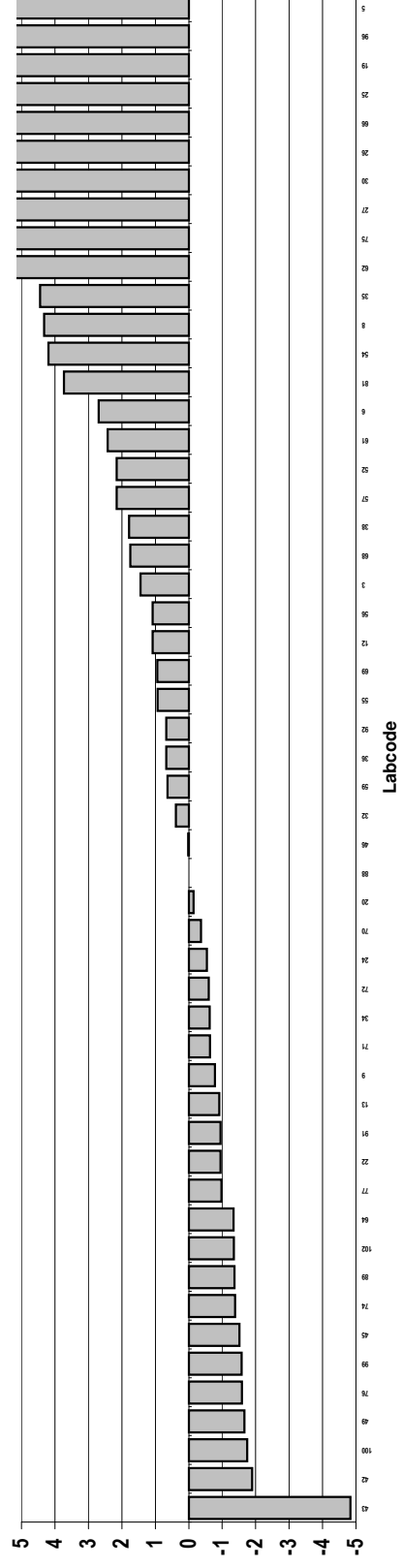
Consensus statistics

Consensus median, pg/g	37
Median all values pg/g	42
Consensus mean, pg/g	40
Standard deviation, pg/g	15
Relative standard deviation, %	39
No. of values reported	53
No. of values removed	9
No. of reported non-detects	3

CB 52



Z-score: CB 52



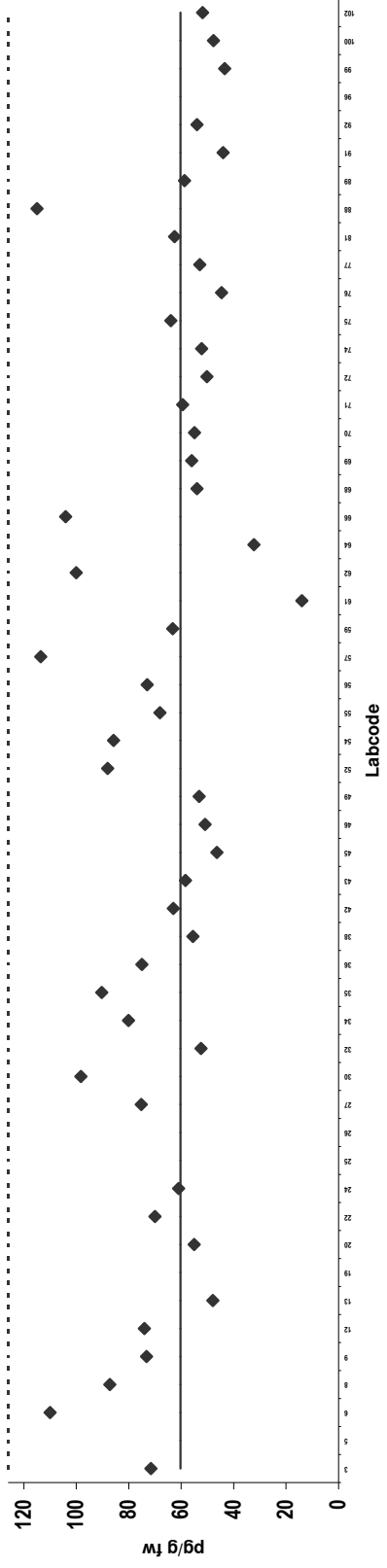
Beef
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	72		88	115	
5	526	Outlier	89	59	
6	110		91	44	
8	87		92	54	
9	73		96	600	Outlier,ND
12	74		99	43	
13	48		100	48	
19	204	Outlier	102	52	
20	55				
22	70				
24	61				
25	500				
26	381	Outlier,ND			
27	75	Outlier			
30	98				
32	52				
34	80				
35	90				
36	75				
38	56				
42	63				
43	58				
45	46				
46	51				
49	53				
52	88				
54	86				
55	68				
56	73				
57	113				
59	63				
61	14				
62	100				
64	32				
66	104				
68	54				
69	56				
70	55				
71	60				
72	50				
74	52				
75	64				
76	45				
77	53				
81	63				

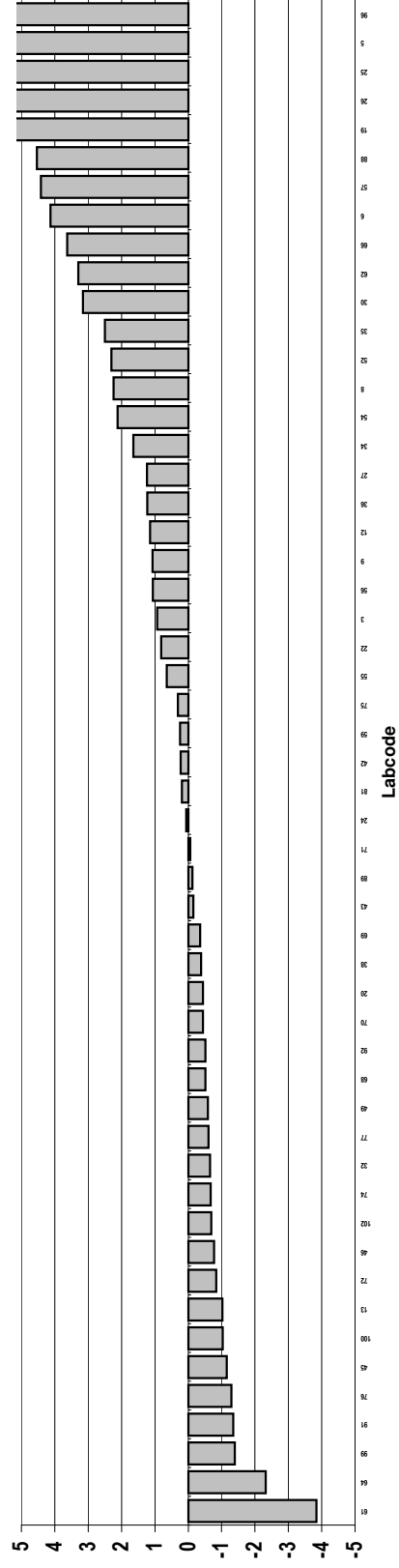
Consensus statistics

Consensus median, pg/g	60
Median all values pg/g	63
Consensus mean, pg/g	66
Standard deviation, pg/g	21
Relative standard deviation, %	32
No. of values reported	53
No. of values removed	5
No. of reported non-detects	2

CB 101



Z-score: CB 101



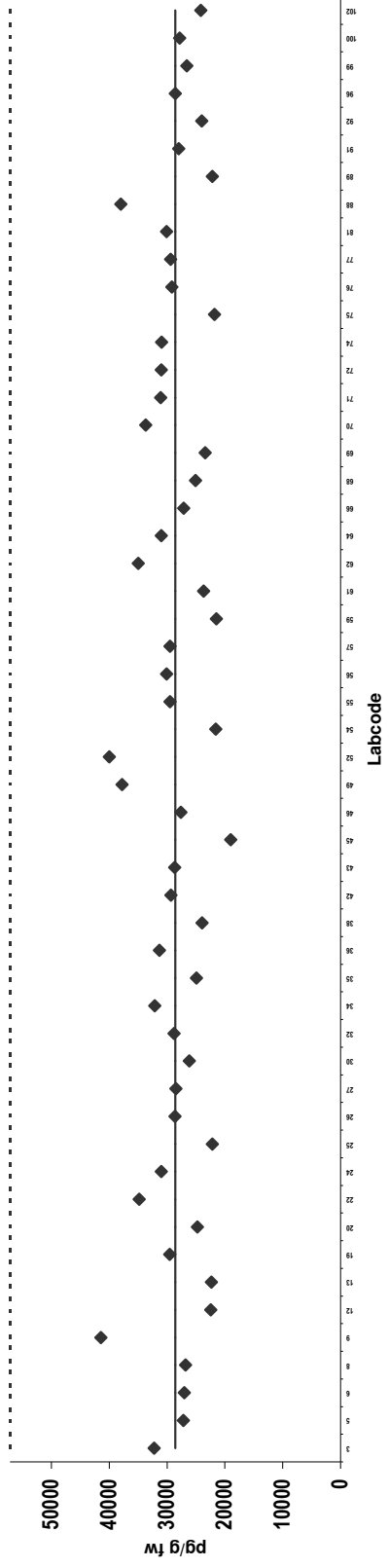
Beef
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	32238		88	38012	
5	27191		89	22184	
6	27000		91	28000	
8	26789		92	24000	
9	41429		96	28580	
12	22432		99	26580	
13	22339		100	27843	
19	29526		102	24163	
20	24762				
22	34840				
24	31000				
25	22200				
26	28609				
27	28459				
30	26143				
32	28782				
34	32133				
35	24937				
36	31300				
38	23937				
42	29323				
43	28700				
45	19000				
46	27600				
49	37800				
52	40000				
54	21600				
55	29503				
56	30100				
57	29488				
59	21500				
61	23691				
62	35000				
64	30980				
66	27117				
68	25100				
69	23400				
70	33682				
71	31100				
72	31024				
74	30943				
75	21775				
76	29173				
77	29400				
81	30097				

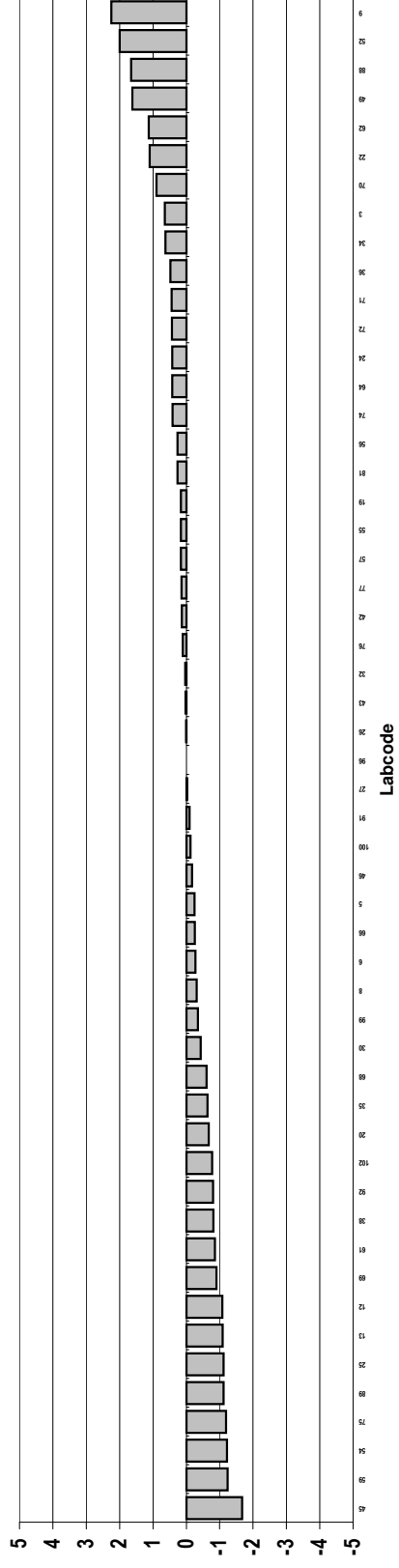
Consensus statistics

Consensus median, pg/g	28580
Median all values pg/g	28580
Consensus mean, pg/g	28349
Standard deviation, pg/g	4833
Relative standard deviation, %	17
No. of values reported	53
No. of values removed	0
No. of reported non-detects	0

CB 138



Z-score: CB 138



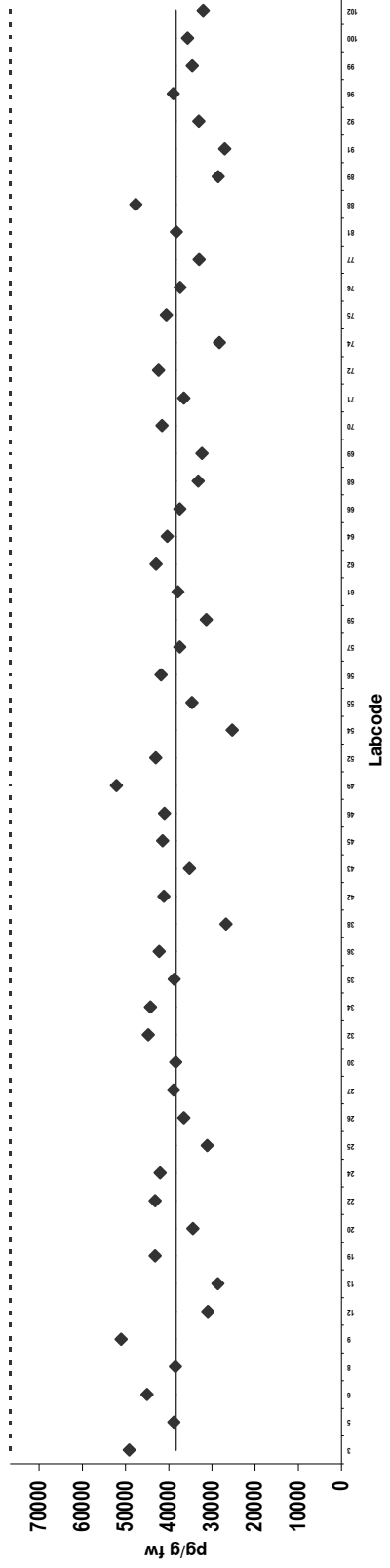
Beef
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	49167		88	47603	
5	38822		89	28516	
6	45000		91	27000	
8	38416		92	33000	
9	51039		96	38950	
12	30899		99	34565	
13	28604		100	35653	
19	43126		102	31992	
20	34399				
22	43140				
24	42000				
25	31100				
26	36468				
27	38912				
30	38376				
32	44702				
34	44231				
35	38710				
36	42200				
38	26736				
42	41143				
43	35200				
45	41400				
46	41000				
49	52100				
52	43000				
54	25300				
55	34586				
56	41800				
57	37463				
59	31300				
61	37834				
62	42900				
64	40360				
66	37431				
68	33200				
69	32300				
70	41522				
71	36500				
72	42366				
74	28239				
75	40530				
76	37332				
77	32959				
81	38257				

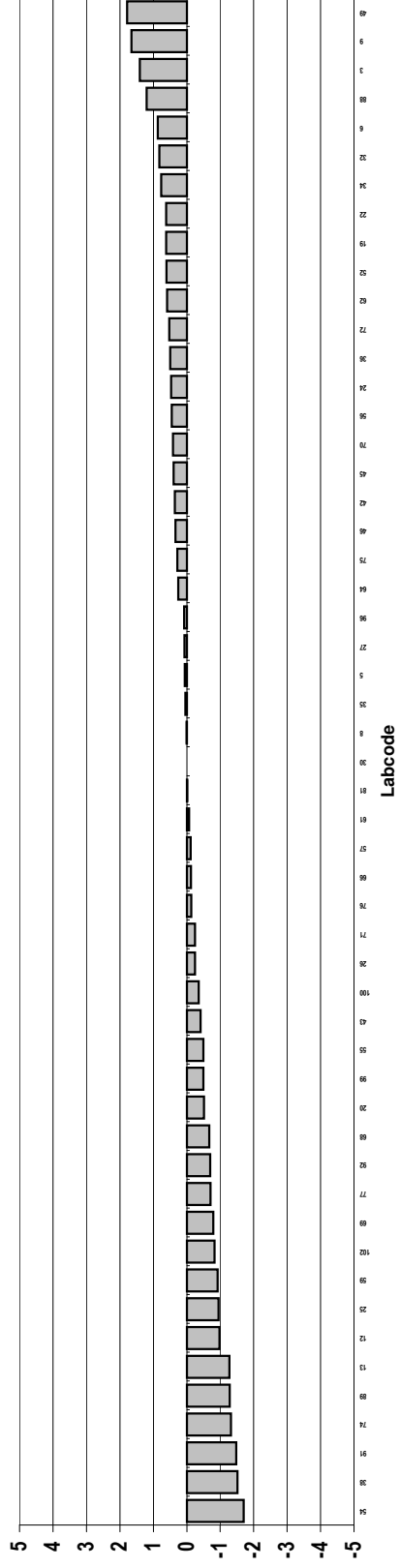
Consensus statistics

Consensus median, pg/g	38376
Median all values pg/g	38376
Consensus mean, pg/g	37912
Standard deviation, pg/g	6152
Relative standard deviation, %	16
No. of values reported	53
No. of values removed	0
No. of reported non-detects	0

CB 153



Z-score: CB 153



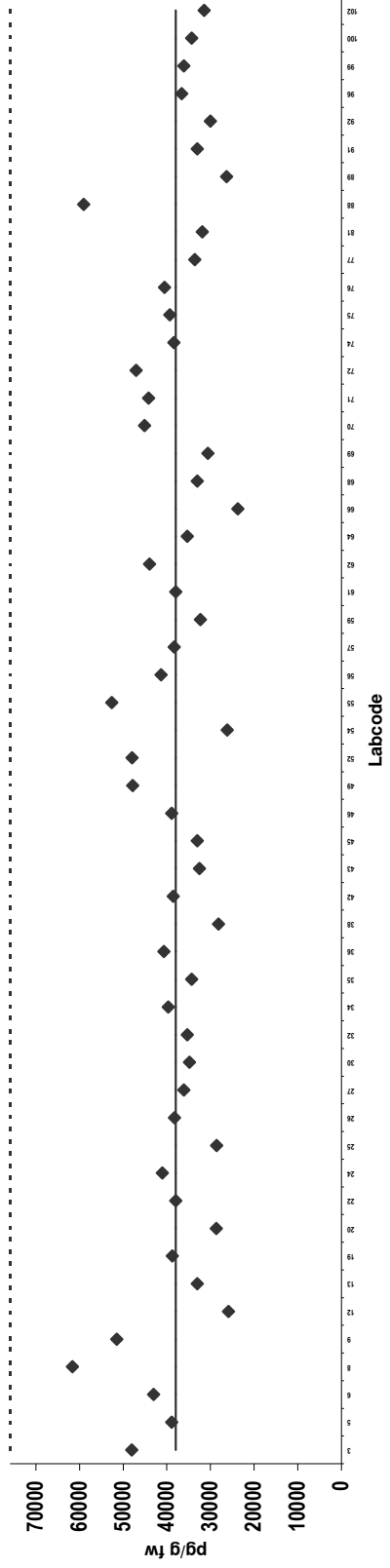
Beef
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	48054		88	59083	
5	38871		89	26277	
6	43000		91	33000	
8	61645		92	30000	
9	51486		96	36610	
12	25882		99	36096	
13	33063		100	34316	
19	38743		102	31473	
20	28654				
22	37960				
24	41000				
25	28600				
26	38245				
27	36132				
30	34822				
32	35343				
34	39666				
35	34281				
36	40700				
38	28143				
42	38567				
43	32500				
45	33000				
46	38900				
49	47800				
52	48000				
54	26200				
55	52635				
56	41300				
57	38288				
59	32300				
61	37972				
62	44000				
64	35320				
66	23732				
68	33000				
69	30600				
70	45086				
71	44200				
72	47011				
74	38419				
75	39293				
76	40516				
77	33614				
81	31895				

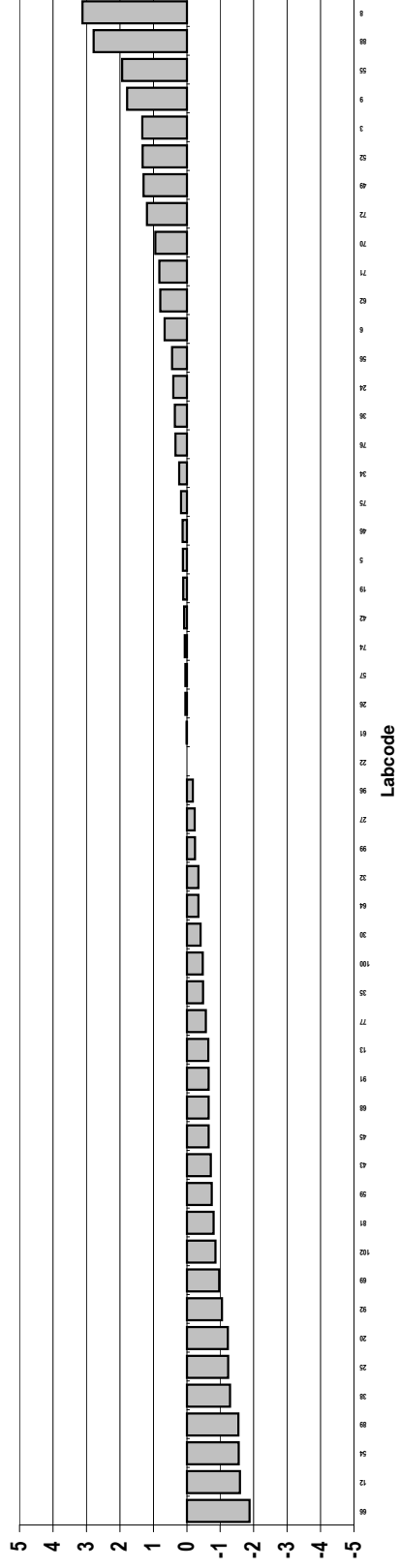
Consensus statistics

Consensus median, pg/g	37960
Median all values pg/g	37960
Consensus mean, pg/g	37836
Standard deviation, pg/g	7975
Relative standard deviation, %	21
No. of values reported	53
No. of values removed	0
No. of reported non-detects	0

CB 180



Z-score: CB 180



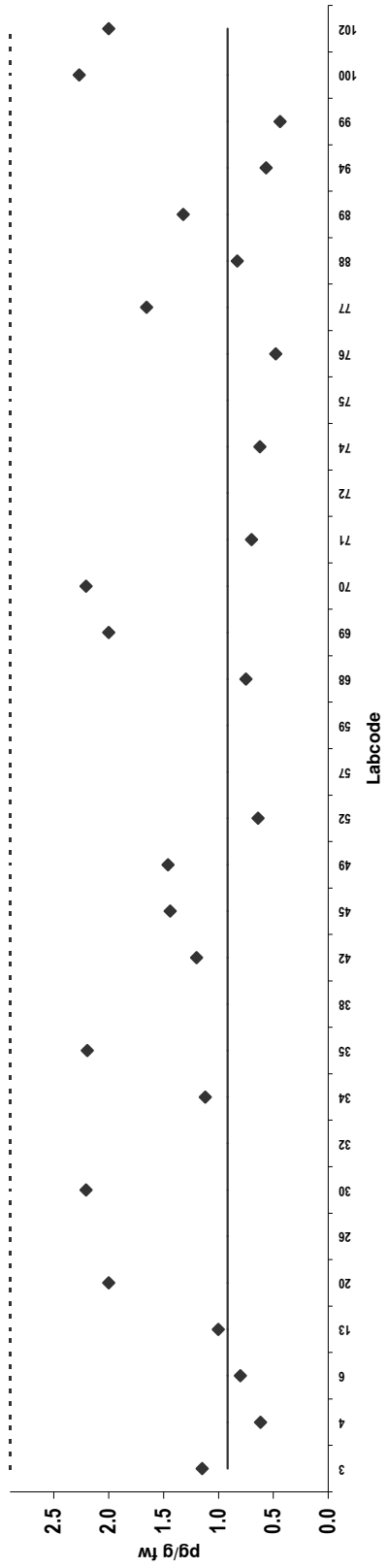
Beef
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	1.2				
4	0.62				
6	0.80				
13	1.0				
20	2.0	ND			
26	2.1	Outlier,ND			
30	2.2				
32	3.2	Outlier			
34	1.1				
35	2.2				
38	4.1	Outlier			
42	1.2	ND			
45	1.4				
49	1.5				
52	0.64				
57	3.8	Outlier,ND			
59	10	Outlier,ND			
68	0.75				
69	2.0				
70	2.2	ND			
71	0.70				
72	3.2	Outlier			
74	0.62				
75	9.0	Outlier,ND			
76	0.48				
77	1.7	ND			
88	0.83				
89	1.3				
94	0.56				
99	0.44				
100	2.3				
102	2.0	ND			

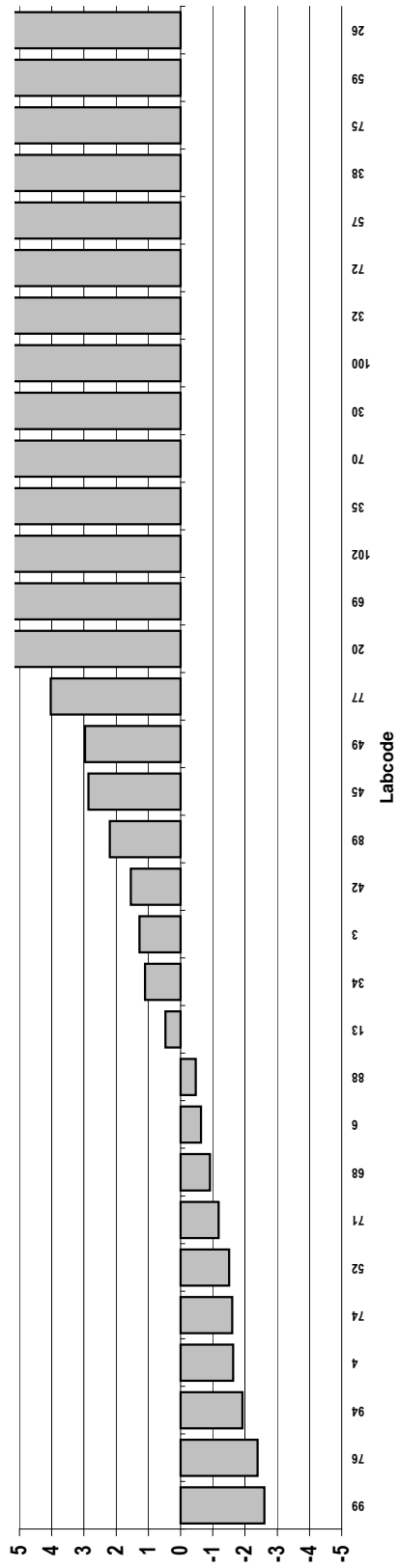
Consensus statistics

Consensus median, pg/g	0.92
Median all values pg/g	1.5
Consensus mean, pg/g	1.3
Standard deviation, pg/g	0.63
Relative standard deviation, %	50
No. of values reported	32
No. of values removed	7
No. of reported non-detects	9

BDE 28



Z-score: BDE 28



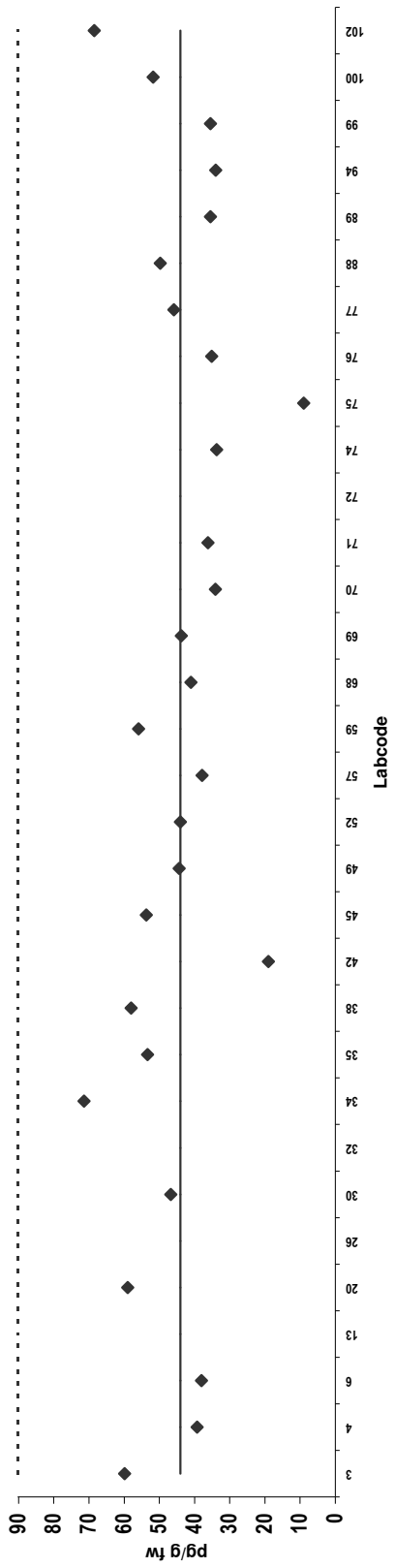
Beef
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	60				
4	39				
6	38				
13	117	Outlier			
20	59				
26	167	Outlier			
30	47				
32	125	Outlier			
34	71				
35	53				
38	58				
42	19				
45	54				
49	44				
52	44				
57	38				
59	56				
68	41				
69	44				
70	34				
71	36				
72	106	Outlier			
74	34				
75	9.0	ND			
76	35				
77	46				
88	50				
89	36				
94	34				
99	35				
100	52				
102	69				

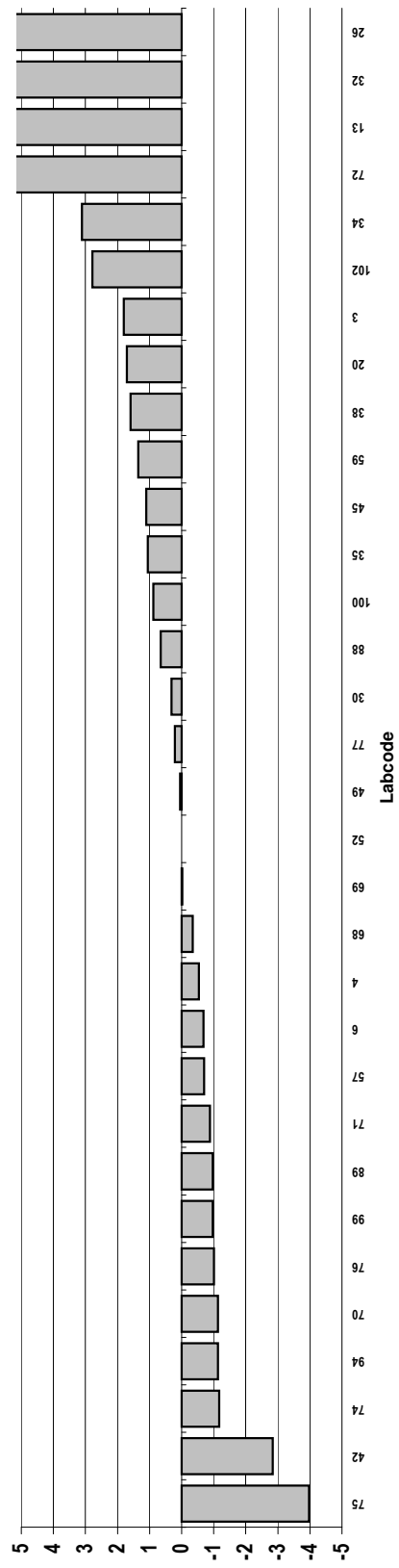
Consensus statistics

Consensus median, pg/g	44
Median all values pg/g	45
Consensus mean, pg/g	44
Standard deviation, pg/g	14
Relative standard deviation, %	31
No. of values reported	32
No. of values removed	4
No. of reported non-detects	1

BDE 47



Z-score: BDE 47



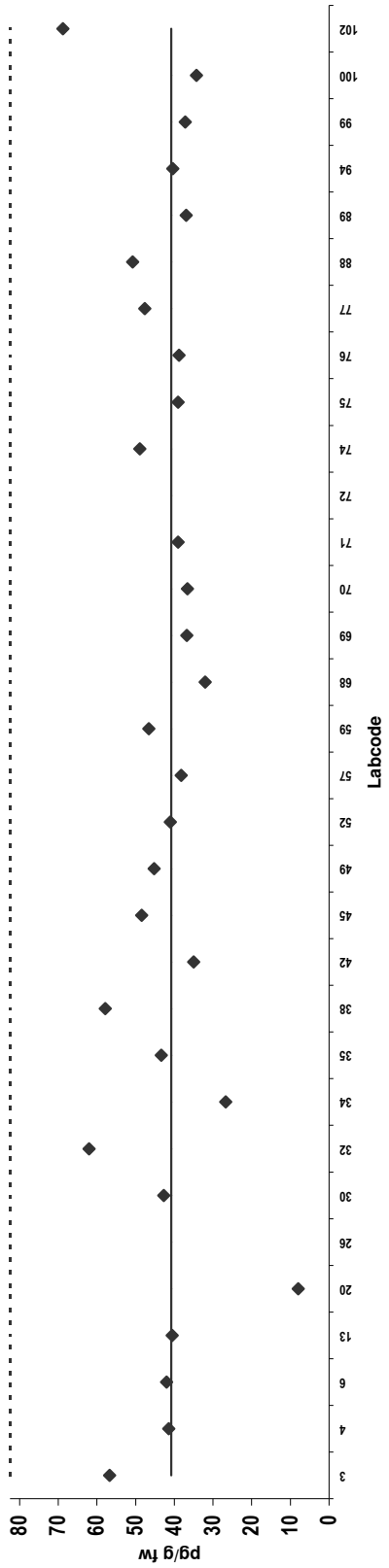
Beef
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	57				
4	41				
6	42				
13	41				
20	8.0				
26	92				
30	43	Outlier			
32	62				
34	27				
35	43				
38	58				
42	35				
45	48				
49	45				
52	41				
57	38				
59	47				
68	32				
69	37				
70	37				
71	39				
72	114	Outlier			
74	49				
75	39				
76	39				
77	48				
88	51				
89	37				
94	40				
99	37				
100	34				
102	69				

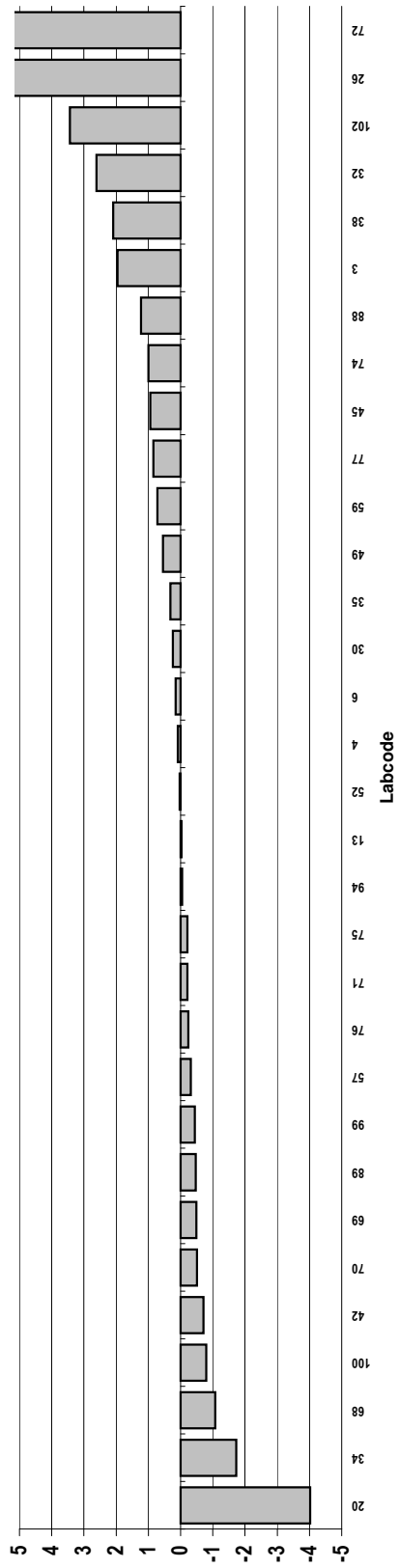
Consensus statistics

Consensus median, pg/g	41
Median all values pg/g	41
Consensus mean, pg/g	42
Standard deviation, pg/g	11
Relative standard deviation, %	26
No. of values reported	32
No. of values removed	2
No. of reported non-detects	0

BDE 99



Z-score: BDE 99



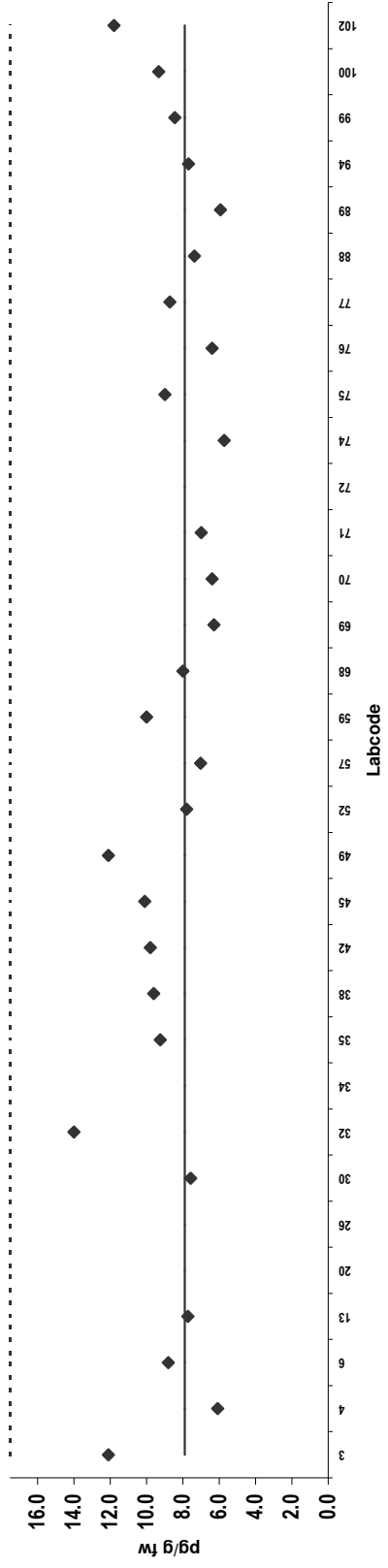
Beef
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	12				
4	6.1				
6	8.8				
13	7.7				
20	60	Outlier			
26	28	Outlier			
30	7.6				
32	14				
34	27				
35	9.2				
38	9.6				
42	9.8				
45	10				
49	12				
52	7.8				
57	7.0				
59	10				
68	8.0	ND			
69	6.3				
70	6.4				
71	7.0				
72	25				
74	5.7	Outlier			
75	9.0				
76	6.4				
77	8.7				
88	7.4				
89	5.9				
94	7.7				
99	8.5				
100	9.3				
102	12				

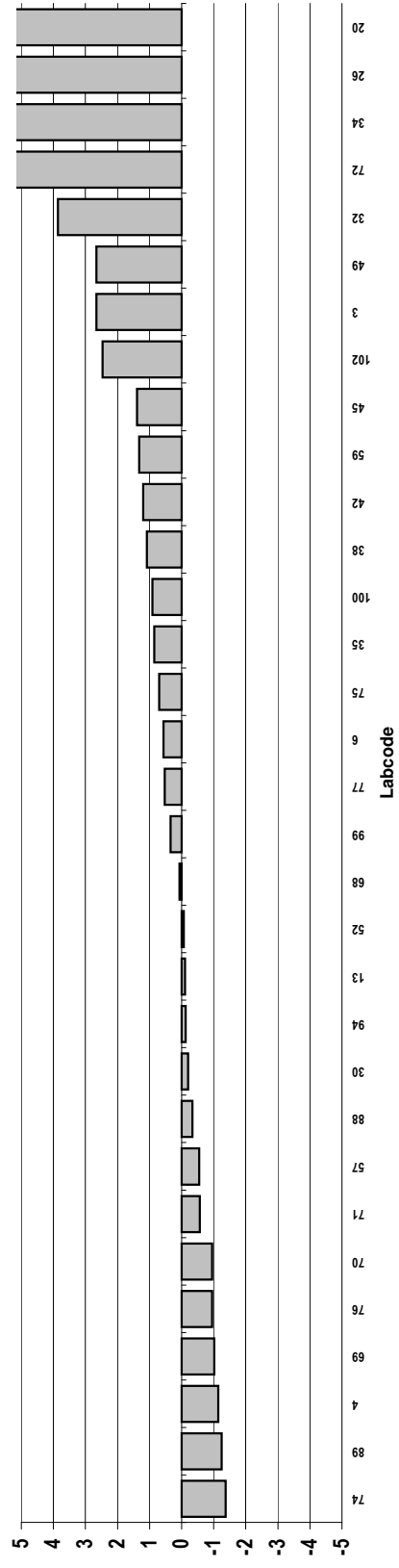
Consensus statistics

Consensus median, pg/g	7.9
Median all values pg/g	8.8
Consensus mean, pg/g	8.6
Standard deviation, pg/g	2.1
Relative standard deviation, %	24
No. of values reported	32
No. of values removed	4
No. of reported non-detects	2

BDE 100



Z-score: BDE 100



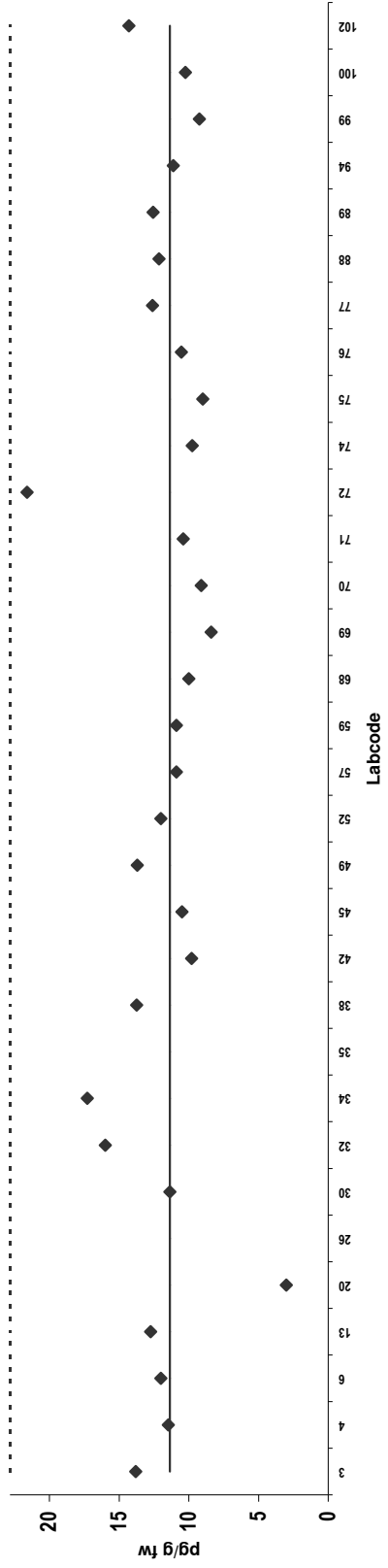
Beef
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	14				
4	11				
6	12				
13	13				
20	3.0				
26	25	Outlier,ND			
30	11				
32	16				
34	17				
35	26	Outlier			
38	14				
42	9.8				
45	11				
49	14				
52	12				
57	11				
59	11				
68	10				
69	8.4				
70	9.1				
71	10				
72	22				
74	9.8				
75	9.0	ND			
76	11				
77	13				
88	12				
89	13				
94	11				
99	9.2				
100	10				
102	14				

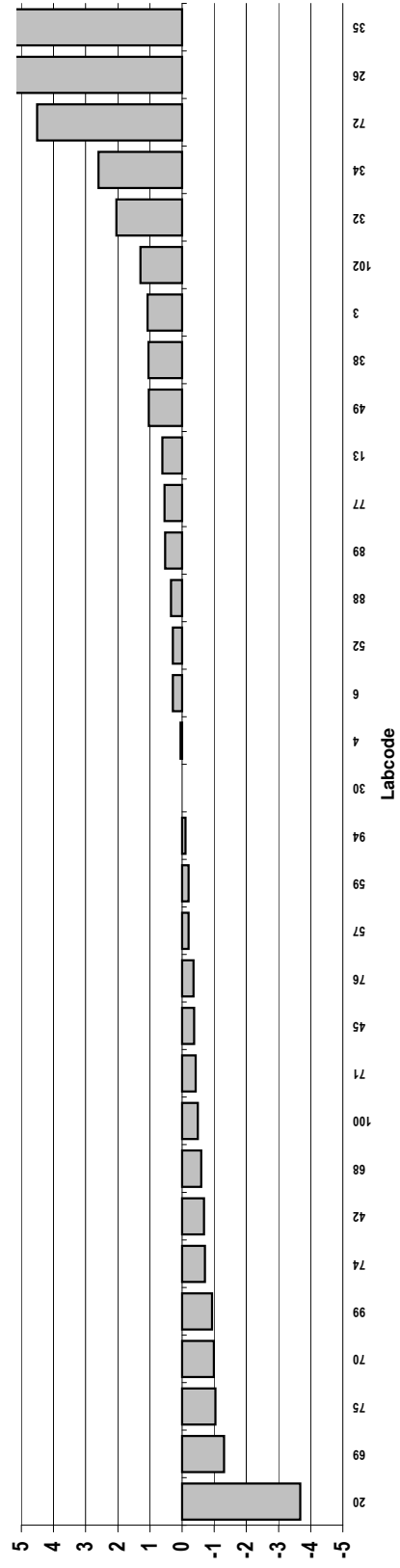
Consensus statistics

Consensus median, pg/g	11
Median all values pg/g	11
Consensus mean, pg/g	12
Standard deviation, pg/g	3.2
Relative standard deviation, %	27
No. of values reported	32
No. of values removed	2
No. of reported non-detects	2

BDE 153



Z-score: BDE 153



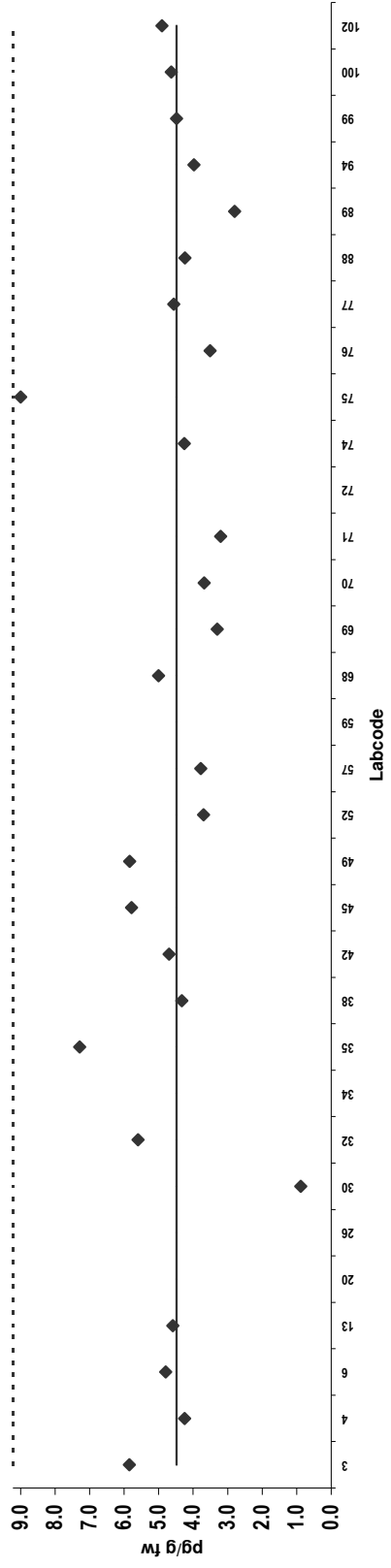
Beef
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5.9				
4	4.2				
6	4.8				
13	4.6				
20	11	Outlier			
26	30	Outlier,ND			
30	0.88				
32	5.6				
34	9.5	Outlier			
35	7.3				
38	4.3				
42	4.7				
45	5.8				
49	5.8				
52	3.7				
57	3.8	ND			
59	10	Outlier,ND			
68	5.0				
69	3.3				
70	3.7				
71	3.2	Outlier			
72	15				
74	4.3				
75	9.0	ND			
76	3.5				
77	4.6				
88	4.2				
89	2.8				
94	4.0				
99	4.5				
100	4.6				
102	4.9				

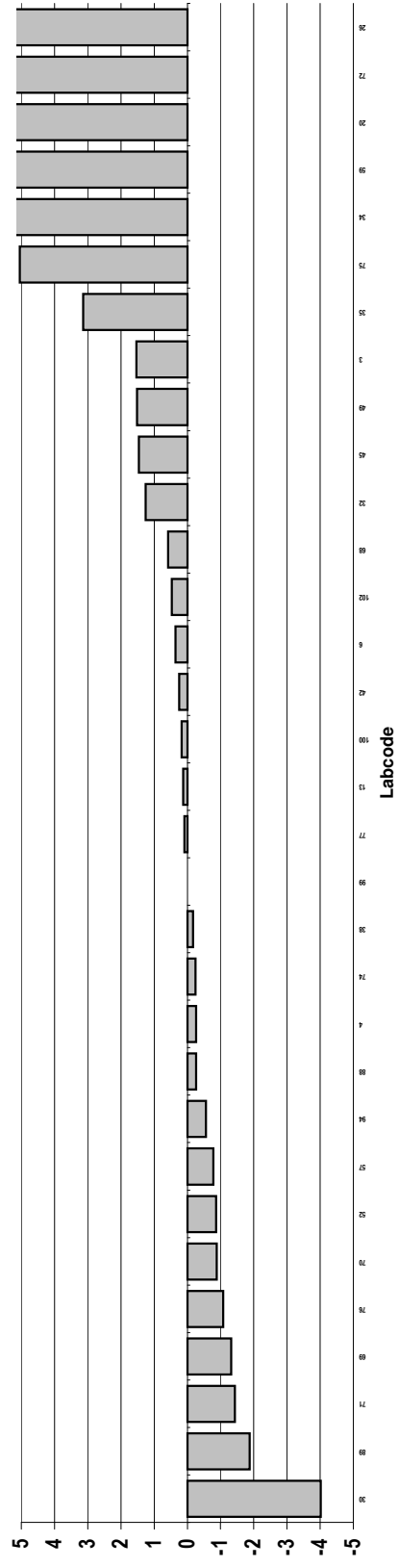
Consensus statistics

Consensus median, pg/g	4.5
Median all values pg/g	4.6
Consensus mean, pg/g	4.6
Standard deviation, pg/g	1.5
Relative standard deviation, %	33
No. of values reported	32
No. of values removed	5
No. of reported non-detects	4

BDE 154



Z-score: BDE 154



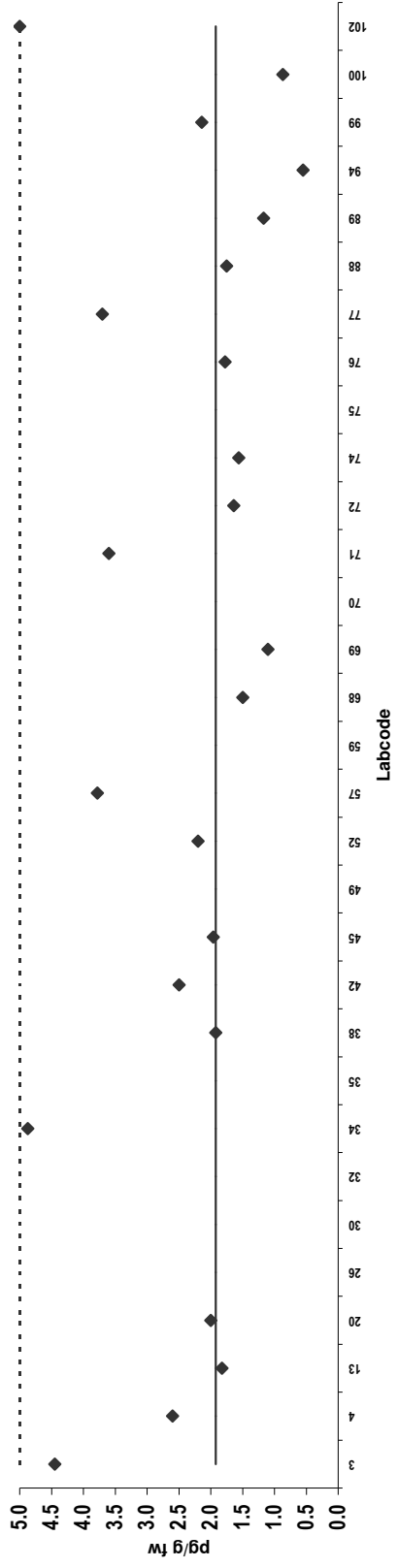
Beef
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	4.5				
4	2.6				
13	1.8				
20	2.0	ND			
26	22	Outlier,ND			
30	13	Outlier			
32	9.0	Outlier			
34	4.9				
35	42	Outlier			
38	1.9				
42	2.5	ND			
45	2.0				
49	5.2	Outlier			
52	2.2				
57	3.8	ND			
59	10	Outlier,ND			
68	1.5				
69	1.1				
70	7.3	Outlier,ND			
71	3.6				
72	1.6	ND			
74	1.6				
75	9.0	Outlier,ND			
76	1.8				
77	3.7				
88	1.8				
89	1.2				
94	0.55				
99	2.1				
100	0.87	ND			
102	5.0	ND			

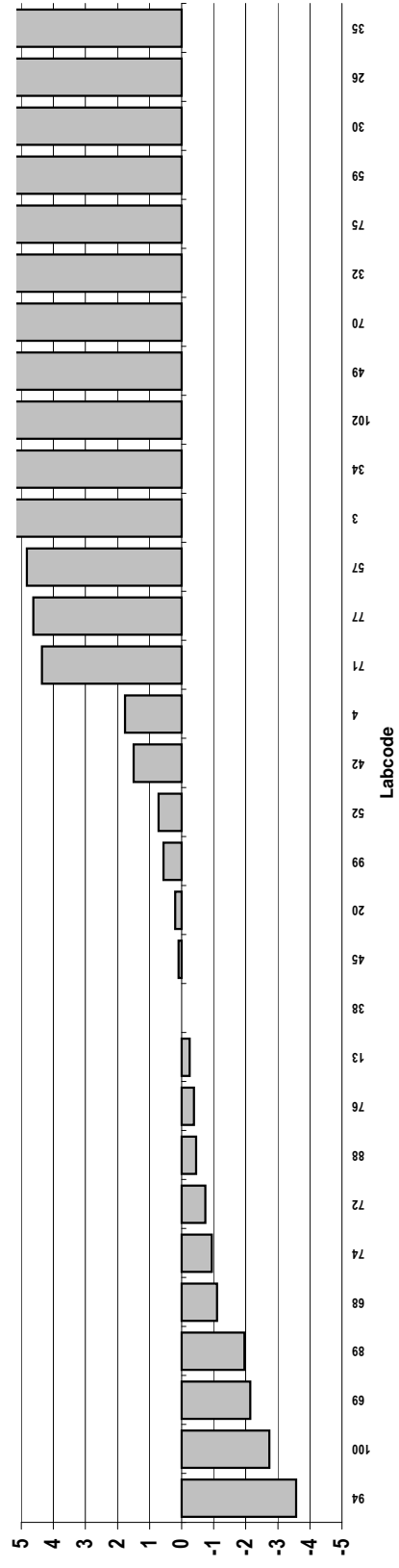
Consensus statistics

Consensus median, pg/g	1.9
Median all values pg/g	2.5
Consensus mean, pg/g	2.4
Standard deviation, pg/g	1.3
Relative standard deviation, %	53
No. of values reported	31
No. of values removed	8
No. of reported non-detects	10

BDE 183



Z-score: BDE 183

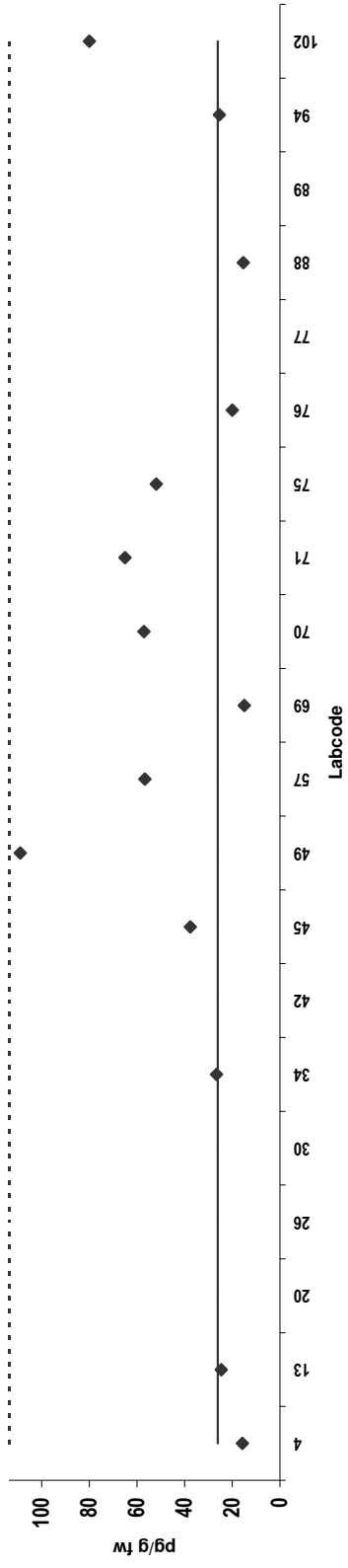


Beef
Congener: BDE 209

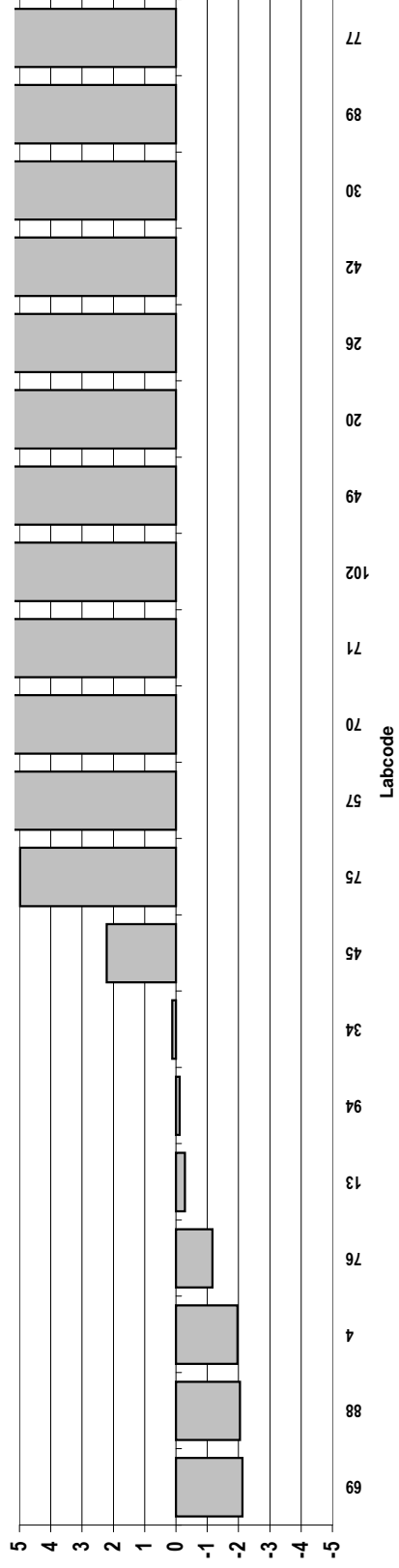
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	16				
13	25				
20	121	Outlier			
26	130	Outlier,ND			
30	167	Outlier,ND			
34	27				
42	145	Outlier			
45	38				
49	109				
57	57	ND			
69	15				
70	57				
71	65	ND			
75	52				
76	20	ND			
77	266	Outlier			
88	15				
89	210	Outlier			
94	25				
102	80	ND			

Consensus statistics	
Consensus median, pg/g	26
Median all values pg/g	57
Consensus mean, pg/g	43
Standard deviation, pg/g	28
Relative standard deviation, %	66
No. of values reported	20
No. of values removed	6
No. of reported non-detects	6

BDE 209



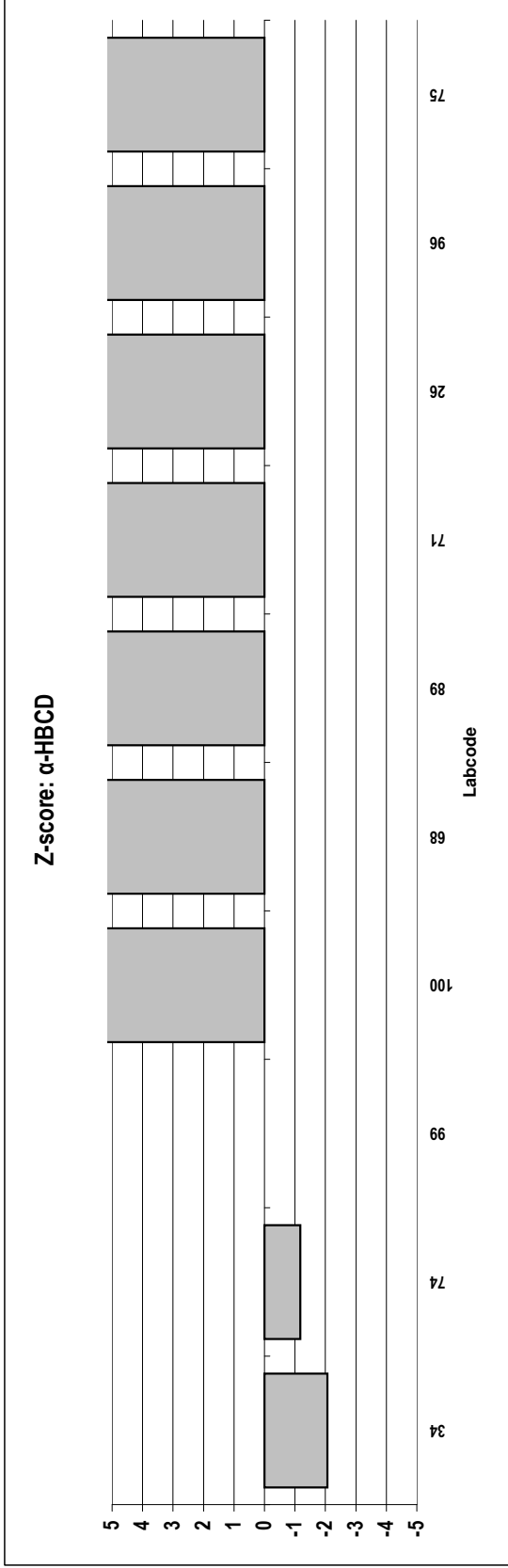
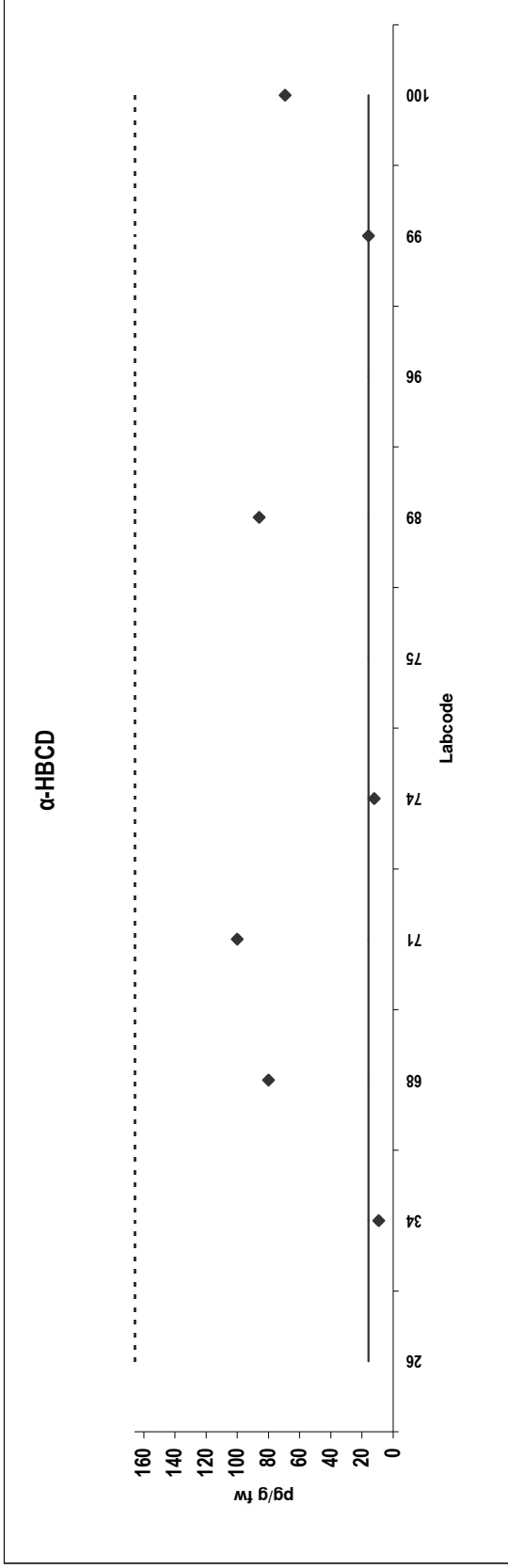
Z-score: BDE 209



Beef
Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	214	Outlier,ND			
34	9.3				
68	80	ND			
71	100	ND			
74	12	ND			
75	1109	Outlier			
89	86				
96	250	Outlier,ND			
99	16				
100	69	ND			

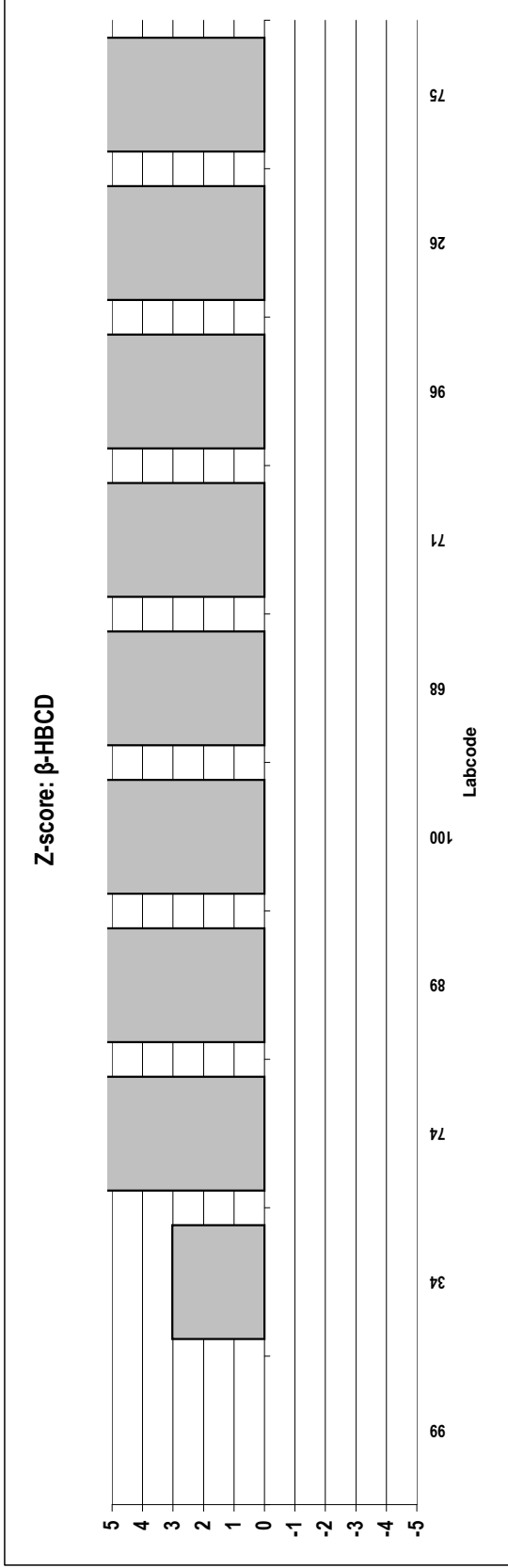
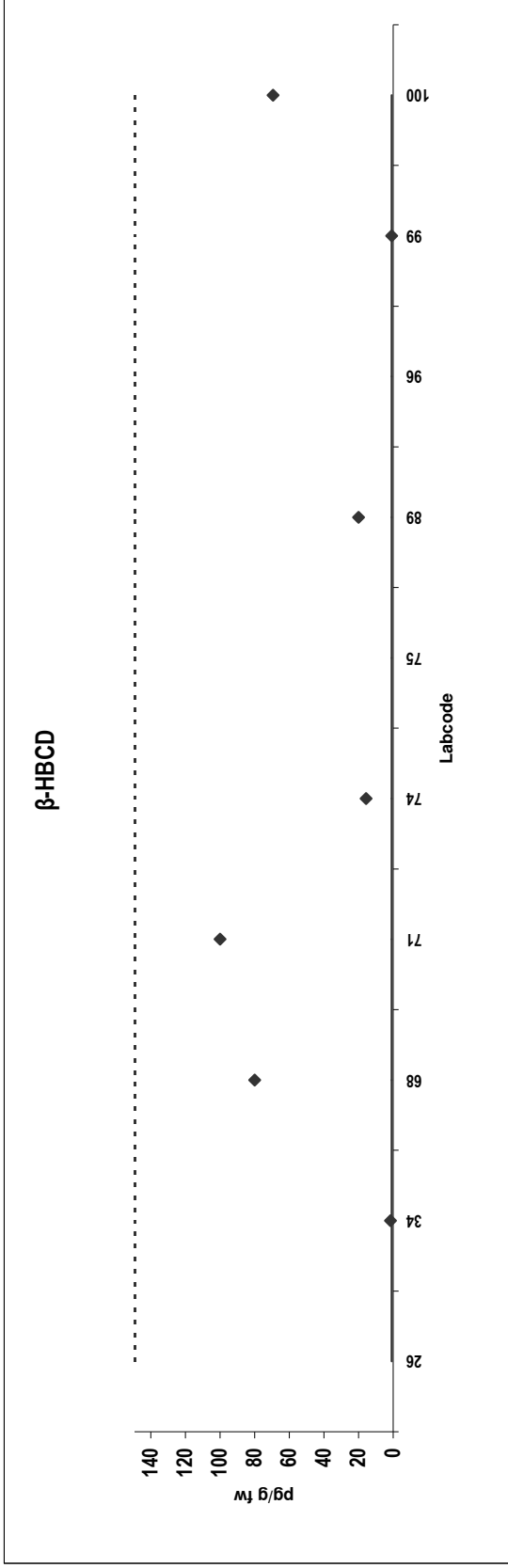
Consensus statistics	
Consensus median, pg/g	16
Median all values pg/g	83
Consensus mean, pg/g	53
Standard deviation, pg/g	39
Relative standard deviation, %	74
No. of values reported	10
No. of values removed	3
No. of reported non-detects	6



Beef
Congener: β -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	625	Outlier,ND			
34	1.5	ND			
68	80	ND			
71	100	ND			
74	16	ND			
75	799	Outlier			
89	20	ND			
96	150	Outlier,ND			
99	0.94				
100	69	ND			

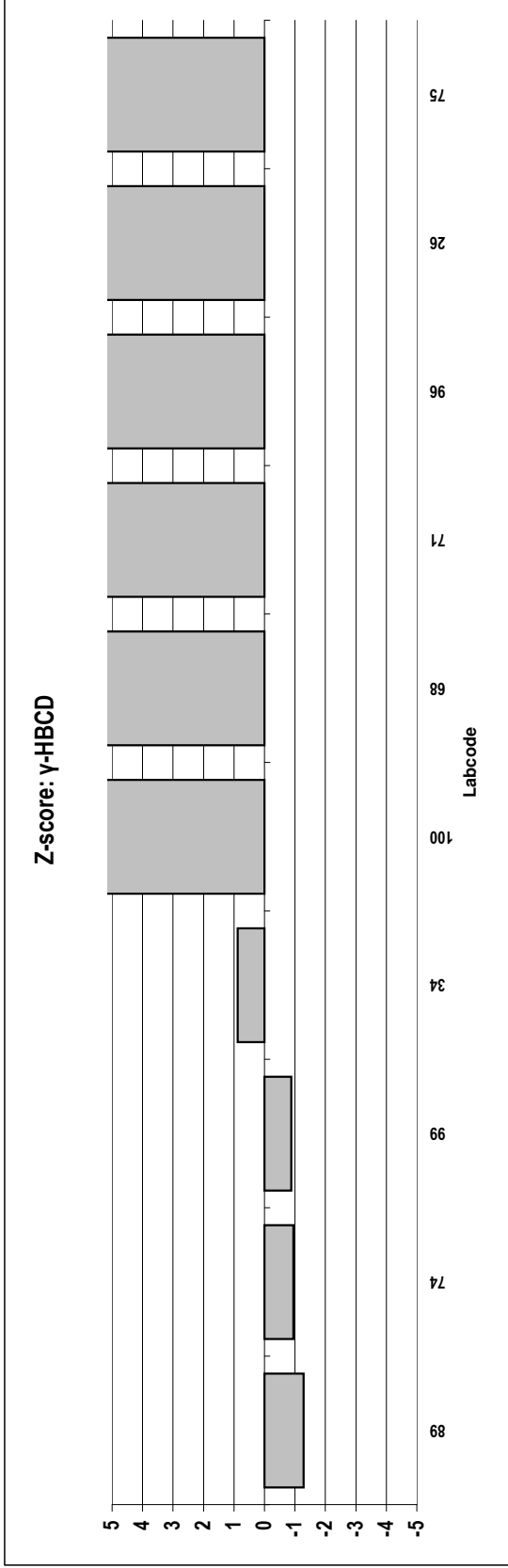
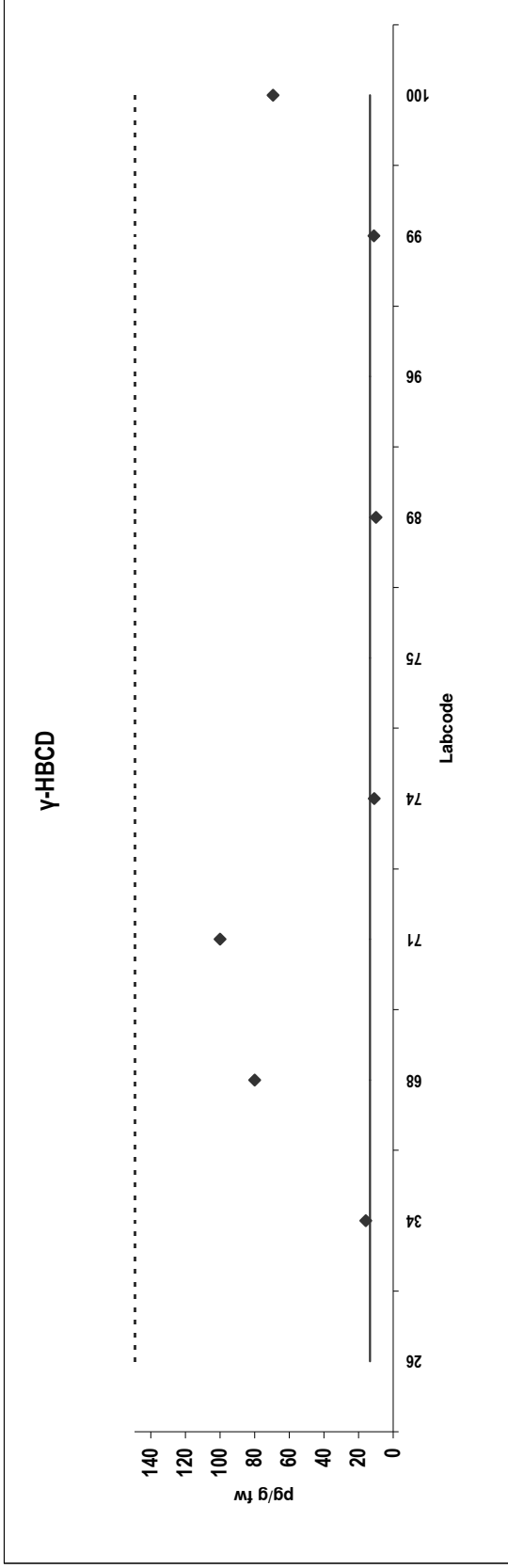
Consensus statistics	
Consensus median, pg/g	0.94
Median all values pg/g	75
Consensus mean, pg/g	41
Standard deviation, pg/g	41
Relative standard deviation, %	100
No. of values reported	10
No. of values removed	3
No. of reported non-detects	8



Beef
Congener: γ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	259	Outlier,ND			
34	16	ND			
68	80	ND			
71	100	ND			
74	11	ND			
75	810	Outlier			
89	10	ND			
96	150	Outlier,ND			
99	11				
100	69	ND			

Consensus statistics	
Consensus median, pg/g	13
Median all values pg/g	75
Consensus mean, pg/g	42
Standard deviation, pg/g	39
Relative standard deviation, %	92
No. of values reported	10
No. of values removed	3
No. of reported non-detects	7

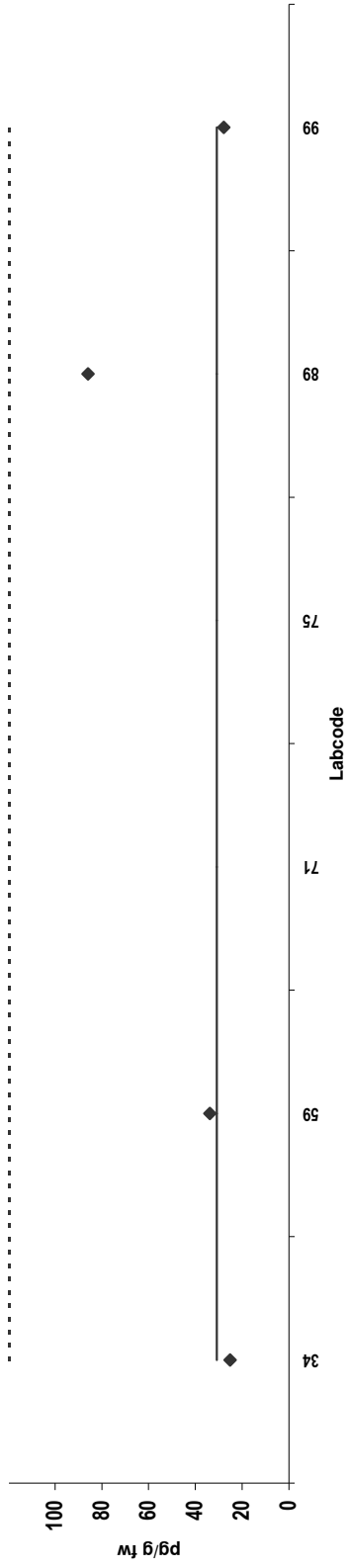


Beef
Congener: total HBCD

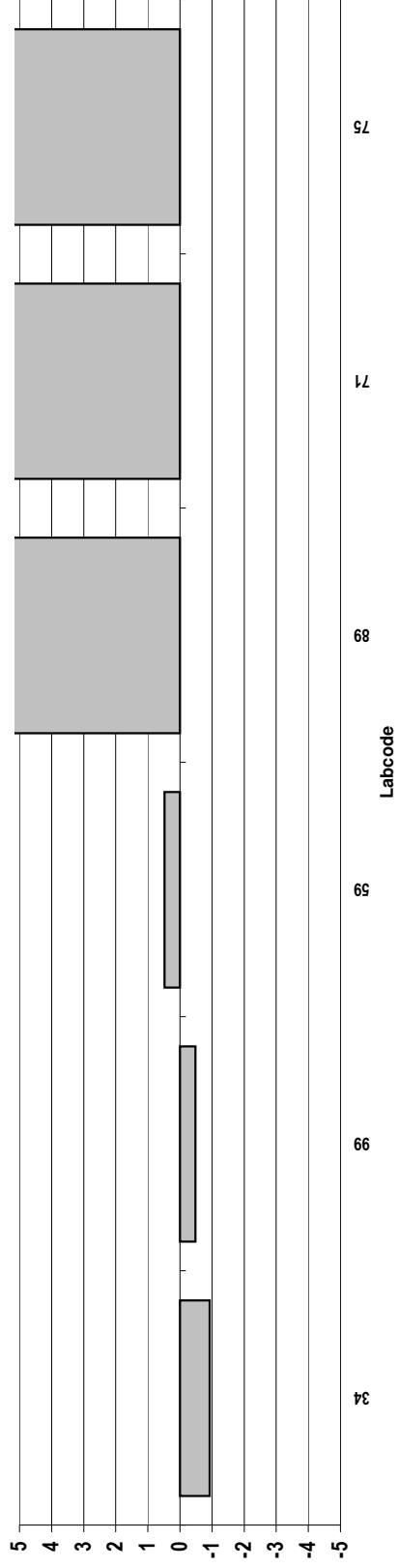
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
34	25				
59	34				
71	300	Outlier,ND			
75	2718	Outlier			
89	86				
99	28				

Consensus statistics	
Consensus median, pg/g	31
Median all values pg/g	60
Consensus mean, pg/g	43
Standard deviation, pg/g	29
Relative standard deviation, %	67
No. of values reported	6
No. of values removed	2
No. of reported non-detects	1

total HBCD



Z-score: total HBCD



Appendix 3:

Presentation of results
for butter oil

Appendix 3: Presentation of results: Butter oil

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:

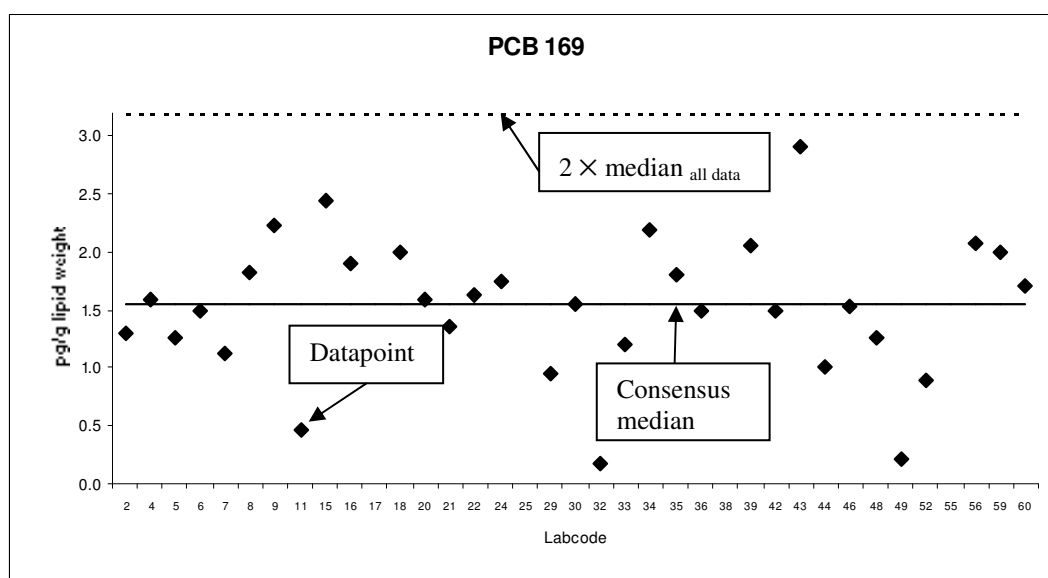
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding $2 \times$ this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

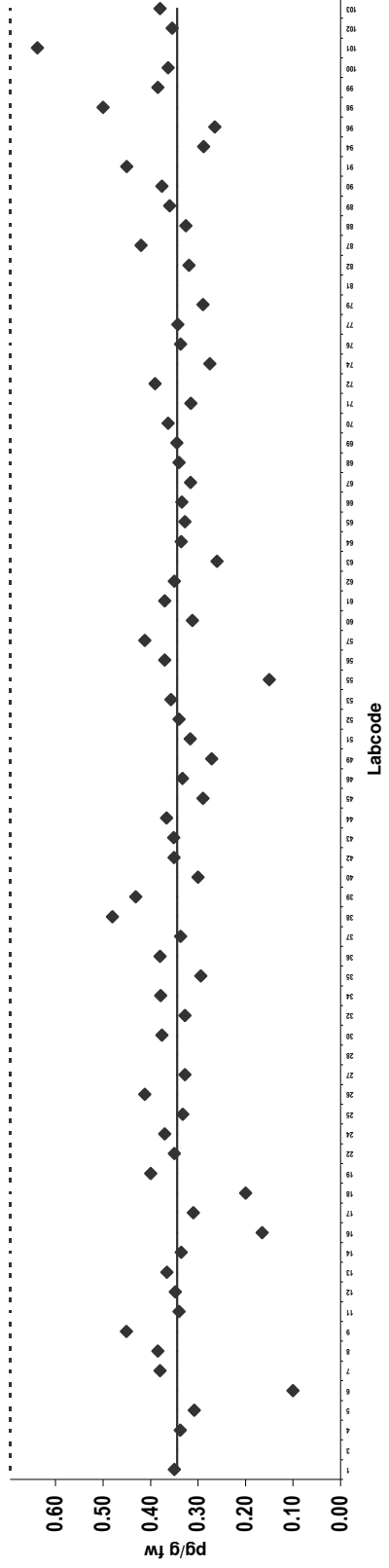
Butteroil
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.35		62	0.35	
3	0.71	Outlier	63	0.26	
4	0.34		64	0.34	
5	0.31		65	0.33	
6	0.10	ND	66	0.33	
7	0.38		67	0.32	
8	0.38		68	0.34	
9	0.45		69	0.35	
11	0.34		70	0.36	
12	0.35		71	0.32	
13	0.37		72	0.39	
14	0.34		74	0.28	
16	0.17		76	0.34	
17	0.31		77	0.34	
18	0.20		79	0.29	
19	0.40	ND	81	1.0	Outlier
22	0.35		82	0.32	
24	0.37		87	0.42	
25	0.33		88	0.33	
26	0.41		89	0.36	
27	0.33		90	0.38	
28	1.9	Outlier	91	0.45	
30	0.38		94	0.29	
32	0.33		96	0.27	
34	0.38		98	0.50	ND
35	0.29		99	0.38	
36	0.38		100	0.36	
37	0.34		101	0.64	
38	0.48		102	0.35	
39	0.43		103	0.38	
40	0.30				
42	0.35				
43	0.35				
44	0.37				
45	0.29				
46	0.33				
49	0.27				
51	0.32				
52	0.34				
53	0.36				
55	0.15				
56	0.37				
57	0.41				
60	0.31				
61	0.37				

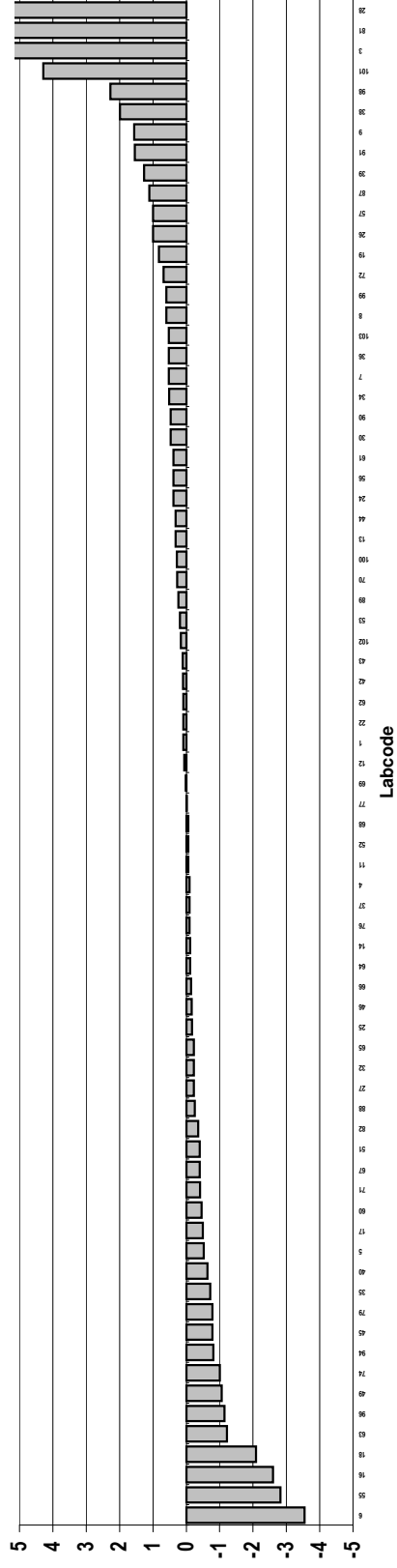
Consensus statistics

Consensus median, pg/g	0.34
Median all values pg/g	0.35
Consensus mean, pg/g	0.34
Standard deviation, pg/g	0.074
Relative standard deviation, %	22
No. of values reported	75
No. of values removed	3
No. of reported non-detects	3

2,3,7,8 TCDD



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



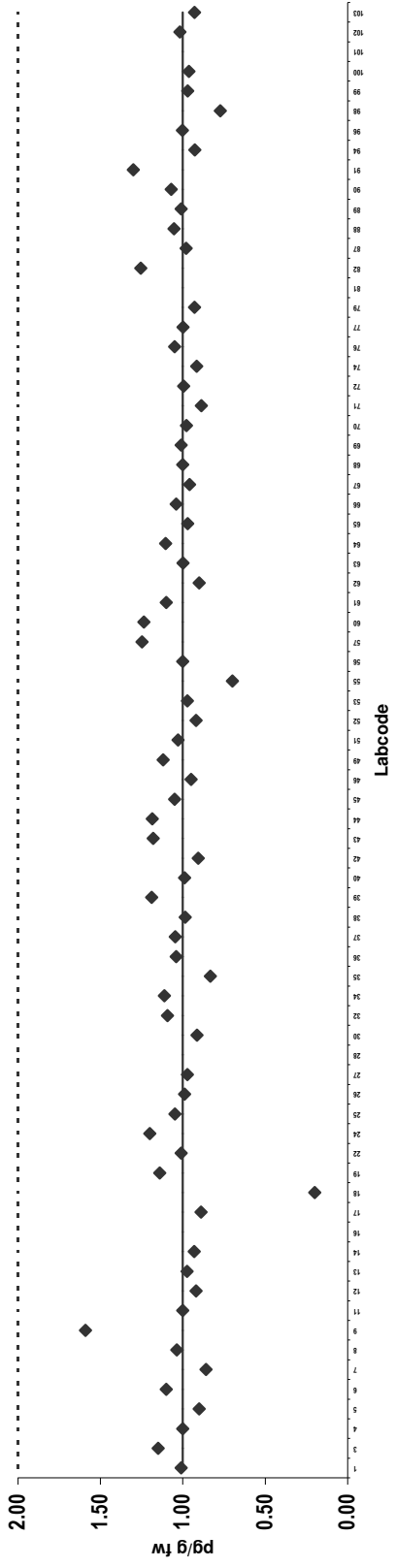
Butteroil
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.0		62	0.90	
3	1.2		63	1.0	
4	1.0		64	1.1	
5	0.90		65	0.97	
6	1.1		66	1.0	
7	0.86		67	0.96	
8	1.0		68	1.0	
9	1.6		69	1.0	
11	1.0		70	0.98	
12	0.92		71	0.89	
13	0.98		72	1.0	
14	0.93		74	0.92	
16	2.2	Outlier	76	1.0	
17	0.89		77	1.0	
18	0.20	ND	79	0.93	Outlier
19	1.1		81	4.0	
22	1.0		82	1.3	
24	1.2		87	0.98	
25	1.0		88	1.1	
26	0.99		89	1.0	
27	0.97		90	1.1	
28	5.4	Outlier	91	1.3	
30	0.91		94	0.93	
32	1.1		96	1.0	
34	1.1		98	0.77	
35	0.83		99	0.97	
36	1.0		100	0.96	
37	1.0		101	2.0	Outlier
38	0.99		102	1.0	
39	1.2		103	0.93	
40	0.99				
42	0.91				
43	1.2				
44	1.2				
45	1.1				
46	0.95				
49	1.1				
51	1.0				
52	0.92				
53	0.97				
55	0.70				
56	1.0				
57	1.2				
60	1.2				
61	1.1				

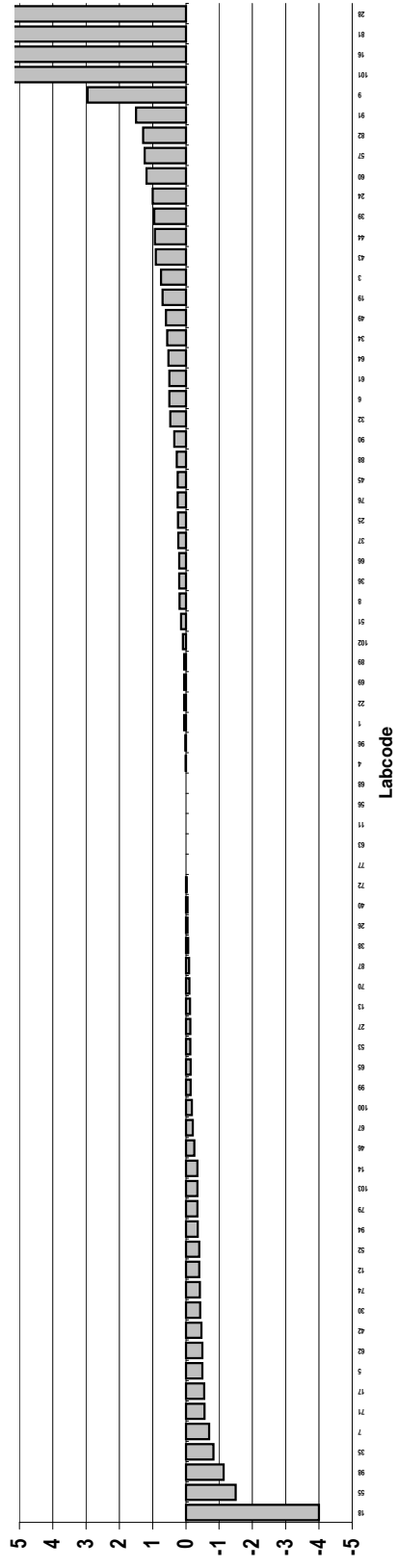
Consensus statistics

Consensus median, pg/g	1.0
Median all values pg/g	1.0
Consensus mean, pg/g	1.0
Standard deviation, pg/g	0.16
Relative standard deviation, %	16
No. of values reported	75
No. of values removed	4
No. of reported non-detects	1

1,2,3,7,8 PeCDD



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



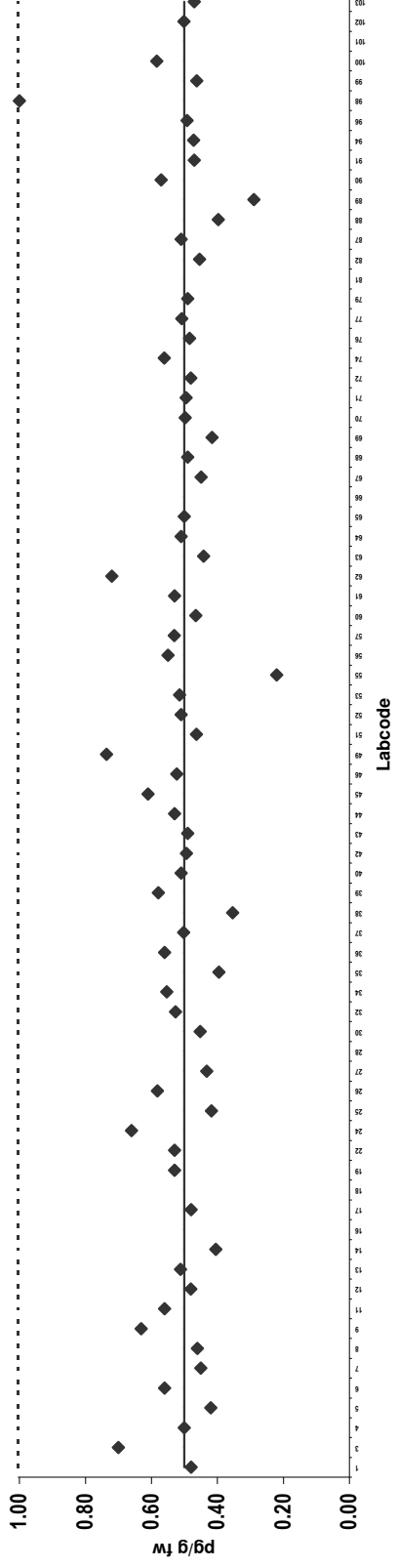
Butteroil
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.48		62	0.72	
3	0.70		63	0.44	
4	0.50		64	0.51	
5	0.42		65	0.50	
6	0.56		66	1.0	Outlier
7	0.45		67	0.45	
8	0.46		68	0.49	
9	0.63		69	0.42	
11	0.56		70	0.50	ND
12	0.48		71	0.49	
13	0.51		72	0.48	
14	0.41		74	0.56	
16	1.1	Outlier	76	0.48	
17	0.48		77	0.51	
18	2.1	Outlier	79	0.49	
19	0.53		81	3.2	Outlier
22	0.53		82	0.45	
24	0.66		87	0.51	
25	0.42		88	0.40	
26	0.58		89	0.29	
27	0.43		90	0.57	
28	1.1		91	0.47	
30	0.45		94	0.47	
32	0.53		96	0.49	
34	0.55		98	1.0	ND
35	0.40		99	0.46	
36	0.56		100	0.58	
37	0.50		101	1.5	Outlier
38	0.35		102	0.50	
39	0.58		103	0.47	
40	0.51				
42	0.49				
43	0.49				
44	0.53				
45	0.61				
46	0.52				
49	0.74				
51	0.46				
52	0.51				
53	0.52				
55	0.22				
56	0.55				
57	0.53				
60	0.47				
61	0.53				

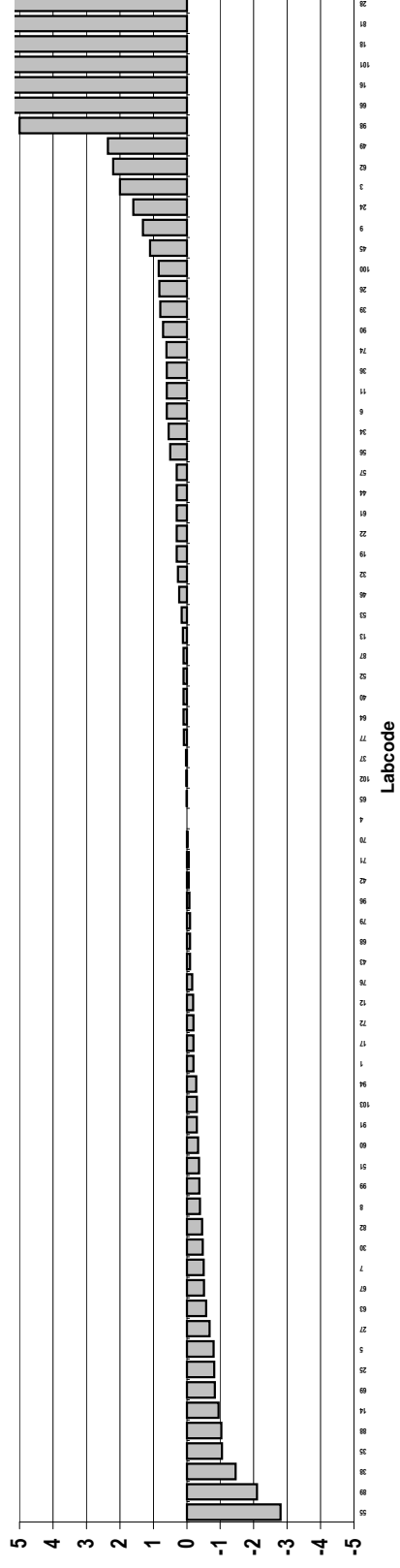
Consensus statistics

Consensus median, pg/g	0.50
Median all values pg/g	0.50
Consensus mean, pg/g	0.51
Standard deviation, pg/g	0.10
Relative standard deviation, %	20
No. of values reported	75
No. of values removed	6
No. of reported non-detects	2

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



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



Butteroil

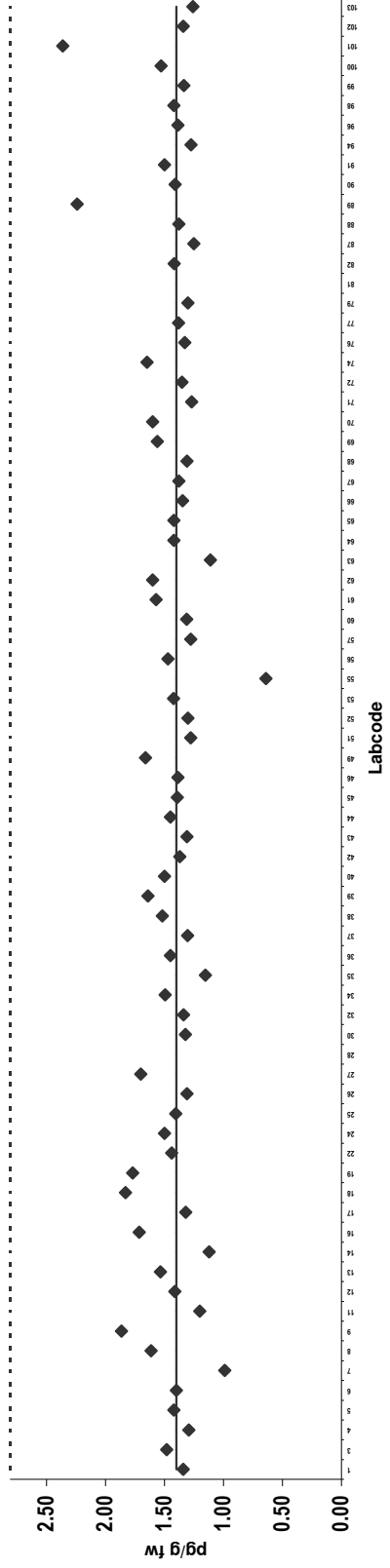
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.3		62	1.6	
3	1.5		63	1.1	
4	1.3		64	1.4	
5	1.4		65	1.4	
6	1.4		66	1.3	
7	0.99		67	1.4	
8	1.6		68	1.3	
9	1.9		69	1.6	
11	1.2		70	1.6	
12	1.4		71	1.3	
13	1.5		72	1.4	
14	1.1		74	1.6	
16	1.7		76	1.3	
17	1.3		77	1.4	
18	1.8		79	1.3	
19	1.8		81	3.4	Outlier
22	1.4		82	1.4	
24	1.5		87	1.3	
25	1.4		88	1.4	
26	1.3		89	2.2	
27	1.7		90	1.4	
28	2.0		91	1.5	
30	1.3	Outlier	94	1.3	
32	1.3		96	1.4	
34	1.5		98	1.4	
35	1.2		99	1.3	
36	1.5		100	1.5	
37	1.3		101	2.4	
38	1.5		102	1.3	
39	1.6		103	1.3	
40	1.5				
42	1.4				
43	1.3				
44	1.4				
45	1.4				
46	1.4				
49	1.7				
51	1.3				
52	1.3				
53	1.4				
55	0.64				
56	1.5				
57	1.3				
60	1.3				
61	1.6				

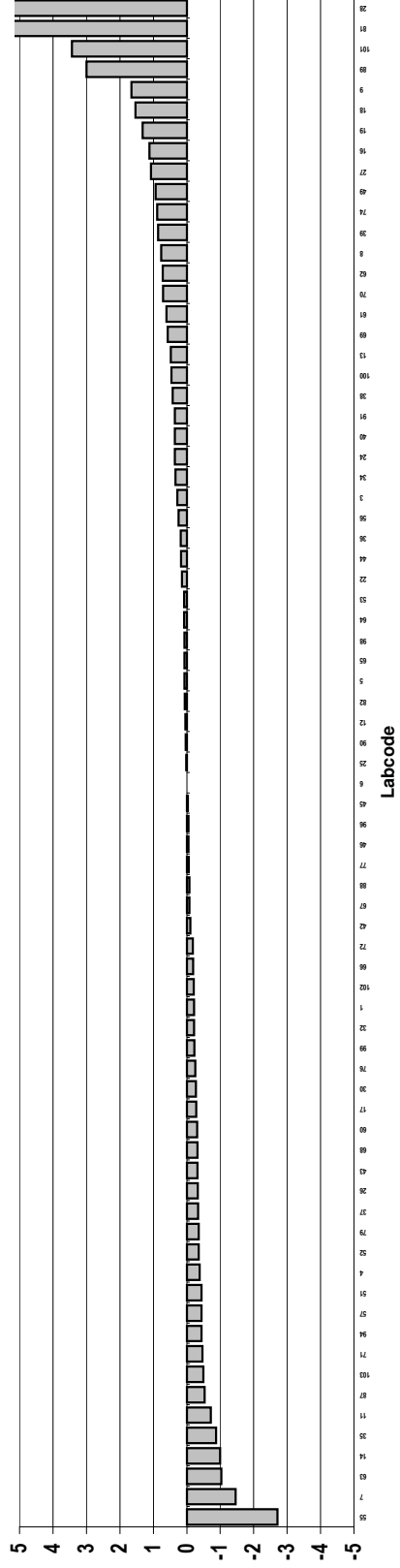
Consensus statistics

Consensus median, pg/g	1.4
Median all values pg/g	1.4
Consensus mean, pg/g	1.4
Standard deviation, pg/g	0.24
Relative standard deviation, %	16
No. of values reported	75
No. of values removed	2
No. of reported non-detects	0

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



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



Butteroil

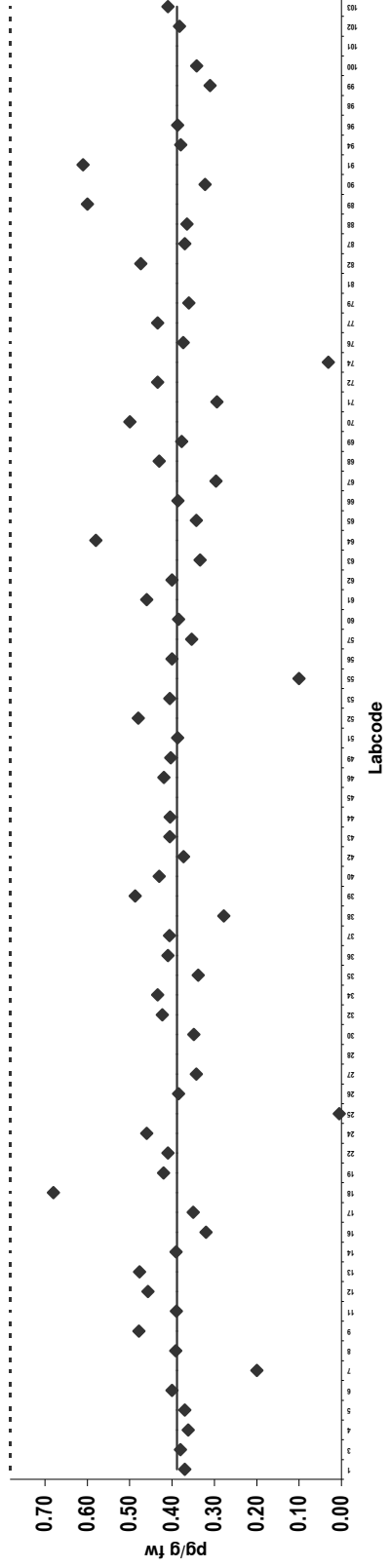
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.37		62	0.40	
3	0.38		63	0.33	
4	0.36		64	0.58	
5	0.37		65	0.34	
6	0.40		66	0.39	
7	0.20		67	0.30	
8	0.39	ND	68	0.43	
9	0.48		69	0.38	
11	0.39		70	0.50	ND
12	0.46		71	0.29	
13	0.48		72	0.43	
14	0.39		74	0.031	ND
16	0.32		76	0.37	
17	0.35		77	0.43	
18	0.68		79	0.36	
19	0.42		81	3.0	Outlier
22	0.41		82	0.47	
24	0.46		87	0.37	
25	0.0050		88	0.37	
26	0.38	ND	89	0.60	
27	0.34		90	0.32	
28	1.3	Outlier	91	0.61	
30	0.35		94	0.38	
32	0.42		96	0.39	
34	0.43		98	1.0	Outlier,ND
35	0.34		99	0.31	
36	0.41		100	0.34	
37	0.41		101	1.3	Outlier
38	0.28		102	0.38	
39	0.49		103	0.41	
40	0.43				
42	0.37				
43	0.41				
44	0.40				
45	1.1	Outlier			
46	0.42				
49	0.40				
51	0.39				
52	0.48				
53	0.41				
55	0.10	ND			
56	0.40				
57	0.35				
60	0.39				
61	0.46				

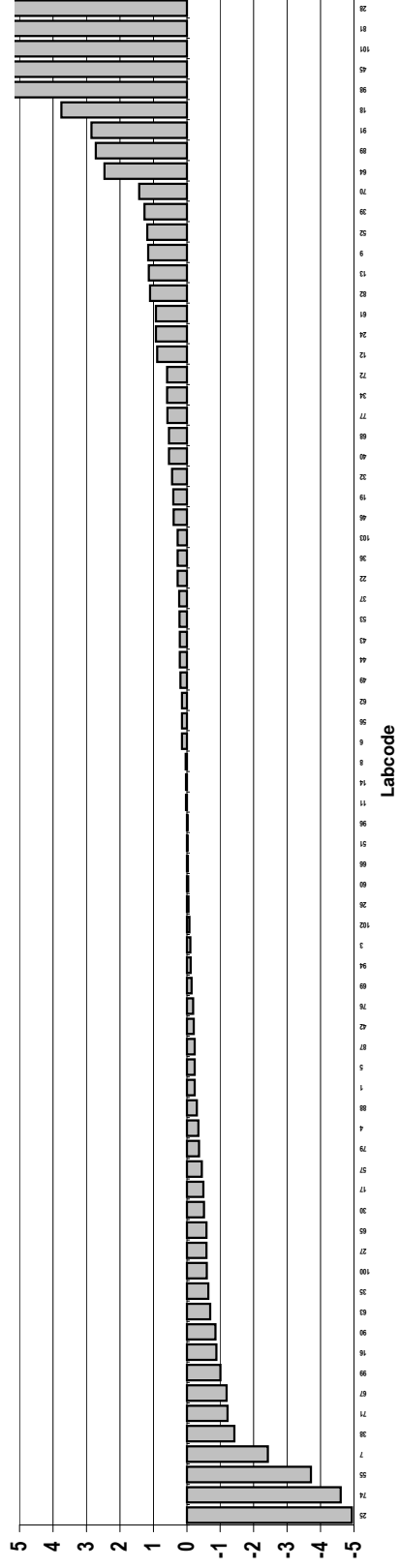
Consensus statistics

Consensus median, pg/g	0.39
Median all values pg/g	0.39
Consensus mean, pg/g	0.39
Standard deviation, pg/g	0.10
Relative standard deviation, %	27
No. of values reported	75
No. of values removed	5
No. of reported non-detects	6

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



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



Butteroil

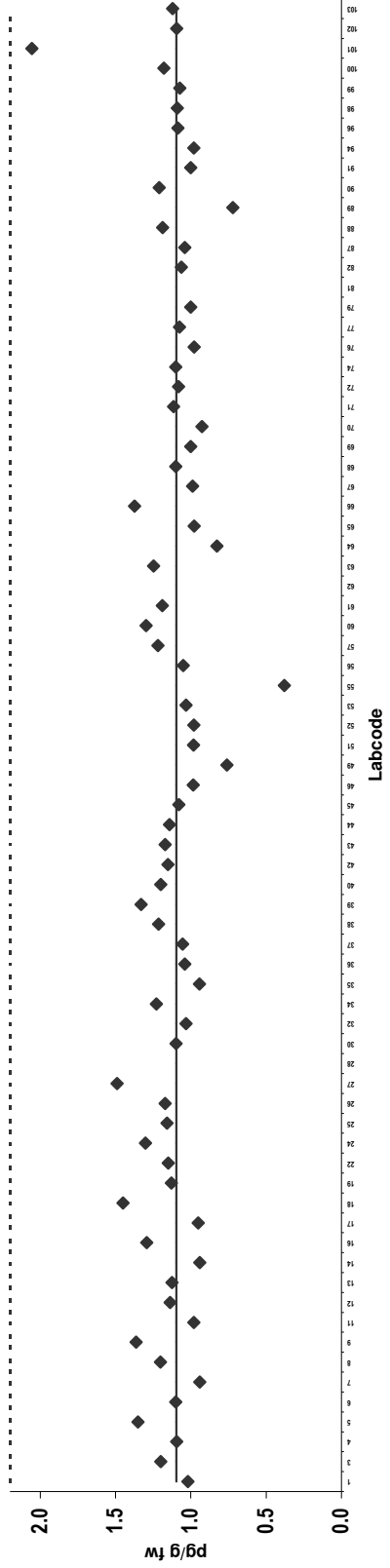
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.0		62	2.4	Outlier
3	1.2		63	1.2	
4	1.1		64	0.83	
5	1.4		65	0.98	
6	1.1		66	1.4	
7	0.94		67	0.99	
8	1.2		68	1.1	
9	1.4		69	1.0	
11	0.98		70	0.93	
12	1.1		71	1.1	
13	1.1		72	1.1	
14	0.94		74	1.1	
16	1.3		76	0.98	
17	0.95		77	1.1	
18	1.5		79	1.0	
19	1.1		81	3.2	Outlier
22	1.2		82	1.1	
24	1.3		87	1.0	
25	1.2		88	1.2	
26	1.2		89	0.72	
27	1.5		90	1.2	
28	1.66		91	1.0	
30	1.1		94	0.98	
32	1.0		96	1.1	
34	1.2		98	1.1	
35	0.94		99	1.1	
36	1.0		100	1.2	
37	1.1		101	2.1	
38	1.2		102	1.1	
39	1.3		103	1.1	
40	1.2				
42	1.2				
43	1.2				
44	1.1				
45	1.1				
46	0.98				
49	0.76				
51	0.98				
52	0.98				
53	1.0				
55	0.38				
56	1.1				
57	1.2				
60	1.3				
61	1.2				

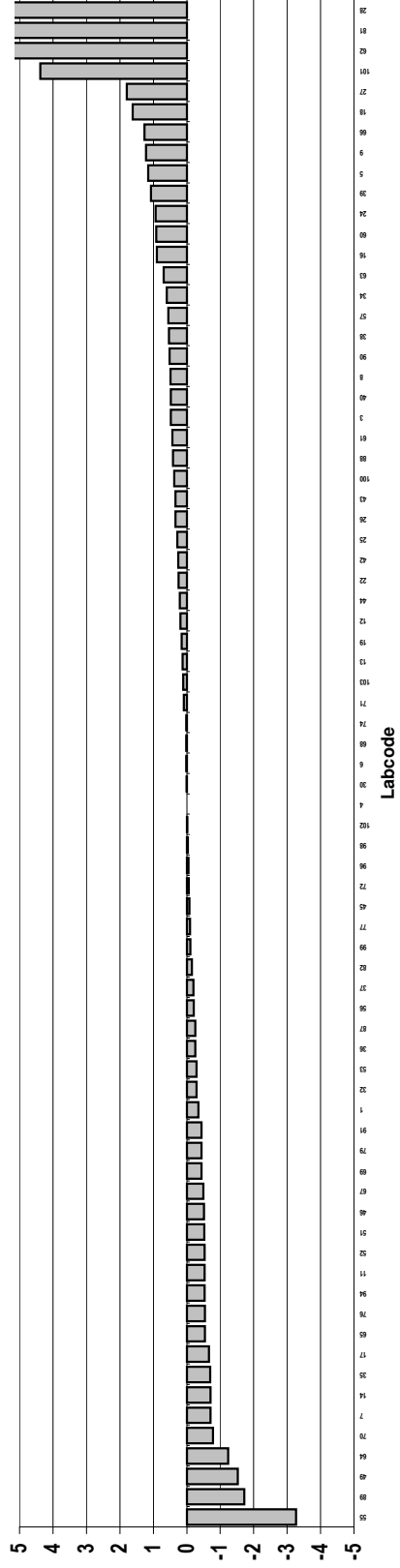
Consensus statistics

Consensus median, pg/g	1.1
Median all values pg/g	1.1
Consensus mean, pg/g	1.1
Standard deviation, pg/g	0.20
Relative standard deviation, %	18
No. of values reported	75
No. of values removed	3
No. of reported non-detects	0

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



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



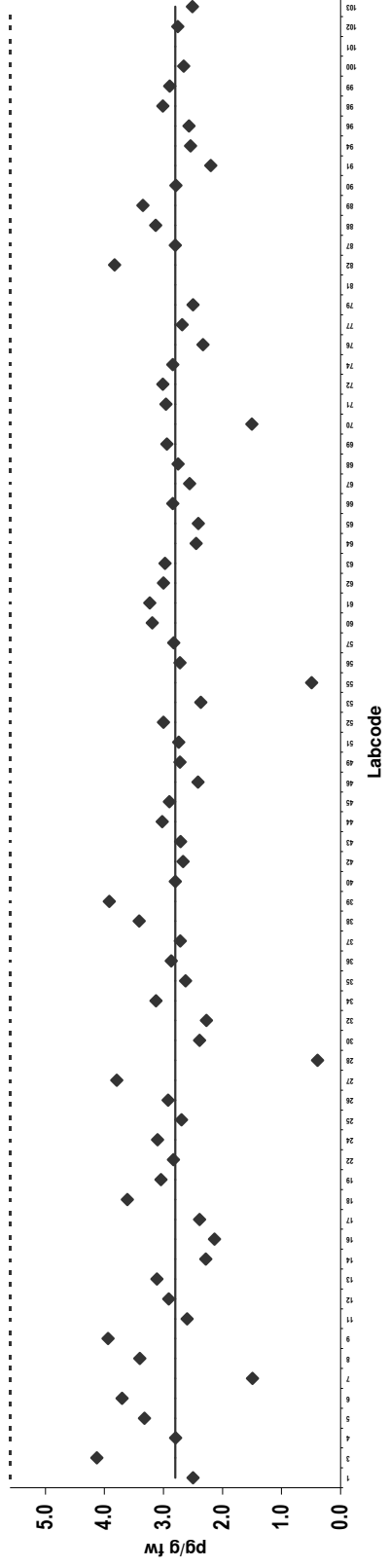
Butteroil
Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.5		62	3.0	
3	4.1		63	3.0	
4	2.8		64	2.4	
5	3.3		65	2.4	
6	3.7		66	2.8	
7	1.5		67	2.6	
8	3.4		68	2.8	
9	3.9		69	2.9	
11	2.6		70	1.5	ND
12	2.9		71	3.0	
13	3.1		72	3.0	
14	2.3		74	2.8	
16	2.1		76	2.3	
17	2.4		77	2.7	
18	3.6		79	2.5	
19	3.0		81	8.8	Outlier
22	2.8		82	3.8	
24	3.1		87	2.8	
25	2.7		88	3.1	
26	2.9		89	3.4	
27	3.8		90	2.8	
28	0.39	ND	91	2.2	
30	2.4		94	2.5	
32	2.3		96	2.6	
34	3.1		98	3.0	
35	2.6		99	2.9	
36	2.9		100	2.7	
37	2.7		101	5.7	Outlier
38	3.4		102	2.8	
39	3.9		103	2.5	
40	2.8				
42	2.7				
43	2.7				
44	3.0				
45	2.9				
46	2.4				
49	2.7				
51	2.7				
52	3.0				
53	2.4				
55	0.49				
56	2.7				
57	2.8				
60	3.2				
61	3.2				

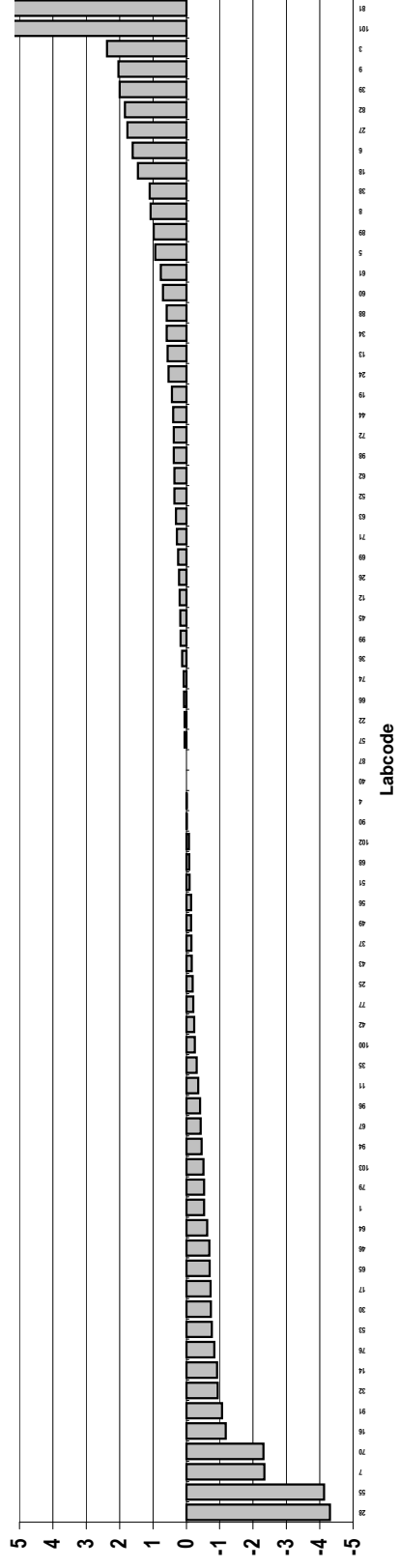
Consensus statistics

Consensus median, pg/g	2.8
Median all values pg/g	2.8
Consensus mean, pg/g	2.8
Standard deviation, pg/g	0.62
Relative standard deviation, %	22
No. of values reported	75
No. of values removed	2
No. of reported non-detects	2

OCDD



Z-score: OCDD



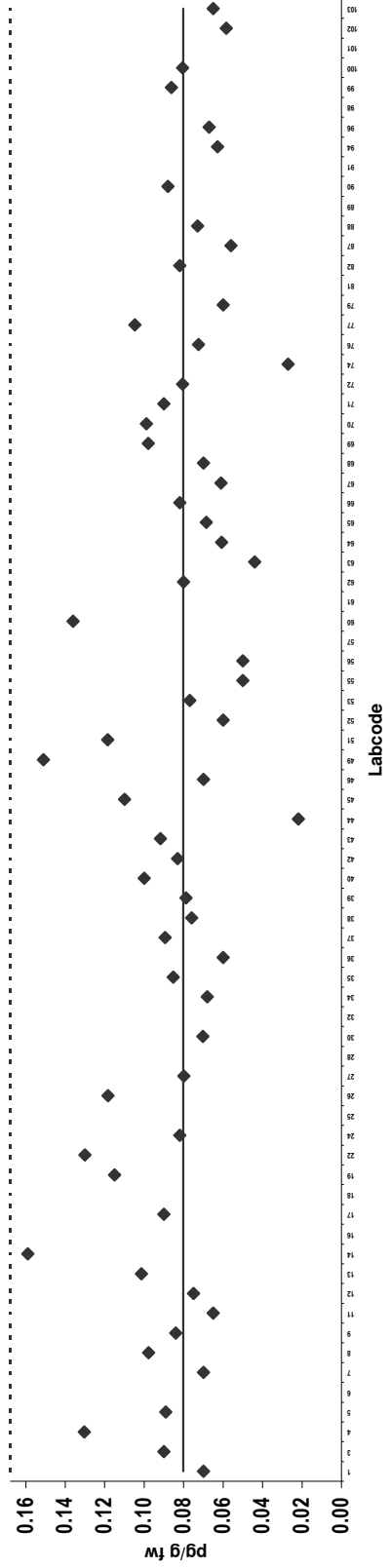
Butteroil
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.070		62	0.080	
3	0.090	ND	63	0.044	ND
4	0.13		64	0.061	
5	0.089		65	0.069	
6	0.20	Outlier	66	0.082	
7	0.070		67	0.061	
8	0.098		68	0.070	
9	0.084		69	0.098	
11	0.065		70	0.099	ND
12	0.075		71	0.090	ND
13	0.10		72	0.080	
14	0.16		74	0.027	ND
16	0.22	Outlier	76	0.072	
17	0.090		77	0.10	
18	0.20	Outlier,ND	79	0.060	
19	0.12		81	0.66	Outlier
22	0.13		82	0.082	
24	0.082		87	0.056	
25	0.18	Outlier	88	0.073	
26	0.12		89	0.40	Outlier
27	0.080		90	0.088	
28	14		91	0.17	Outlier
30	0.070		94	0.063	
32	0.30	Outlier	96	0.067	
34	0.068		98	0.50	Outlier,ND
35	0.085		99	0.086	
36	0.060		100	0.081	
37	0.089		101	0.39	Outlier
38	0.076		102	0.058	
39	0.079		103	0.065	
40	0.10				
42	0.083				
43	0.092				
44	0.022	ND			
45	0.11				
46	0.070				
49	0.15				
51	0.12				
52	0.060				
53	0.077				
55	0.050	ND			
56	0.050				
57	0.19	Outlier			
60	0.14				
61	0.18	Outlier			

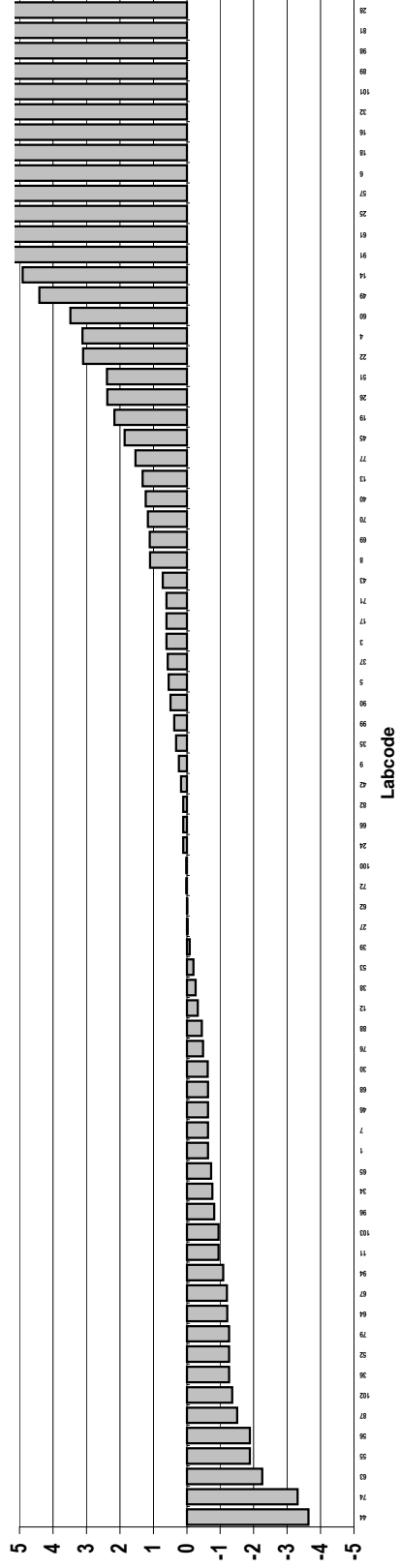
Consensus statistics

Consensus median, pg/g	0.080
Median all values pg/g	0.084
Consensus mean, pg/g	0.082
Standard deviation, pg/g	0.026
Relative standard deviation, %	32
No. of values reported	75
No. of values removed	13
No. of reported non-detects	9

2,3,7,8 TCDF



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



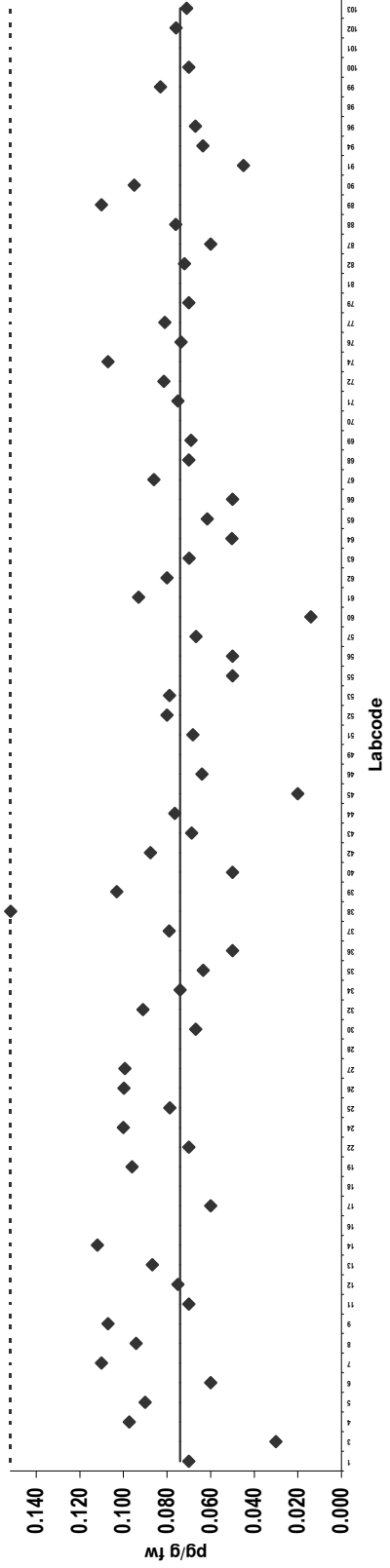
Butteroil
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.070		62	0.080	
3	0.030	ND	63	0.070	ND
4	0.097		64	0.050	
5	0.090	ND	65	0.062	
6	0.060	ND	66	0.050	ND
7	0.11		67	0.086	
8	0.094		68	0.070	
9	0.11		69	0.069	
11	0.070	ND	70	0.16	
12	0.075		71	0.075	
13	0.087		72	0.081	
14	0.11		74	0.11	
16	0.40	Outlier	76	0.074	
17	0.060		77	0.081	
18	0.20	Outlier,ND	79	0.070	
19	0.096		81	2.5	Outlier
22	0.070		82	0.072	
24	0.10		87	0.060	
25	0.079		88	0.076	
26	0.10		89	0.11	
27	0.099		90	0.095	
28	16		91	0.045	
30	0.067		94	0.064	
32	0.091	Outlier	96	0.067	
34	0.074		98	0.50	
35	0.063		99	0.083	
36	0.050		100	0.070	
37	0.079		101	1.2	
38	0.15		102	0.076	Outlier
39	0.10		103	0.071	
40	0.050	ND			
42	0.088	ND			
43	0.069	ND			
44	0.077	ND			
45	0.020	ND			
46	0.064				
49	0.45	Outlier			
51	0.068				
52	0.080				
53	0.079				
55	0.050	ND			
56	0.050				
57	0.067				
60	0.014	ND			
61	0.093				

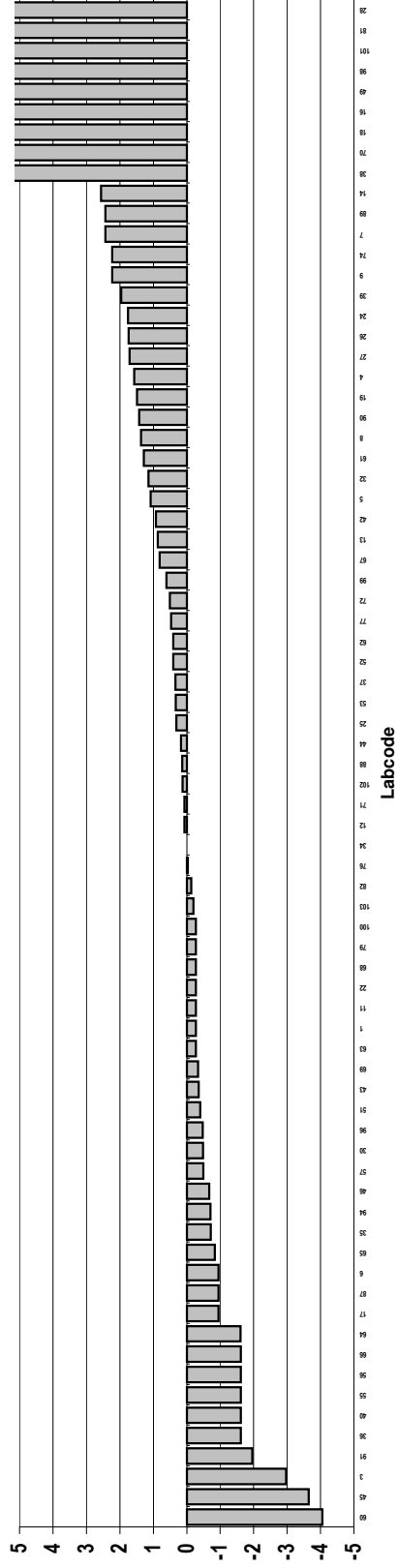
Consensus statistics

Consensus median, pg/g	0.074
Median all values pg/g	0.076
Consensus mean, pg/g	0.076
Standard deviation, pg/g	0.022
Relative standard deviation, %	29
No. of values reported	75
No. of values removed	8
No. of reported non-detects	13

1,2,3,7,8 PeCDF



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



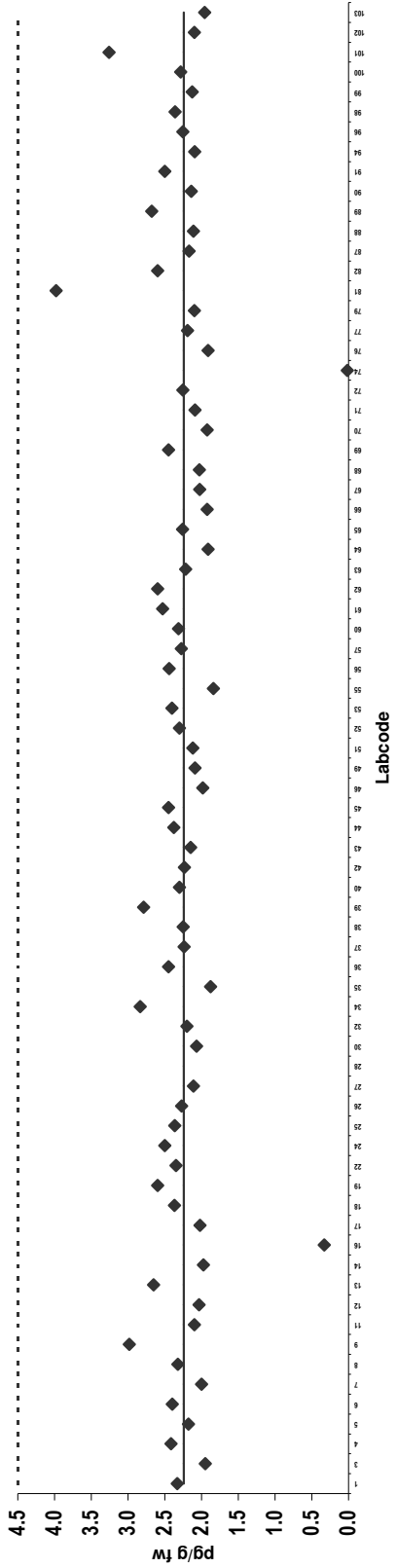
Butteroil
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.3		62	2.6	
3	2.0		63	2.2	
4	2.4		64	1.9	
5	2.2		65	2.3	
6	2.4		66	1.9	
7	2.0		67	2.0	
8	2.3		68	2.0	
9	3.0		69	2.5	
11	2.1		70	1.9	
12	2.0		71	2.1	
13	2.7		72	2.3	
14	2.0		74	0.019	ND
16	0.33		76	1.9	
17	2.0		77	2.2	
18	2.4		79	2.1	
19	2.6		81	4.0	
22	2.4		82	2.6	
24	2.5		87	2.2	
25	2.4		88	2.1	
26	2.3		89	2.7	
27	2.1		90	2.1	
28	92	Outlier	91	2.5	
30	2.1		94	2.1	
32	2.2		96	2.3	
34	2.8		98	2.4	
35	1.9		99	2.1	
36	2.5		100	2.3	
37	2.2		101	3.3	
38	2.3		102	2.1	
39	2.8		103	2.0	
40	2.3				
42	2.2				
43	2.2				
44	2.4				
45	2.5				
46	2.0				
49	2.1				
51	2.1				
52	2.3				
53	2.4				
55	1.8				
56	2.4				
57	2.3				
60	2.3				
61	2.5				

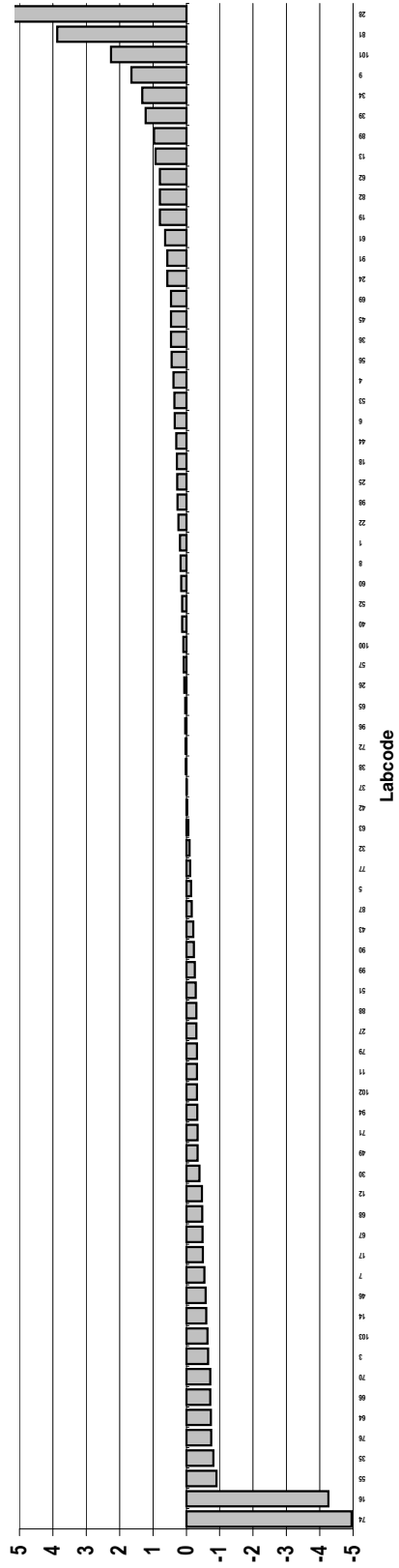
Consensus statistics

Consensus median, pg/g	2.2
Median all values pg/g	2.3
Consensus mean, pg/g	2.2
Standard deviation, pg/g	0.48
Relative standard deviation, %	21
No. of values reported	75
No. of values removed	1
No. of reported non-detects	1

2,3,4,7,8 PeCDF



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



Butteroil

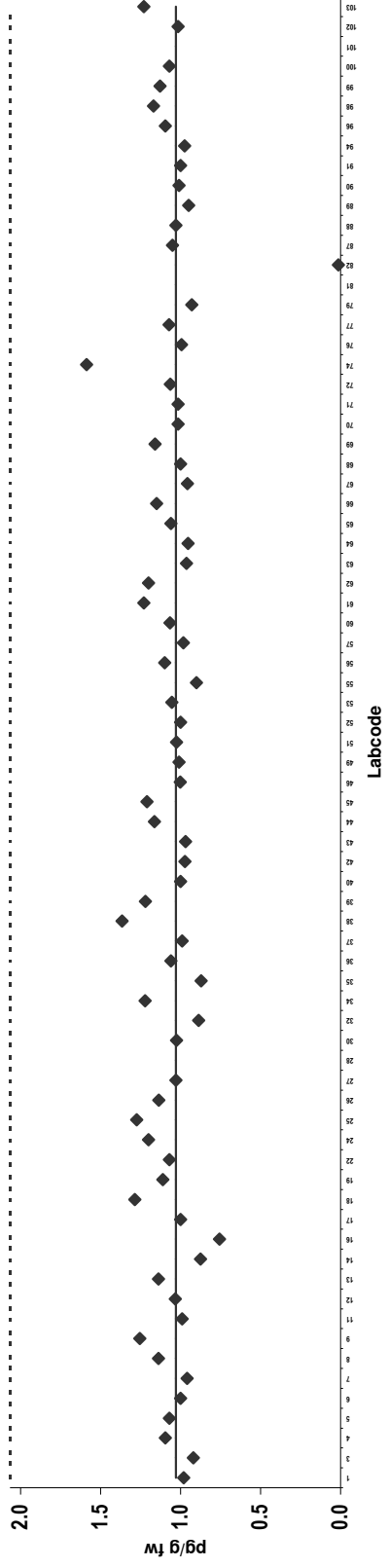
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.98		62	1.2	
3	0.92		63	0.96	
4	1.1		64	0.95	
5	1.1		65	1.1	
6	1.0		66	1.2	
7	0.96		67	0.96	
8	1.1		68	1.0	
9	1.3		69	1.2	
11	0.99		70	1.0	
12	1.0		71	1.0	
13	1.1		72	1.1	
14	0.87		74	1.6	
16	0.76		76	0.99	
17	1.0		77	1.1	
18	1.3		79	0.93	
19	1.1		81	2.7	
22	1.1		82	0.013	Outlier ND
24	1.2		87	1.1	
25	1.3		88	1.0	
26	1.1		89	0.95	
27	1.0		90	1.0	
28	58		91	1.0	
30	1.0		94	0.97	
32	0.89		96	1.1	
34	1.2		98	1.2	
35	0.87		99	1.1	
36	1.1		100	1.1	
37	0.99		101	2.2	
38	1.4		102	1.0	
39	1.2		103	1.2	
40	1.0				
42	0.97				
43	0.97				
44	1.2				
45	1.2				
46	1.0				
49	1.0				
51	1.0				
52	1.0				
53	1.1				
55	0.90				
56	1.1				
57	0.98				
60	1.1				
61	1.2				

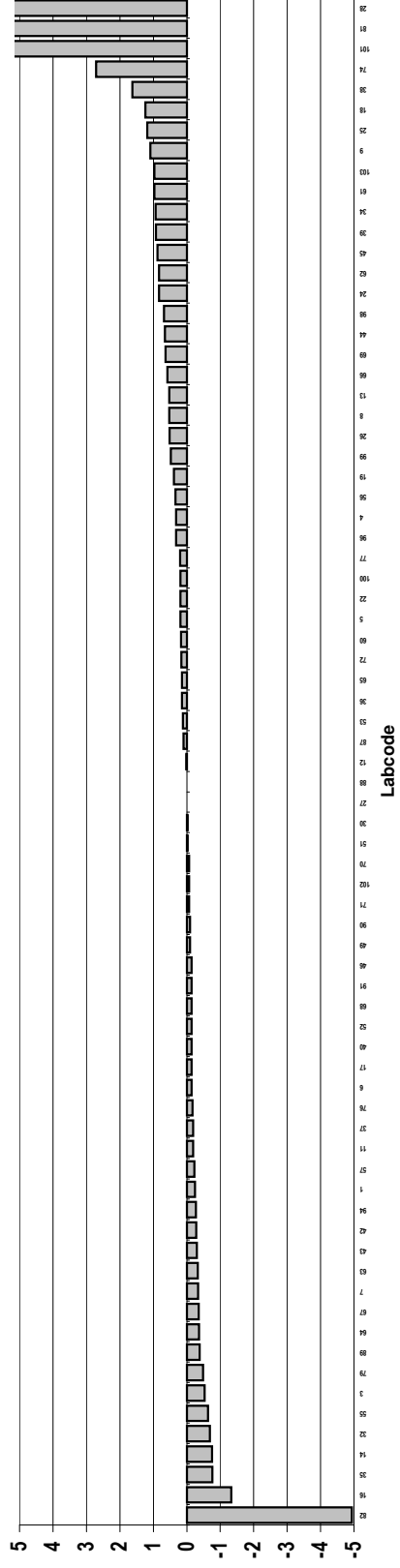
Consensus statistics

Consensus median, pg/g	1.0
Median all values pg/g	1.0
Consensus mean, pg/g	1.0
Standard deviation, pg/g	0.18
Relative standard deviation, %	17
No. of values reported	75
No. of values removed	3
No. of reported non-detects	1

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



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



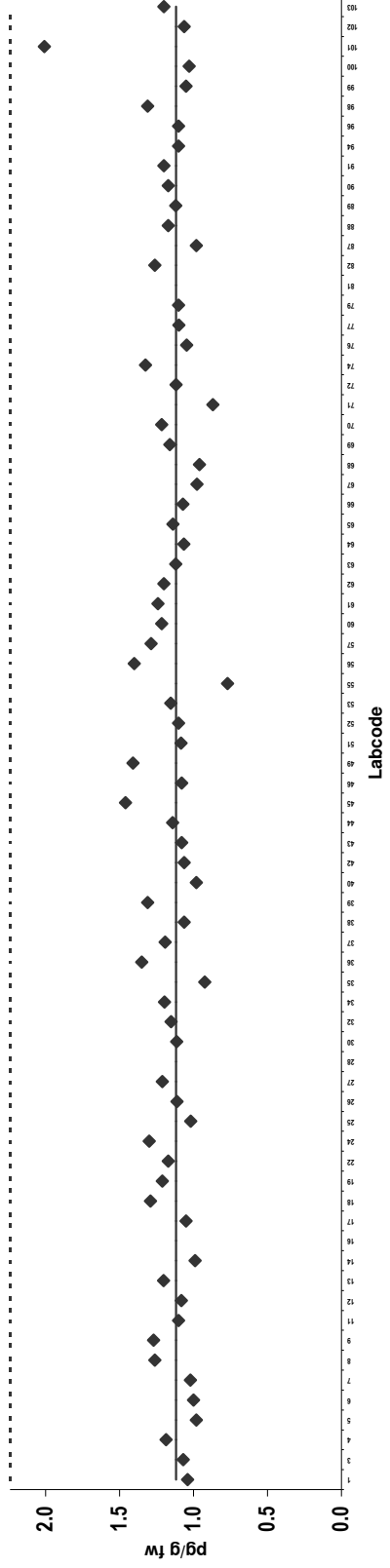
Butteroil
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.0		62	1.2	
3	1.1		63	1.1	
4	1.2		64	1.1	
5	0.98		65	1.1	
6	1.0		66	1.1	
7	1.0		67	0.98	
8	1.3		68	0.96	
9	1.3		69	1.2	
11	1.1		70	1.2	
12	1.1		71	0.87	
13	1.2		72	1.1	
14	0.99		74	1.3	
16	3.6		76	1.0	
17	1.1		77	1.1	
18	1.3		79	1.1	
19	1.2		81	3.3	
22	1.2		82	1.3	
24	1.3		87	0.98	
25	1.0		88	1.2	
26	1.1		89	1.1	
27	1.2		90	1.2	
28	51		91	1.2	
30	1.1		94	1.1	
32	1.2		96	1.1	
34	1.2		98	1.3	
35	0.92		99	1.1	
36	1.4		100	1.0	
37	1.2		101	2.0	
38	1.1		102	1.1	
39	1.3		103	1.2	
40	0.98				
42	1.1				
43	1.1				
44	1.1				
45	1.5				
46	1.1				
49	1.4				
51	1.1				
52	1.1				
53	1.2				
55	0.77				
56	1.4				
57	1.3				
60	1.2				
61	1.2				

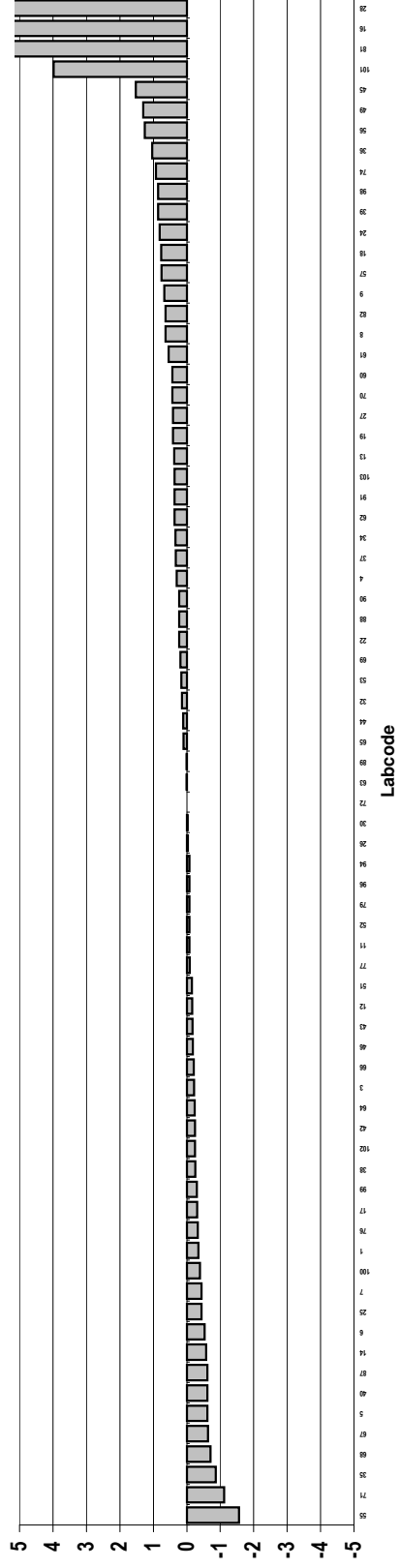
Consensus statistics

Consensus median, pg/g	1.1
Median all values pg/g	1.1
Consensus mean, pg/g	1.1
Standard deviation, pg/g	0.16
Relative standard deviation, %	14
No. of values reported	75
No. of values removed	3
No. of reported non-detects	0

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



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



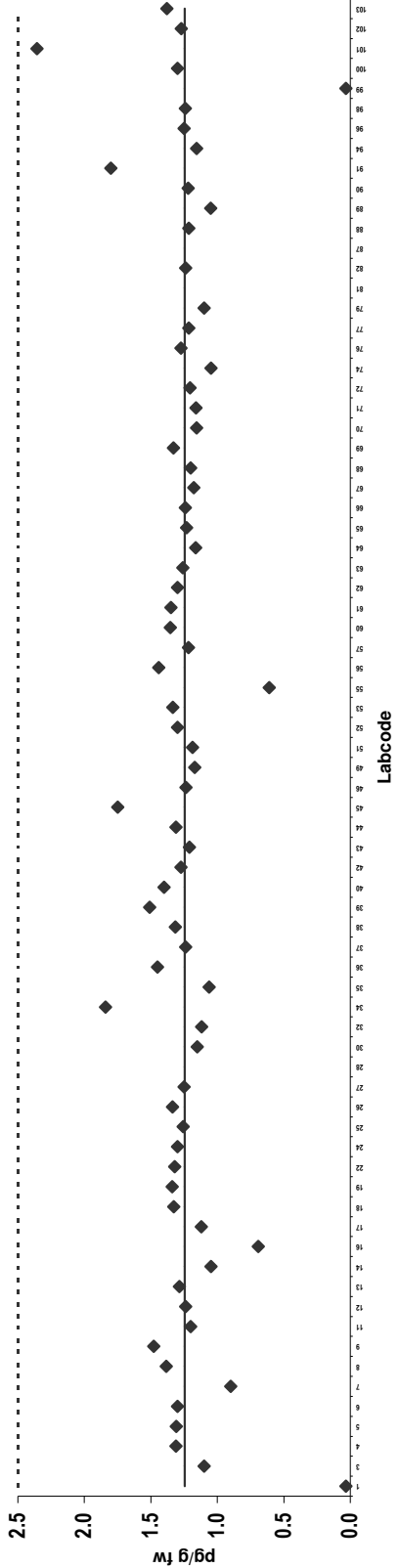
Butteroil
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.032	ND	62	1.3	
3	1.1		63	1.3	
4	1.3		64	1.2	
5	1.3		65	1.2	
6	1.3		66	1.2	
7	0.90		67	1.2	
8	1.4		68	1.2	
9	1.5		69	1.3	
11	1.2		70	1.2	
12	1.2		71	1.2	
13	1.3		72	1.2	
14	1.0		74	1.0	
16	0.69		76	1.3	
17	1.1		77	1.2	
18	1.3		79	1.1	
19	1.3		81	3.5	Outlier
22	1.3		82	1.2	
24	1.3		87	3.4	Outlier
25	1.3		88	1.2	
26	1.3		89	1.1	
27	1.3		90	1.2	
28	1.54		91	1.8	
30	1.2		94	1.2	
32	1.1		96	1.3	
34	1.8		98	1.2	
35	1.1		99	0.032	
36	1.5		100	1.3	
37	1.2		101	2.4	
38	1.3		102	1.3	
39	1.5		103	1.4	
40	1.4				
42	1.3				
43	1.2				
44	1.3				
45	1.8				
46	1.2				
49	1.2				
51	1.2				
52	1.3				
53	1.3				
55	0.61				
56	1.4				
57	1.2				
60	1.4				
61	1.4				

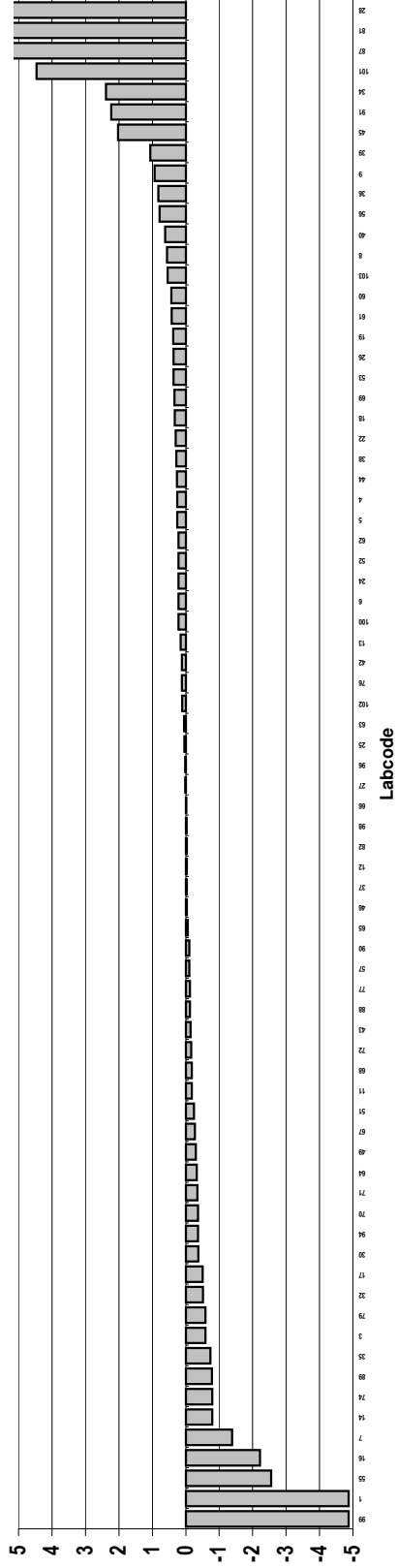
Consensus statistics

Consensus median, pg/g	1.2
Median all values pg/g	1.3
Consensus mean, pg/g	1.2
Standard deviation, pg/g	0.30
Relative standard deviation, %	25
No. of values reported	75
No. of values removed	3
No. of reported non-detects	2

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



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



Butteroil

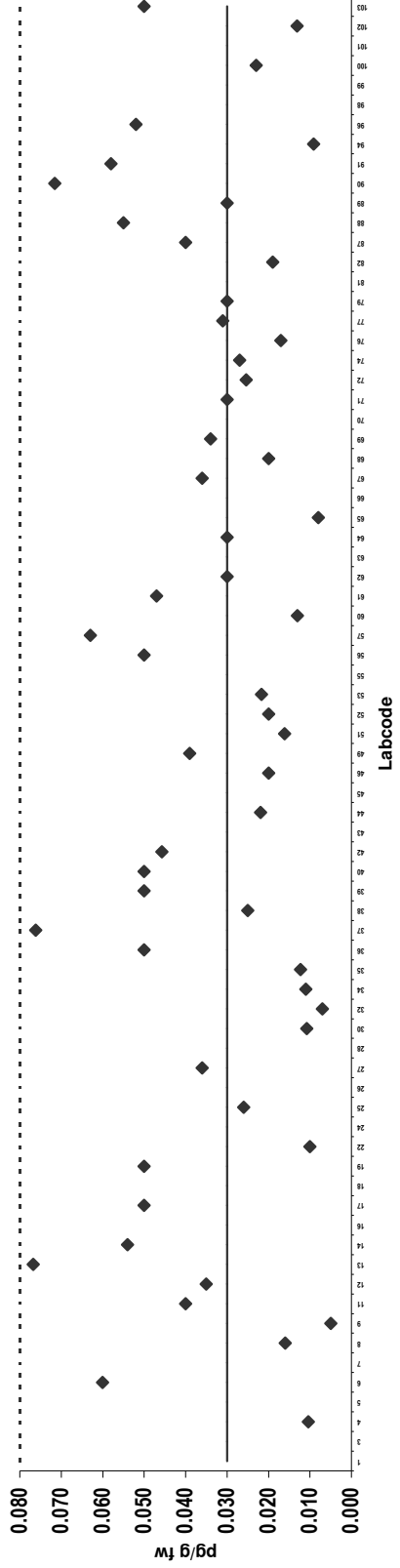
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.48		62	0.030	ND
3	0.12	Outlier,ND	63	0.092	Outlier,ND
4	0.010		64	0.030	ND
5	0.11	Outlier,ND	65	0.0080	ND
6	0.060	ND	66	0.21	Outlier
7	0.10	Outlier,ND	67	0.036	
8	0.016		68	0.020	ND
9	0.0050	ND	69	0.034	
11	0.040	ND	70	0.65	Outlier,ND
12	0.035	ND	71	0.030	ND
13	0.077	ND	72	0.025	ND
14	0.054	ND	74	0.027	ND
16	0.25	Outlier	76	0.017	ND
17	0.050	ND	77	0.031	ND
18	0.20	Outlier,ND	79	0.030	ND
19	0.050	ND	81	2.8	Outlier
22	0.010	ND	82	0.019	ND
24	0.18	Outlier	87	0.040	ND
25	0.026		88	0.055	ND
26	0.10	Outlier,ND	89	0.030	ND
27	0.036	ND	90	0.072	ND
28	0.13	Outlier,ND	91	0.058	
30	0.011		94	0.0091	
32	0.0070		96	0.052	ND
34	0.011	ND	98	1.0	Outlier,ND
35	0.012	ND	99	1.1	Outlier
36	0.050	ND	100	0.023	ND
37	0.076	ND	101	1.0	Outlier
38	0.025		102	0.013	ND
39	0.050	ND	103	0.050	ND
40	0.050	ND			
42	0.046	ND			
43	0.11	Outlier,ND			
44	0.022				
45	0.64	Outlier			
46	0.020	ND			
49	0.039				
51	0.016	ND			
52	0.020	ND			
53	0.022				
55	0.10	Outlier,ND			
56	0.050	ND			
57	0.063	ND			
60	0.013	ND			
61	0.047	ND			

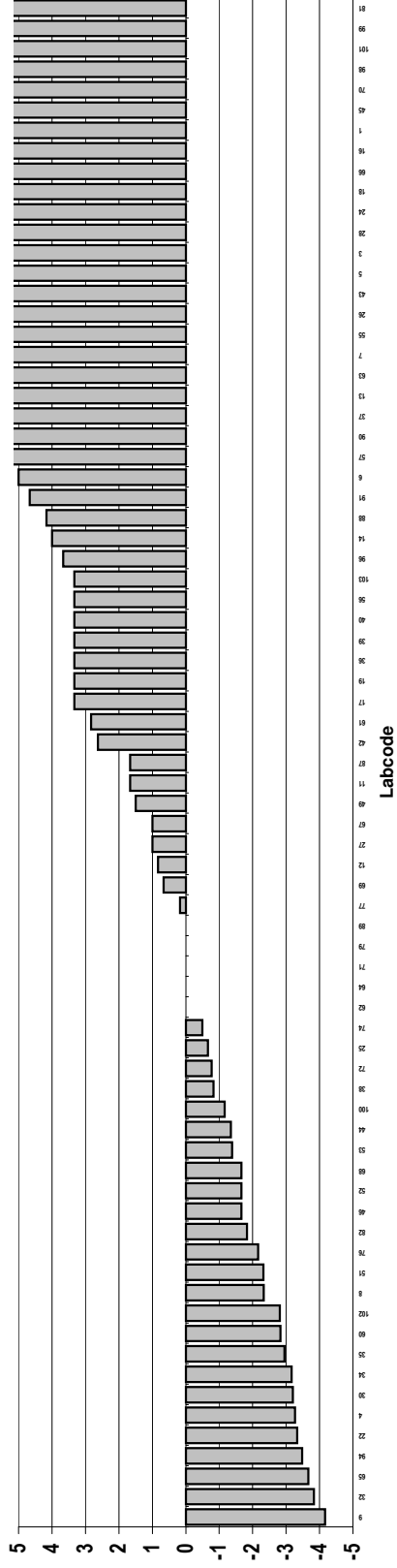
Consensus statistics

Consensus median, pg/g	0.030
Median all values pg/g	0.040
Consensus mean, pg/g	0.033
Standard deviation, pg/g	0.019
Relative standard deviation, %	57
No. of values reported	75
No. of values removed	19
No. of reported non-detects	54

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



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



Butteroil

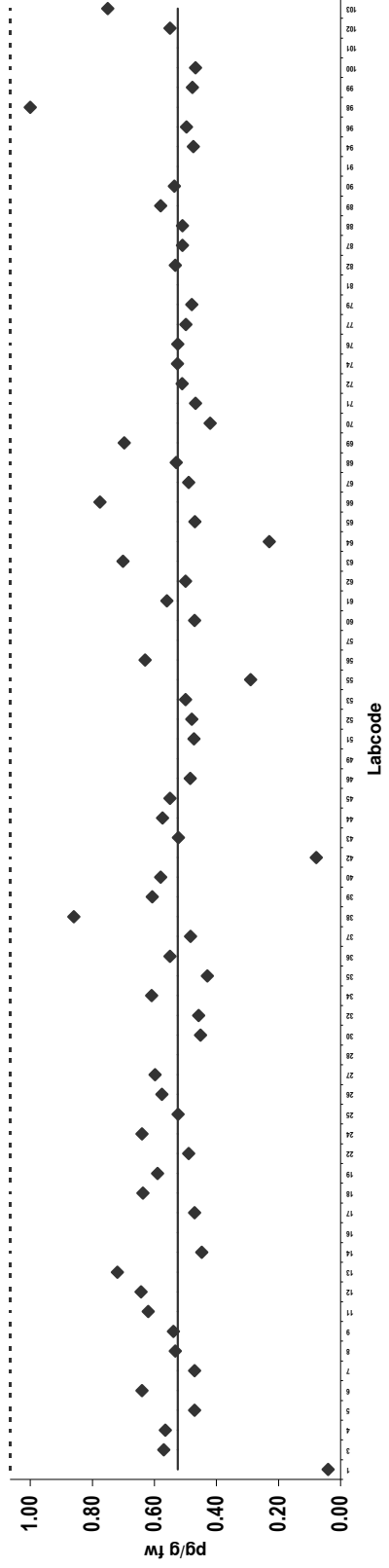
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.040		62	0.50	
3	0.57		63	0.70	
4	0.56		64	0.23	
5	0.47		65	0.47	
6	0.64		66	0.78	
7	0.47		67	0.49	
8	0.53		68	0.53	
9	0.54		69	0.70	
11	0.62		70	0.42	
12	0.64		71	0.47	
13	0.72		72	0.51	
14	0.45		74	0.53	
16	2.1	Outlier	76	0.52	
17	0.47		77	0.50	
18	0.64		79	0.48	
19	0.59		81	3.1	Outlier
22	0.49		82	0.53	
24	0.64		87	0.51	
25	0.52		88	0.51	
26	0.58		89	0.58	
27	0.60		90	0.54	
28	366	Outlier	91	1.3	
30	0.45		94	0.47	
32	0.46		96	0.50	
34	0.61		98	1.0	ND
35	0.43		99	0.48	
36	0.55		100	0.47	
37	0.48		101	1.8	Outlier
38	0.86		102	0.55	
39	0.61		103	0.75	
40	0.58				
42	0.078	ND			
43	0.52				
44	0.57				
45	0.55				
46	0.49				
49	1.2	Outlier			
51	0.47				
52	0.48				
53	0.50				
55	0.29				
56	0.63				
57	1.1	Outlier			
60	0.47				
61	0.56				

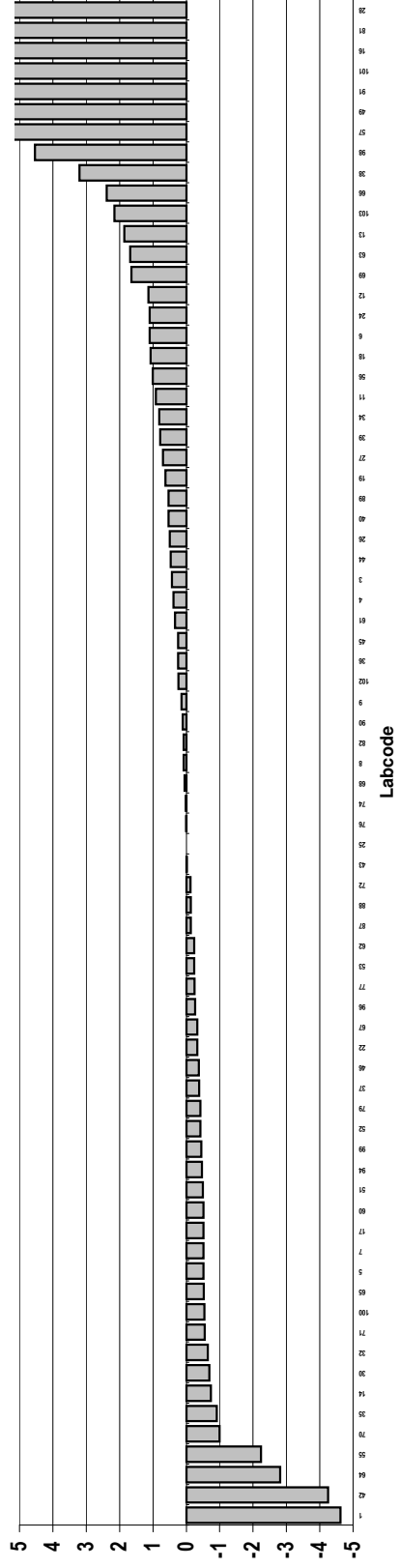
Consensus statistics

Consensus median, pg/g	0.52
Median all values pg/g	0.53
Consensus mean, pg/g	0.53
Standard deviation, pg/g	0.14
Relative standard deviation, %	26
No. of values reported	75
No. of values removed	7
No. of reported non-detects	2

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



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



Butteroil

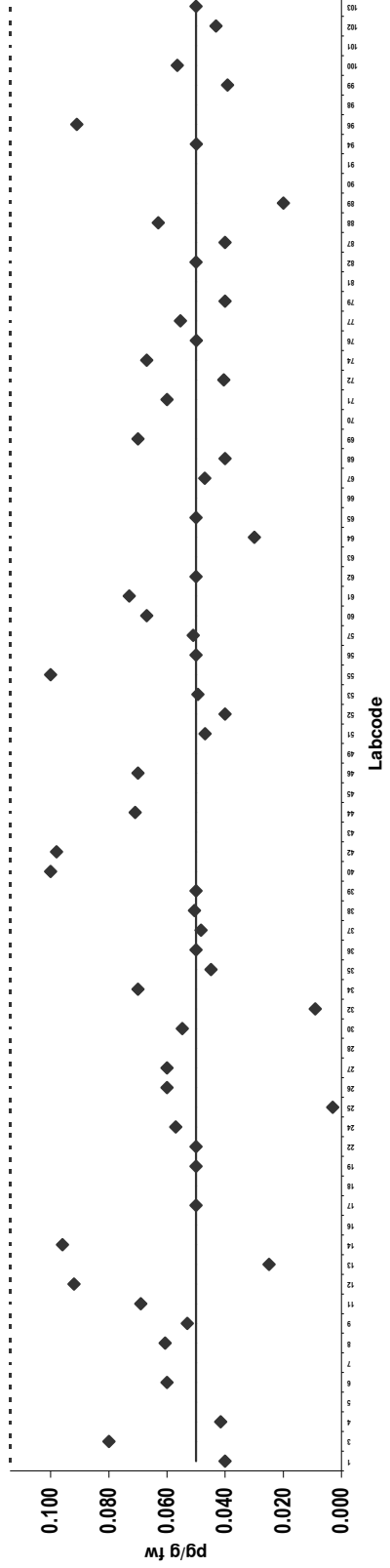
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.040		62	0.050	ND
3	0.080	ND	63	0.17	Outlier,ND
4	0.041		64	0.030	ND
5	0.13	Outlier,ND	65	0.050	
6	0.060	ND	66	0.40	Outlier
7	0.30	Outlier,ND	67	0.047	
8	0.061		68	0.040	
9	0.053		69	0.070	
11	0.069		70	0.69	Outlier,ND
12	0.092		71	0.060	ND
13	0.025		72	0.040	ND
14	0.096		74	0.067	
16	6.2	Outlier	76	0.050	
17	0.050		77	0.055	
18	0.17	Outlier	79	0.040	
19	0.050	ND	81	2.7	Outlier
22	0.050		82	0.050	
24	0.057	ND	87	0.040	
25	0.0030	ND	88	0.063	ND
26	0.060		89	0.020	
27	0.060	ND	90	0.15	Outlier
28	41	Outlier	91	0.12	Outlier
30	0.055		94	0.050	
32	0.0090	ND	96	0.091	ND
34	0.070		98	1.0	Outlier,ND
35	0.045		99	0.039	
36	0.050	ND	100	0.057	
37	0.048		101	1.2	Outlier
38	0.051		102	0.043	
39	0.050	ND	103	0.050	ND
40	0.10	ND			
42	0.098	ND			
43	0.20	Outlier,ND			
44	0.071				
45	0.12	Outlier			
46	0.070				
49	0.14	Outlier			
51	0.047				
52	0.040				
53	0.049				
55	0.10	ND			
56	0.050	ND			
57	0.051				
60	0.067				
61	0.073				

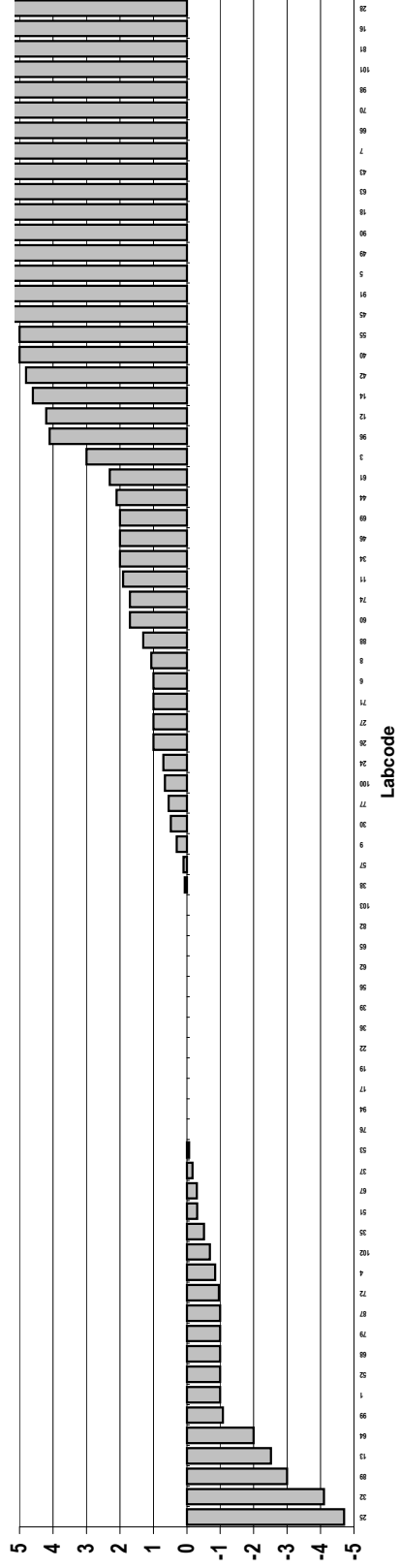
Consensus statistics

Consensus median, pg/g	0.050
Median all values pg/g	0.057
Consensus mean, pg/g	0.055
Standard deviation, pg/g	0.020
Relative standard deviation, %	36
No. of values reported	75
No. of values removed	16
No. of reported non-detects	26

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



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

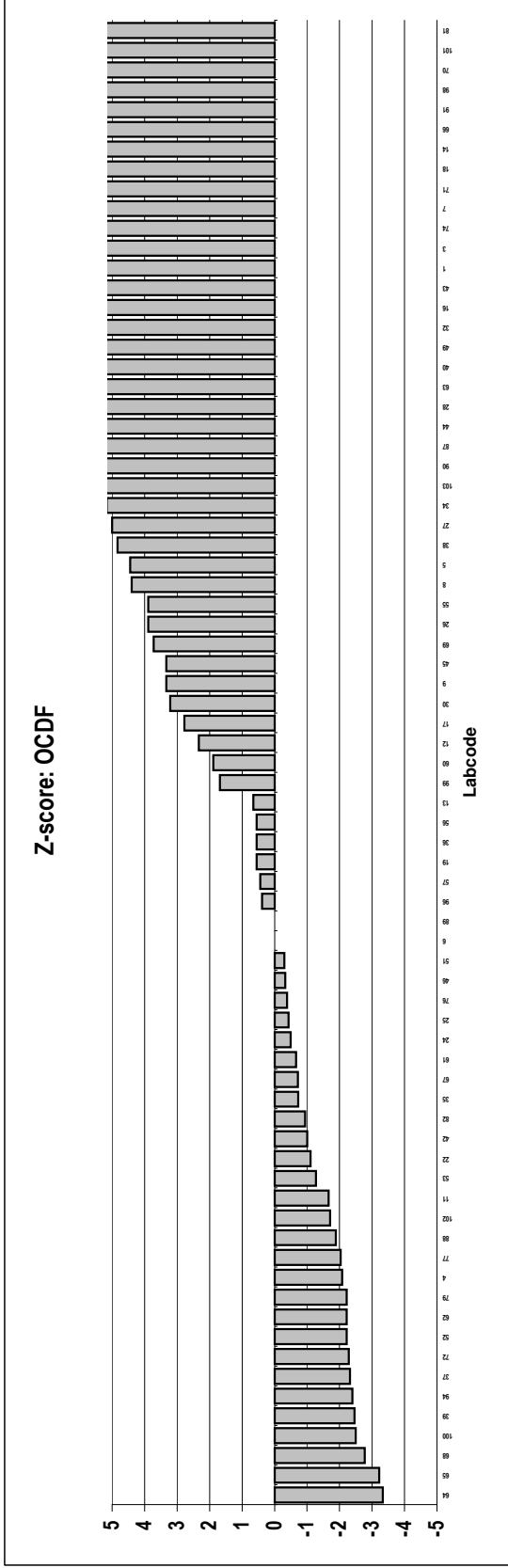
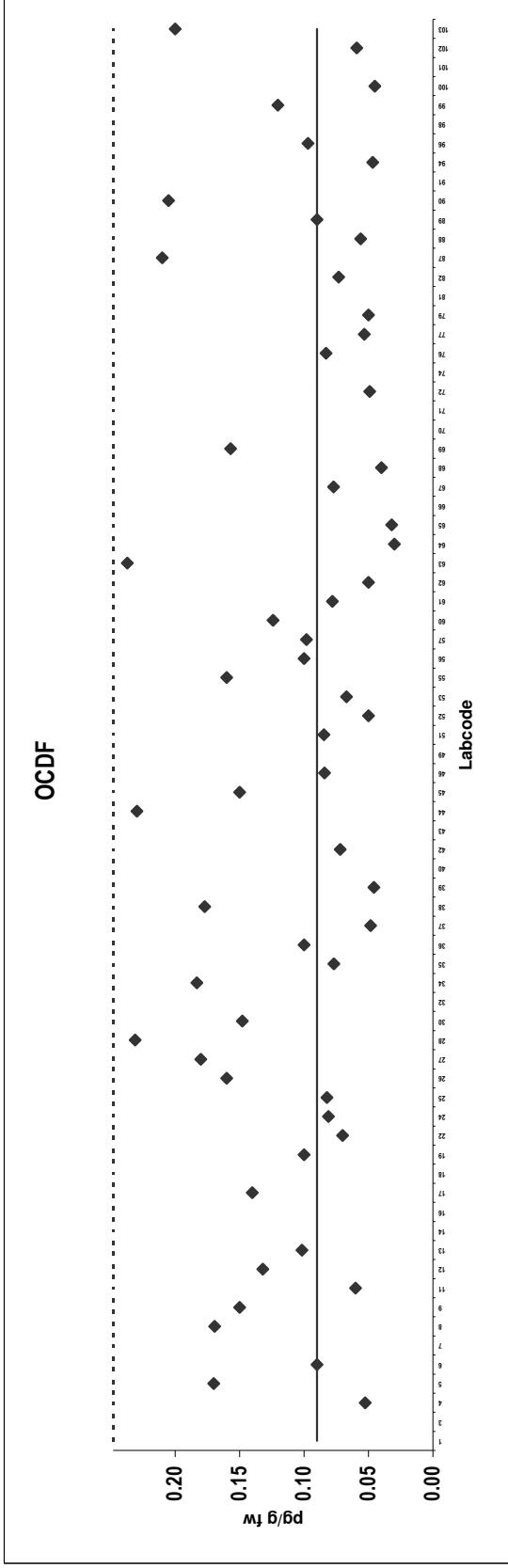


Butteroil
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.35		62	0.050	ND
3	0.35	Outlier	63	0.24	ND
4	0.053	Outlier	64	0.030	ND
5	0.17		65	0.032	
6	0.090	ND	66	0.81	Outlier
7	0.50	ND	67	0.077	
8	0.17	Outlier,ND	68	0.040	
9	0.15		69	0.16	
11	0.060	ND	70	2.3	Outlier,ND
12	0.13	ND	71	0.50	Outlier,ND
13	0.10	ND	72	0.049	ND
14	0.80	Outlier	74	0.37	Outlier
16	0.34	Outlier	76	0.083	ND
17	0.14		77	0.053	
18	0.67	Outlier	79	0.050	ND
19	0.10	ND	81	4.6	Outlier
22	0.070		82	0.073	
24	0.081	ND	87	0.21	
25	0.082	ND	88	0.056	ND
26	0.16	ND	89	0.090	
27	0.18	ND	90	0.21	
28	0.23	ND	91	1.0	Outlier
30	0.15		94	0.047	
32	0.30	Outlier	96	0.097	ND
34	0.18		98	2.0	Outlier,ND
35	0.077		99	0.12	
36	0.10	ND	100	0.045	
37	0.048	ND	101	2.6	Outlier
38	0.18		102	0.059	
39	0.046		103	0.20	ND
40	0.26	Outlier			
42	0.072	ND			
43	0.34	Outlier,ND			
44	0.23				
45	0.15				
46	0.084				
49	0.27	Outlier			
51	0.085				
52	0.050				
53	0.067				
55	0.16				
56	0.10	ND			
57	0.098	ND			
60	0.12				
61	0.078				

Consensus statistics

Consensus median, pg/g	0.090
Median all values pg/g	0.12
Consensus mean, pg/g	0.11
Standard deviation, pg/g	0.057
Relative standard deviation, %	54
No. of values reported	75
No. of values removed	18
No. of reported non-detects	29



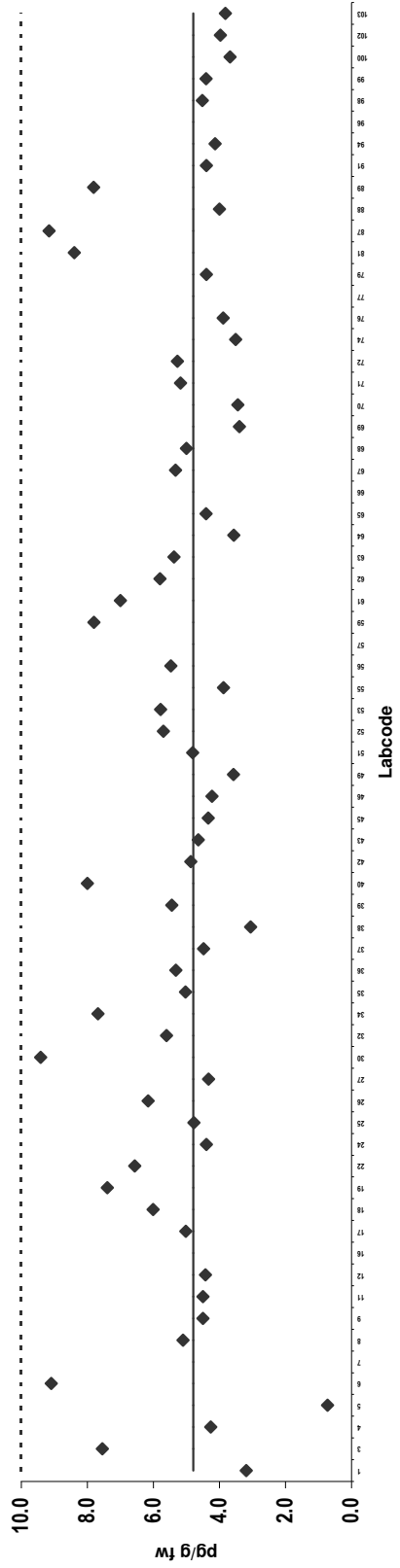
Butteroil
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	3.2		66	10	Outlier
3	7.6		67	5.3	
4	4.3		68	5.0	
5	0.73		69	3.4	
6	9.1		70	3.4	
7	15	Outlier	71	5.2	
8	5.1		72	5.3	
9	4.5		74	3.5	
11	4.5		76	3.9	
12	4.4		77	4.4	Outlier
16	7.1		79	4.4	
17	5.0	Outlier	81	8.4	
18	6.0		87	9.2	
19	7.4		88	4.0	
22	6.6		89	7.8	
24	4.4		91	4.4	
25	4.8		94	4.1	
26	6.2		96	28	Outlier,ND
27	4.3		98	4.5	
30	9.4		99	4.4	
32	5.6		100	3.7	
34	7.7		102	4.0	
35	5.0		103	3.8	
36	5.3				
37	4.5				
38	3.1				
39	5.4				
40	8.0				
42	4.9				
43	4.6				
45	4.3				
46	4.2				
49	3.6				
51	4.8				
52	5.7				
53	5.8				
55	3.9				
56	5.5				
57	17	Outlier			
59	7.8	ND			
61	7.0				
62	5.8				
63	5.4				
64	3.6				
65	4.4				

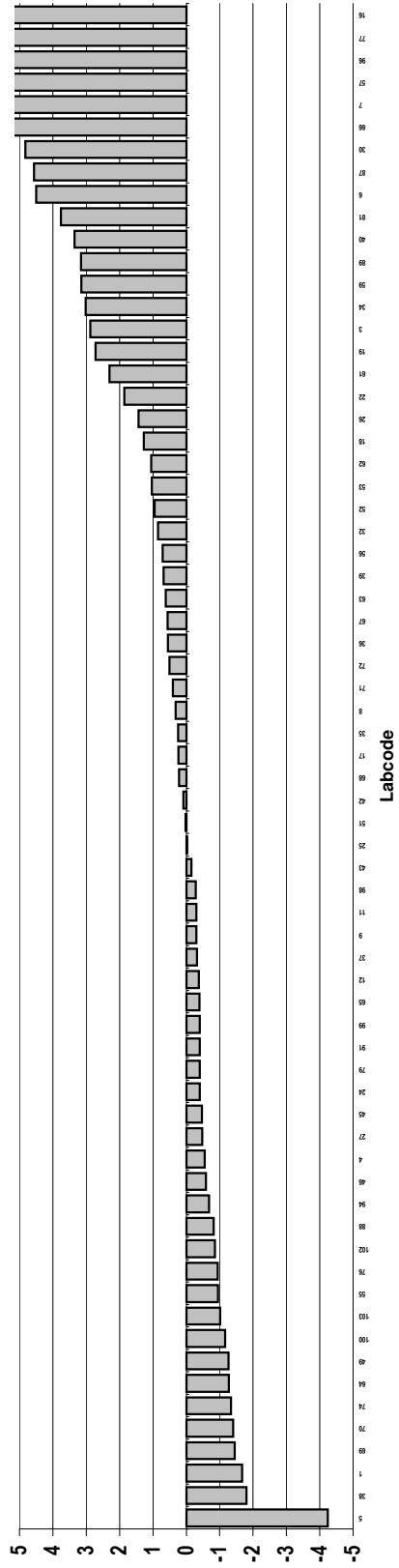
Consensus statistics

Consensus median, pg/g	4.8
Median all values pg/g	5.0
Consensus mean, pg/g	5.2
Standard deviation, pg/g	1.7
Relative standard deviation, %	32
No. of values reported	68
No. of values removed	6
No. of reported non-detects	2

PCB 77



Z-score: PCB 77



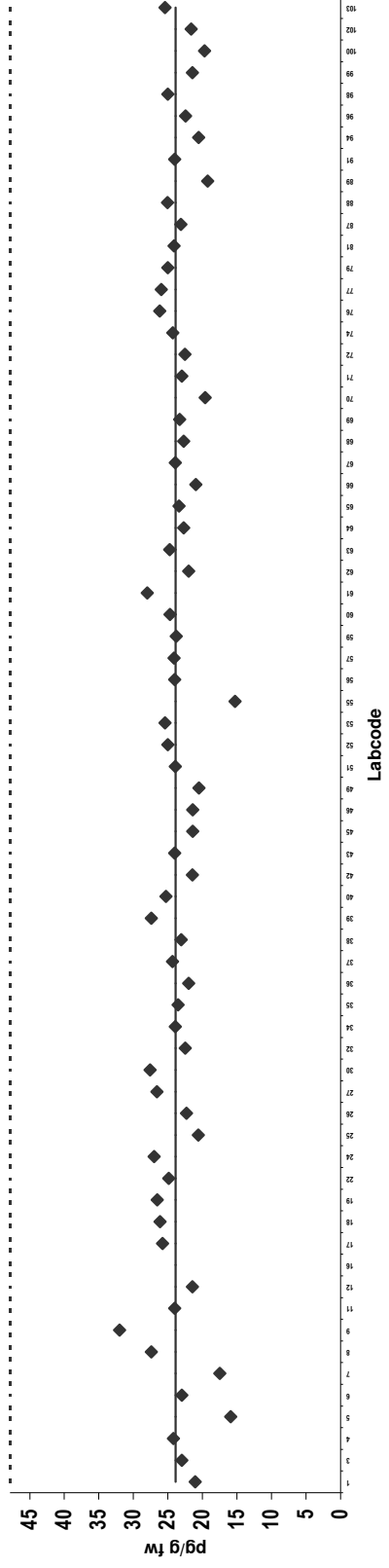
Butteroil
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	21		65	23	
3	23		66	21	
4	24		67	24	
5	16		68	23	
6	23		69	23	
7	17		70	20	
8	27		71	23	
9	32		72	23	
11	24		74	24	
12	21		76	26	
16	354	Outlier	77	26	
17	26		79	25	
18	26		81	24	
19	27		87	23	
22	25		88	25	
24	27		89	19	
25	21		91	24	
26	22		94	21	
27	27		96	22	
30	28		98	25	
32	23		99	21	
34	24		100	20	
35	24		102	22	
36	22		103	25	
37	24				
38	23				
39	27				
40	25				
42	21				
43	24				
45	21				
46	21				
49	21				
51	24				
52	25				
53	25				
55	15				
56	24				
57	24				
59	24				
60	25				
61	28				
62	22				
63	25				
64	23				

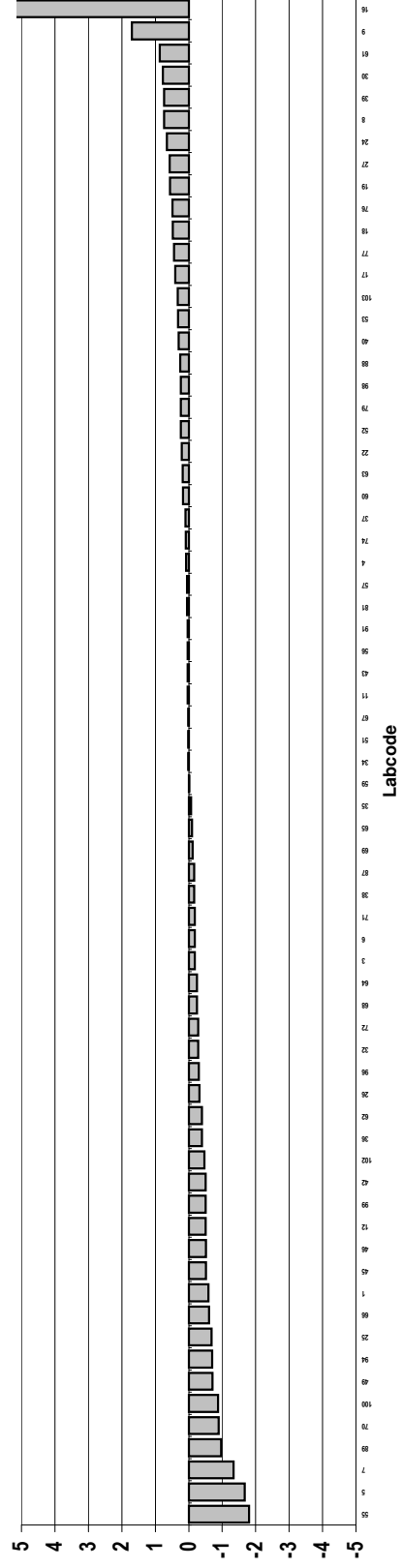
Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	23
Standard deviation, pg/g	2.8
Relative standard deviation, %	12
No. of values reported	69
No. of values removed	1
No. of reported non-detects	0

PCB 126



Z-score: PCB 126



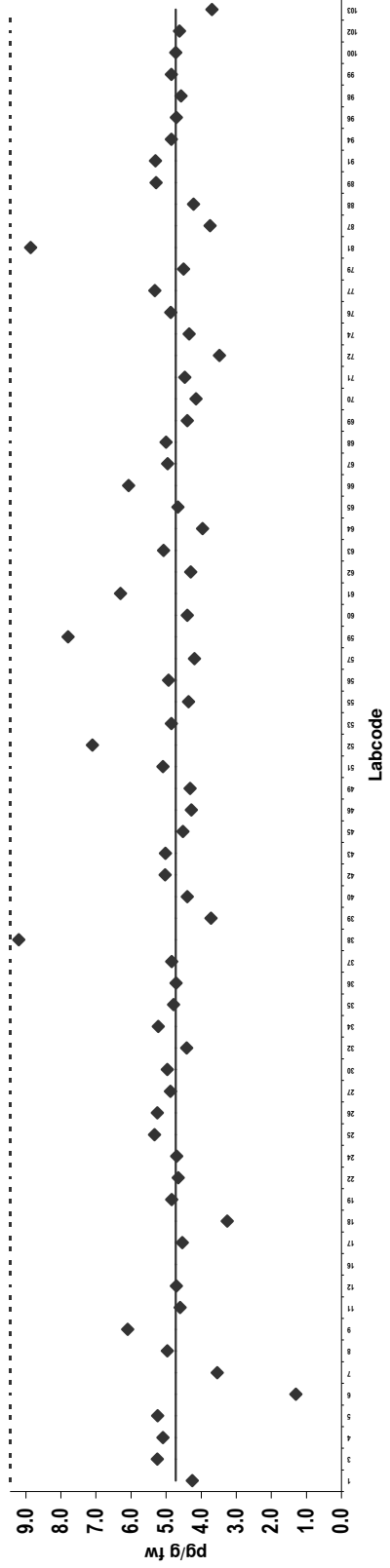
Butteroil
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.3		65	4.7	
3	5.3		66	6.1	
4	5.1		67	5.0	
5	5.2		68	5.0	
6	1.3	ND	69	4.4	
7	3.5		70	4.1	
8	5.0		71	4.5	
9	6.1		72	3.5	ND
11	4.6		74	4.3	
12	4.7		76	4.9	
16	1.5		77	5.3	
17	4.5	Outlier	79	4.5	
18	3.3		81	8.9	ND
19	4.8		87	3.8	
22	4.7		88	4.2	
24	4.7		89	5.3	
25	5.3		91	5.3	
26	5.3		94	4.9	
27	4.9		96	4.7	
30	5.0		98	4.6	
32	4.4		99	4.8	
34	5.2		100	4.7	
35	4.8		102	4.6	
36	4.7		103	3.7	
37	4.8				
38	9.2				
39	3.7				
40	4.4				
42	5.0				
43	5.0				
45	4.5				
46	4.3				
49	4.3				
51	5.1				
52	7.1				
53	4.9				
55	4.4				
56	4.9				
57	4.2				
59	7.8				
60	4.4				
61	6.3				
62	4.3				
63	5.1				
64	4.0				

Consensus statistics

Consensus median, pg/g	4.7
Median all values pg/g	4.7
Consensus mean, pg/g	4.9
Standard deviation, pg/g	1.1
Relative standard deviation, %	23
No. of values reported	69
No. of values removed	1
No. of reported non-detects	4

PCB 169



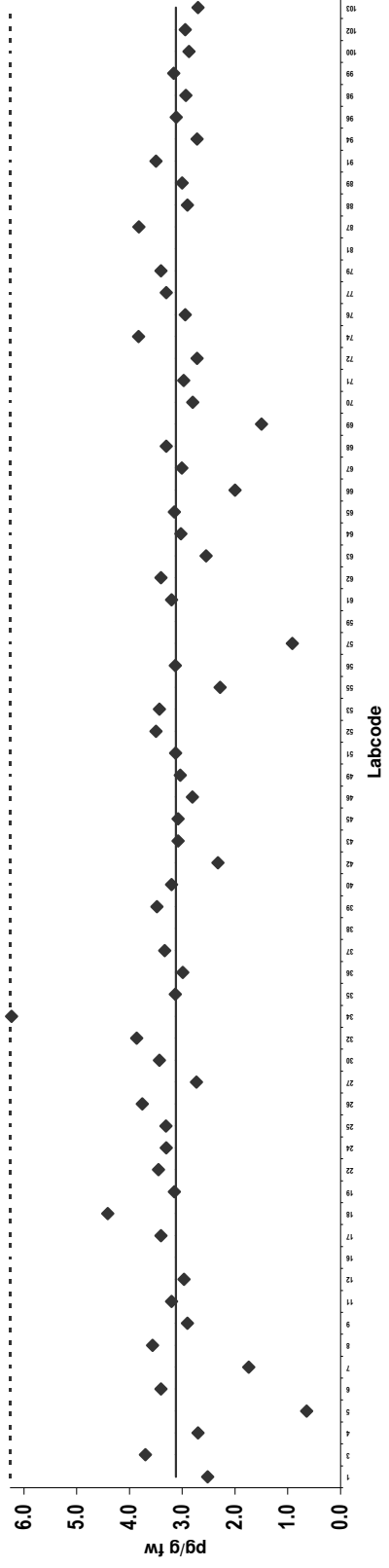
Butteroil
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.5		66	2.0	ND
3	3.7		67	3.0	
4	2.7		68	3.3	
5	0.64		69	1.5	
6	3.4		70	2.8	
7	1.7		71	3.0	
8	3.6		72	2.7	
9	2.9		74	3.8	
11	3.2		76	2.9	
12	3.0		77	3.3	
16	3.2		79	3.4	
17	3.4	Outlier	81	6.5	Outlier
18	4.4		87	3.8	
19	3.2		88	2.9	
22	3.5		89	3.0	
24	3.3		91	3.5	
25	3.3		94	2.7	
26	3.8		96	3.1	
27	2.7		98	2.9	
30	3.4		99	3.2	
32	3.9		100	2.9	
34	6.2		102	2.9	
35	3.1		103	2.7	
36	3.0				
37	3.3				
38	9.8	Outlier			
39	3.5				
40	3.2				
42	2.3				
43	3.1				
45	3.1				
46	2.8				
49	3.0				
51	3.1				
52	3.5				
53	3.4				
55	2.3				
56	3.1				
57	0.91				
59	7.8				
61	3.2				
62	3.4				
63	2.6				
64	3.0	Outlier,ND			
65	3.2				

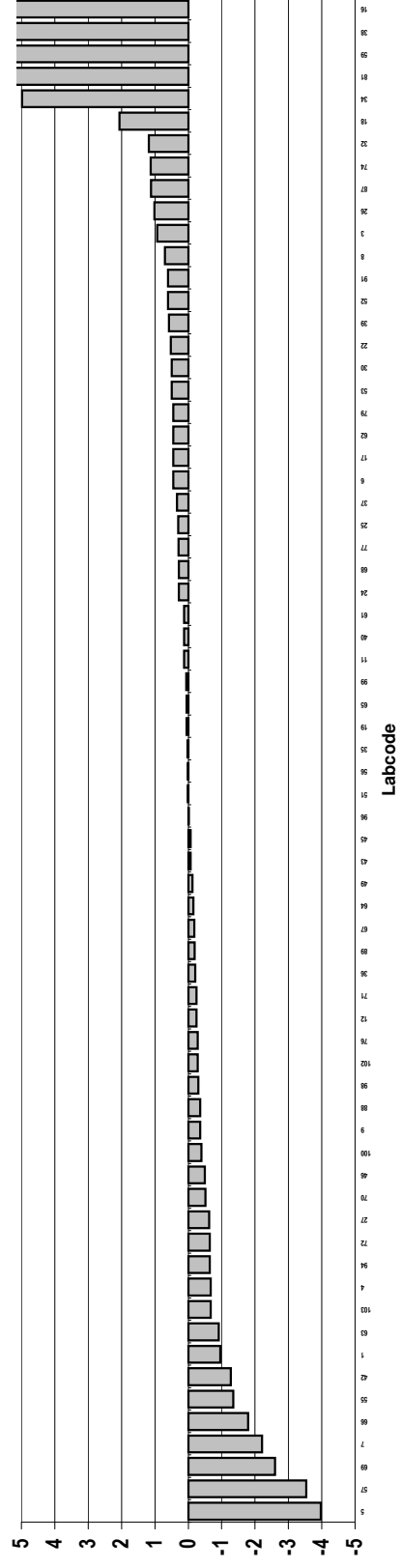
Consensus statistics

Consensus median, pg/g	3.1
Median all values pg/g	3.1
Consensus mean, pg/g	3.1
Standard deviation, pg/g	0.75
Relative standard deviation, %	24
No. of values reported	68
No. of values removed	4
No. of reported non-detects	2

PCB 81



Z-score: PCB 81



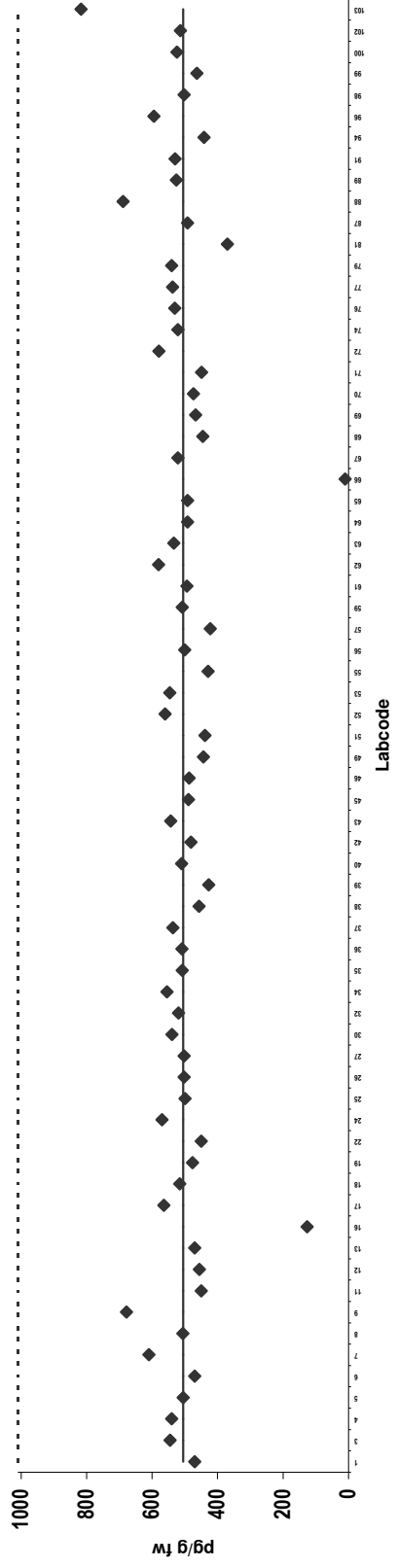
Butteroil
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	470		65	492	
3	545		66	10	
4	540		67	521	
5	505		68	445	
6	470		69	467	
7	610		70	473	
8	506		71	449	
9	678		72	579	
11	450		74	521	
12	455		76	531	
13	470		77	538	
16	127		79	540	
17	564		81	370	
18	516		87	492	
19	476		88	688	
22	450		89	526	
24	570		91	530	
25	499		94	441	
26	502		96	595	
27	502		98	502	
30	540		99	464	
32	519		100	524	
34	555		102	514	
35	508		103	817	
36	509				
37	536				
38	456				
39	427				
40	510				
42	482				
43	543				
45	489				
46	487				
49	443				
51	438				
52	560				
53	546				
55	429				
56	500				
57	422				
59	508				
61	494				
62	580				
63	533				
64	492				

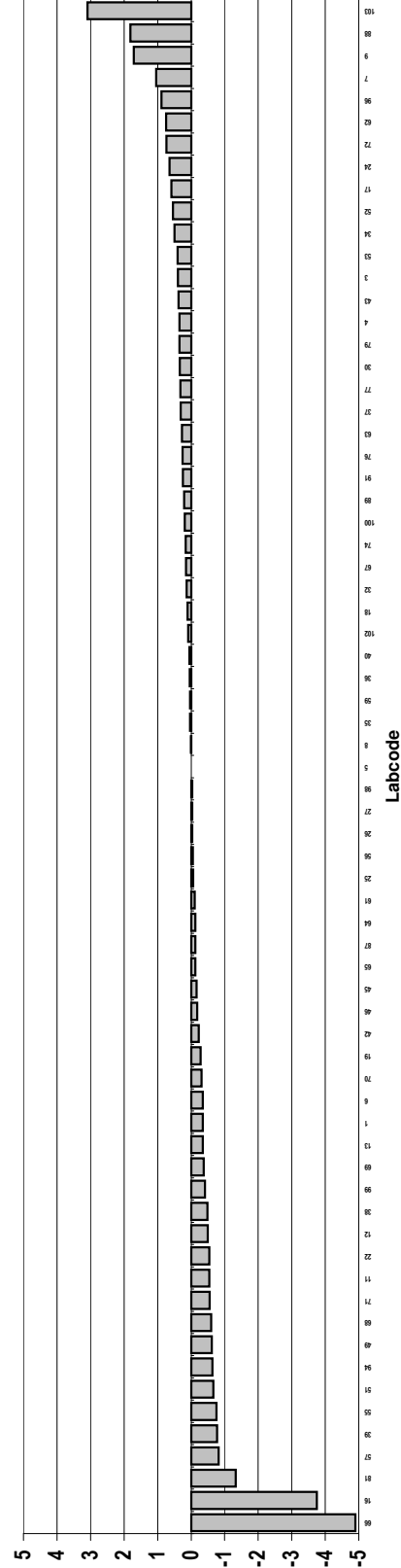
Consensus statistics

Consensus median, pg/g	505
Median all values pg/g	505
Consensus mean, pg/g	499
Standard deviation, pg/g	100
Relative standard deviation, %	20
No. of values reported	69
No. of values removed	0
No. of reported non-detects	0

PCB 105



Z-score: PCB 105



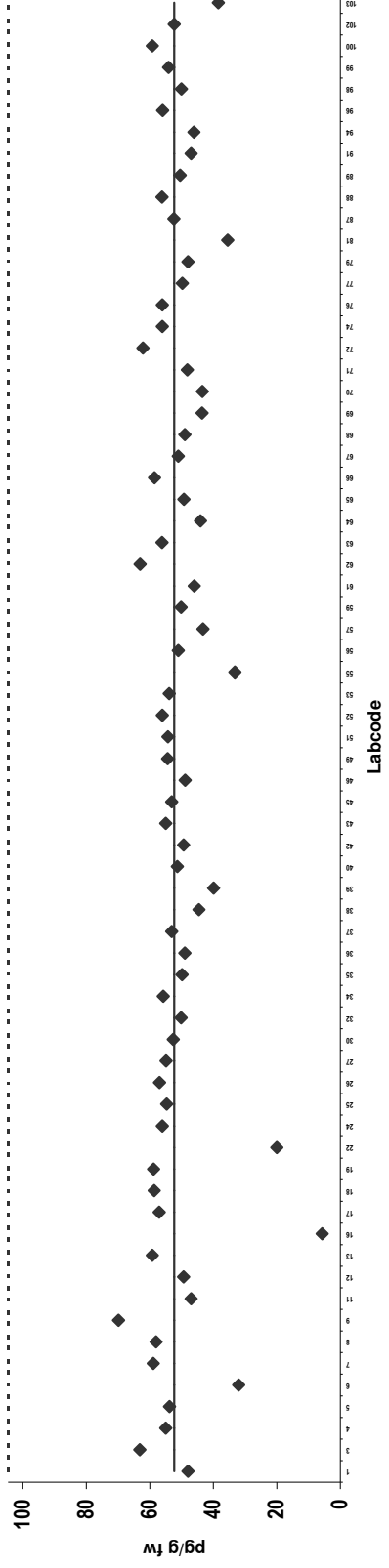
Butteroil
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	48		65	49	
3	63		66	59	
4	55		67	51	
5	54		68	49	
6	32		69	44	
7	59		70	43	
8	58		71	48	
9	70		72	62	
11	47		74	56	
12	49		76	56	
13	59		77	50	
16	5.7		79	48	
17	57		81	35	ND
18	59		87	52	
19	59		88	56	
22	20		89	50	
24	56		91	47	
25	55		94	46	
26	57		96	56	
27	55		98	50	
30	53		99	54	
32	50		100	59	
34	56		102	52	
35	50		103	38	
36	49				
37	53				
38	45				
39	40				
40	51				
42	49				
43	55				
45	53				
46	49				
49	54				
51	54				
52	56				
53	54				
55	33				
56	51				
57	43				
59	50				
61	46				
62	63				
63	56				
64	44				

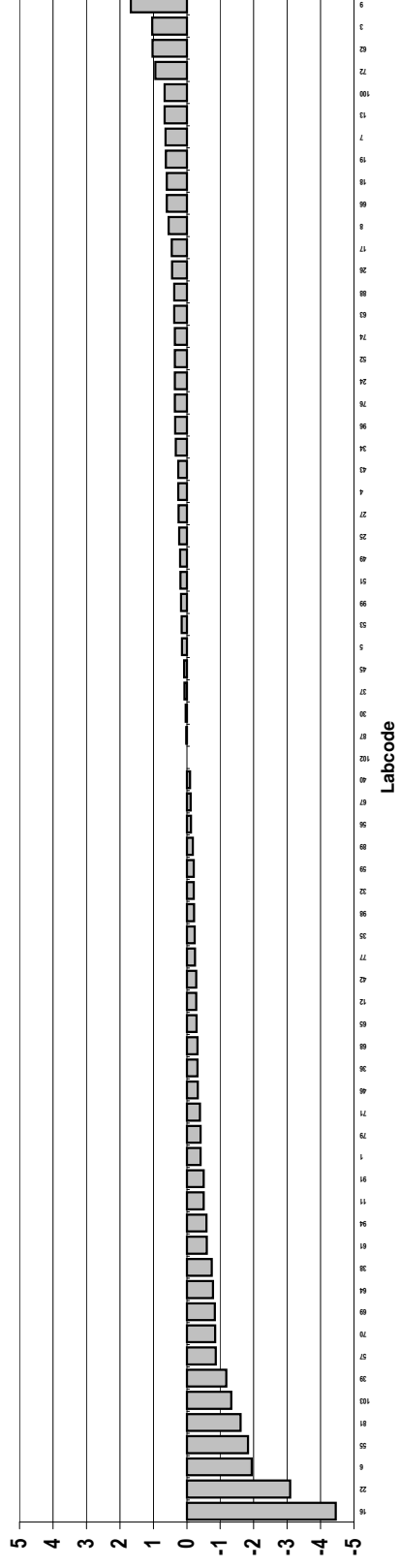
Consensus statistics

Consensus median, pg/g	52
Median all values pg/g	52
Consensus mean, pg/g	51
Standard deviation, pg/g	9.5
Relative standard deviation, %	19
No. of values reported	69
No. of values removed	0
No. of reported non-detects	2

PCB 114



Z-score: PCB 114



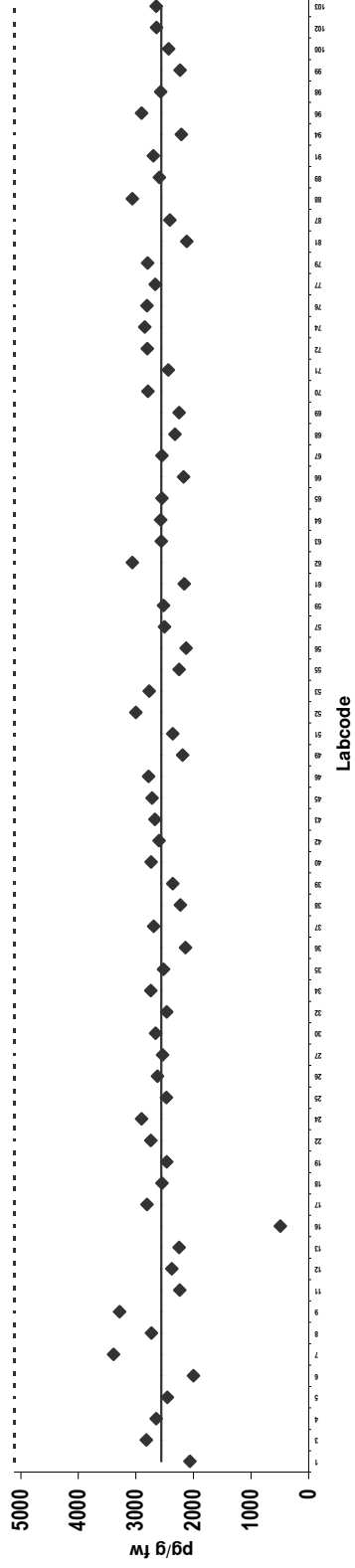
Butteroil
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2064		65	2550	
3	2822		66	2175	
4	2646		67	2550	
5	2457		68	2320	
6	2000		69	2250	
7	3391		70	2792	
8	2733		71	2440	
9	3282		72	2804	
11	2240		74	2848	
12	2379		76	2807	
13	2248		77	2665	
16	495		79	2800	
17	2811		81	2115	
18	2551		87	2410	
19	2464		88	3063	
22	2740		89	2595	
24	2900		91	2700	
25	2470		94	2211	
26	2623		96	2903	
27	2540		98	2570	
30	2657		99	2232	
32	2466		100	2431	
34	2742		102	2641	
35	2520		103	2650	
36	2140				
37	2690				
38	2230				
39	2360				
40	2737				
42	2600				
43	2670				
44	2720				
45	2720				
46	2780				
49	2190				
51	2358				
52	3000				
53	2771				
55	2248				
56	2130				
57	2505				
59	2520				
61	2160				
62	3060				
63	2560				
64	2572				

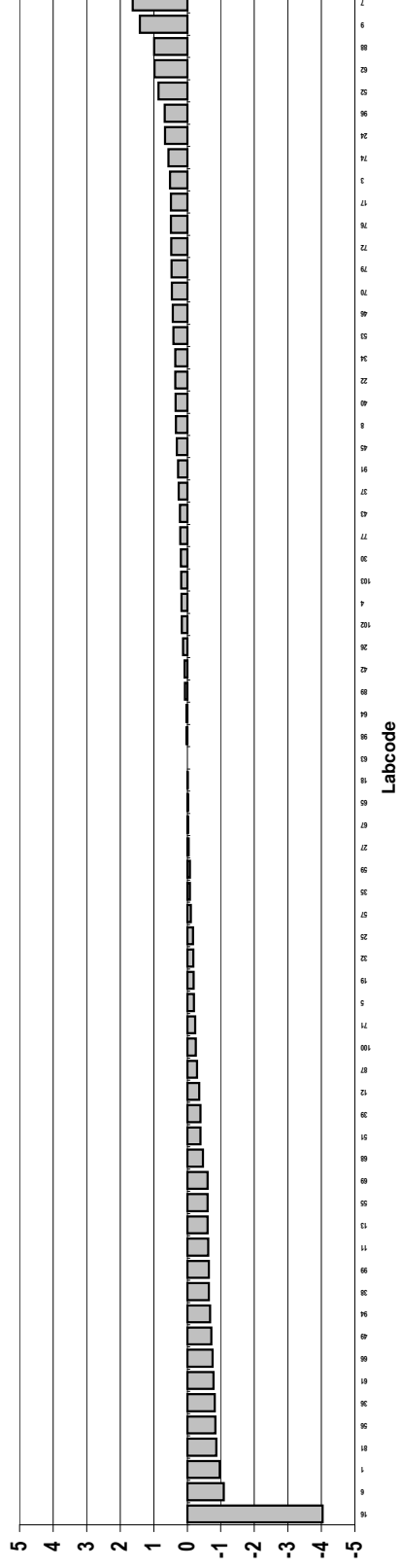
Consensus statistics

Consensus median, pg/g	2560
Median all values pg/g	2560
Consensus mean, pg/g	2533
Standard deviation, pg/g	378
Relative standard deviation, %	15
No. of values reported	69
No. of values removed	0
No. of reported non-detects	0

PCB 118



Z-score: PCB 118



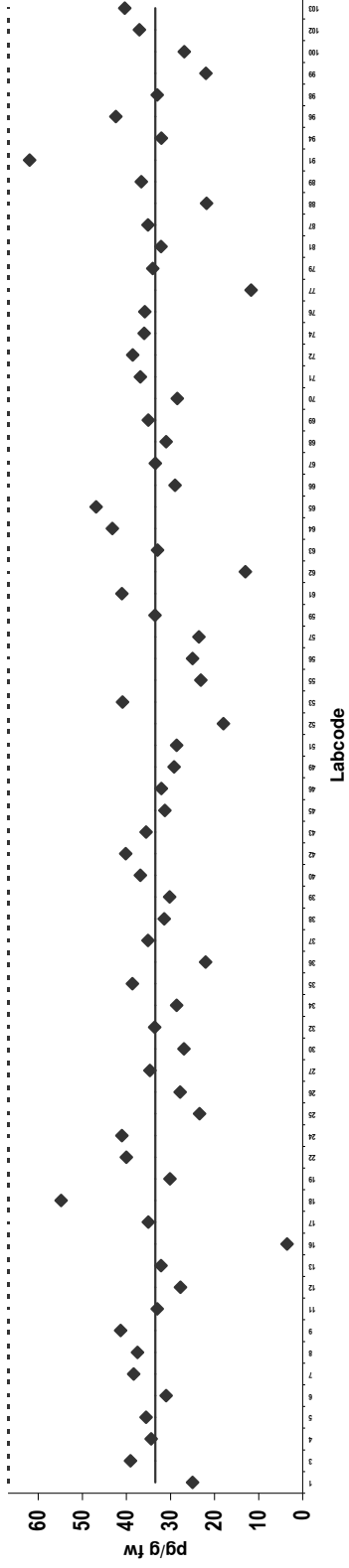
Butteroil
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	25		65	47	
3	39		66	29	
4	34		67	33	
5	36		68	31	
6	31		69	35	
7	38		70	28	
8	38		71	37	
9	41		72	39	
11	33		74	36	
12	28		76	36	
13	32		77	12	
16	3.5		79	34	
17	35		81	32	
18	55		87	35	
19	30		88	22	
22	40		89	37	
24	41		91	62	
25	23		94	32	
26	28		96	42	
27	35		98	33	
30	27		99	22	
32	34		100	27	
34	29		102	37	
35	39		103	40	
36	22				
37	35				
38	31				
39	30				
40	37				
42	40				
43	36				
45	31				
46	32				
49	29				
51	29				
52	18				
53	41				
55	23				
56	25				
57	24				
59	34				
61	41				
62	13				
63	33				
64	43				

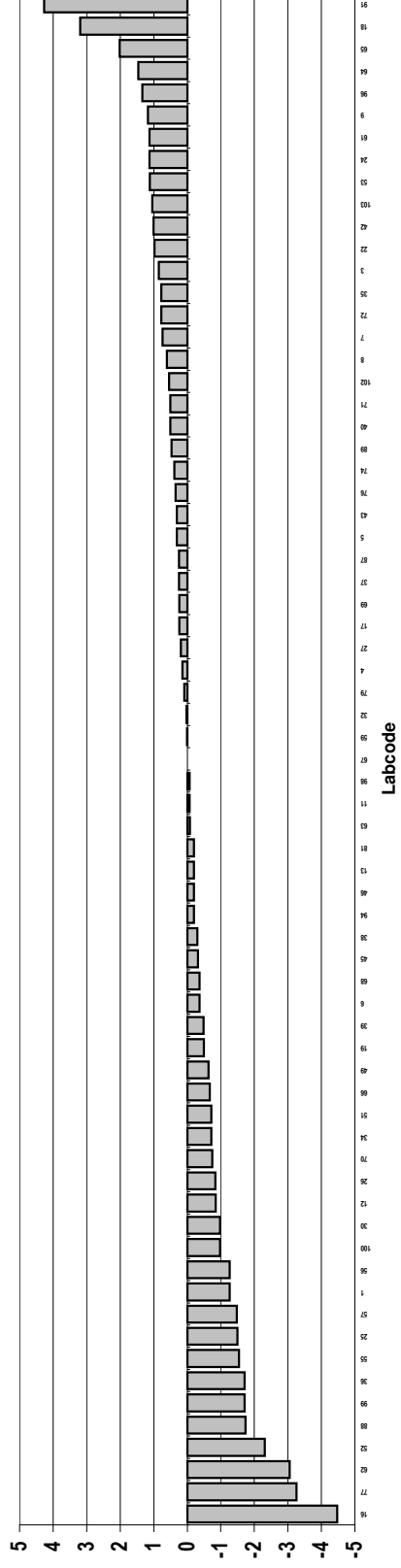
Consensus statistics

Consensus median, pg/g	33
Median all values pg/g	33
Consensus mean, pg/g	33
Standard deviation, pg/g	8.9
Relative standard deviation, %	27
No. of values reported	69
No. of values removed	0
No. of reported non-detects	0

PCB 123



Z-score: PCB 123



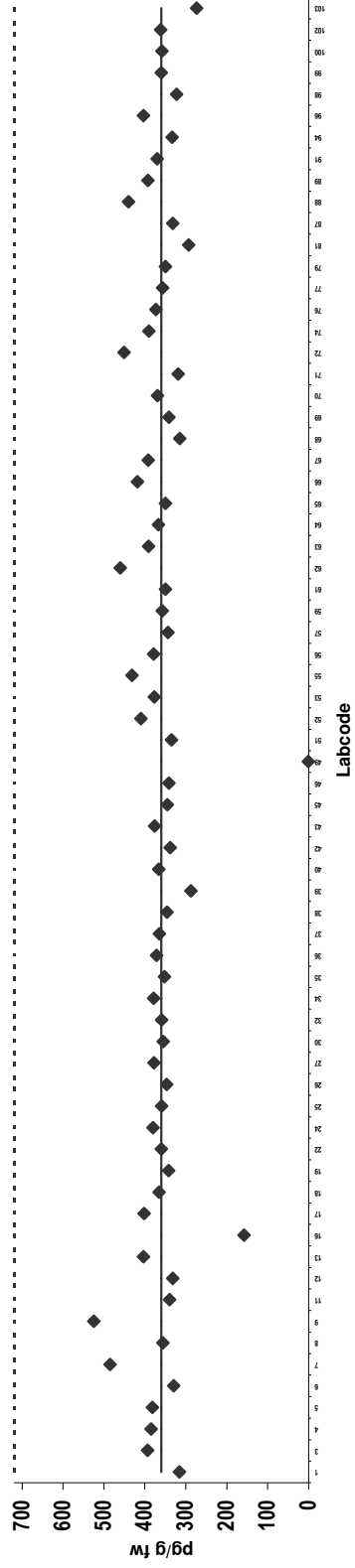
Butteroil
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	316		65	350	
3	393		66	419	
4	385		67	392	
5	382		68	315	
6	330		69	341	
7	485		70	369	
8	356		71	319	
9	525		72	451	
11	340		74	390	
12	332		76	373	
13	403		77	357	
16	158		79	350	
17	402		81	293	
18	366		87	332	
19	342		88	440	
22	360		89	393	
24	380		91	370	
25	359		94	334	
26	347		96	403	
27	378		98	323	
30	355		99	360	
32	359		100	358	
34	378		102	362	
35	353		103	274	
36	372				
37	364				
38	346				
39	288				
40	366				
42	338				
43	376				
45	345				
46	341				
49	053				
51	335				
52	410				
53	377				
55	432				
56	379				
57	344				
59	358				
61	350				
62	460				
63	391				
64	367				

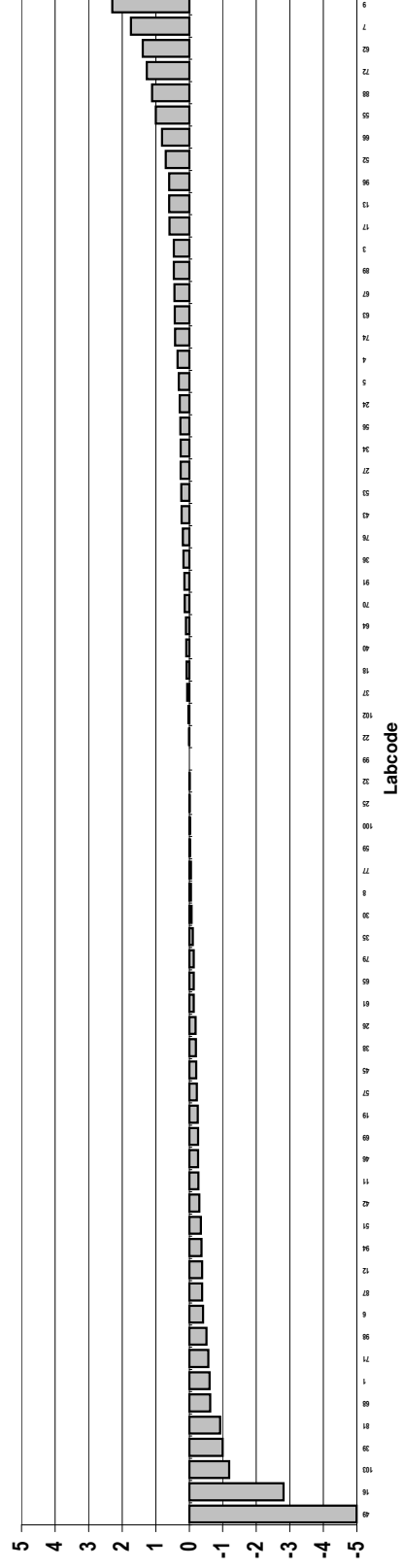
Consensus statistics

Consensus median, pg/g	360
Median all values pg/g	360
Consensus mean, pg/g	359
Standard deviation, pg/g	66
Relative standard deviation, %	18
No. of values reported	69
No. of values removed	0
No. of reported non-detects	0

PCB 156



Z-score: PCB 156



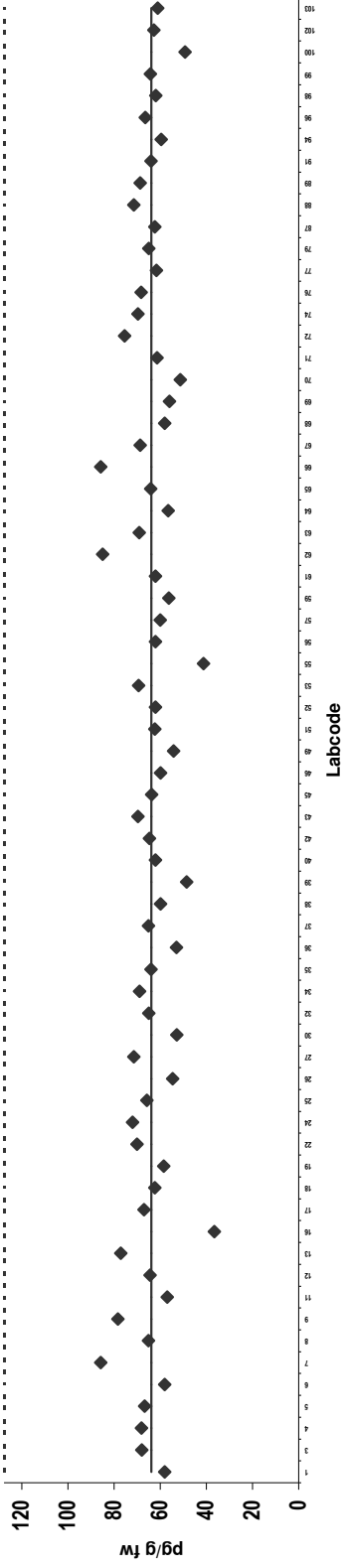
Butteroil
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	58		65	64	
3	68		66	86	
4	68		67	69	
5	67		68	58	
6	58		69	56	
7	86		70	51	
8	65		71	61	
9	78		72	75	
11	57		74	70	
12	64		76	68	
13	77		77	62	
16	37		79	65	
17	67		87	62	
18	62		88	71	
19	59		89	69	
22	70		91	64	
24	72		94	60	
25	66		96	66	
26	55		98	62	
27	71		99	64	
30	53		100	49	
32	65		102	63	
34	69		103	61	
35	64				
36	53				
37	65				
38	60				
39	49				
40	62				
42	65				
43	70				
44	64				
45	60				
46	60				
49	54				
51	62				
52	62				
53	69				
55	41				
56	62				
57	60				
59	56				
61	62				
62	85				
63	69				
64	57				

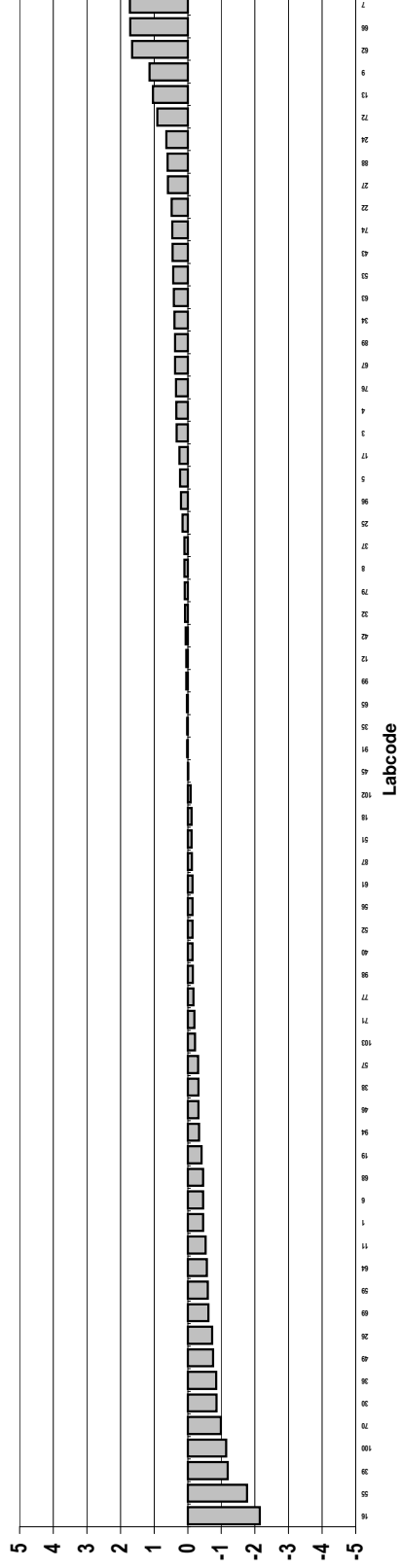
Consensus statistics

Consensus median, pg/g	64
Median all values pg/g	64
Consensus mean, pg/g	64
Standard deviation, pg/g	8.8
Relative standard deviation, %	14
No. of values reported	68
No. of values removed	0
No. of reported non-detects	0

PCB 157



Z-score: PCB 157



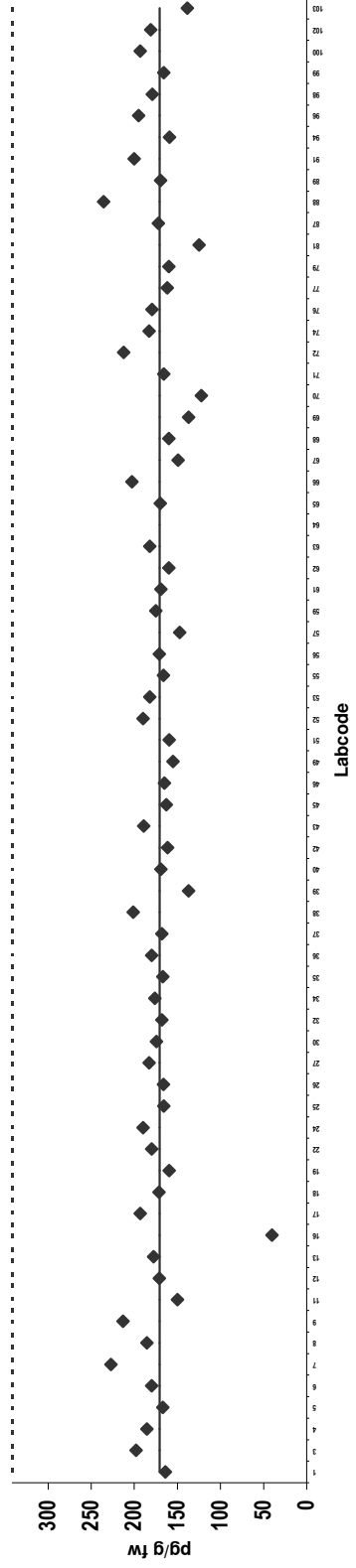
Butteroil
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	164		65	170	
3	198		66	203	
4	185		67	149	
5	167		68	160	
6	180		69	137	
7	227		70	122	
8	185		71	166	
9	213		72	212	
11	150		74	183	
12	171		76	179	
13	178		77	162	
16	40		79	160	
17	193		81	125	
18	171		87	172	
19	159		88	235	
22	180		89	169	
24	190		91	200	
25	166		94	159	
26	166		96	195	
27	183		98	179	
30	174		99	166	
32	168		100	193	
34	176		102	181	
35	167		103	139	
36	180				
37	168				
38	201				
39	137				
40	169				
42	162				
43	189				
45	163				
46	165				
49	155				
51	160				
52	190				
53	182				
55	166				
56	171				
57	147				
59	175				
61	169				
62	160				
63	182				
64	360	Outlier			

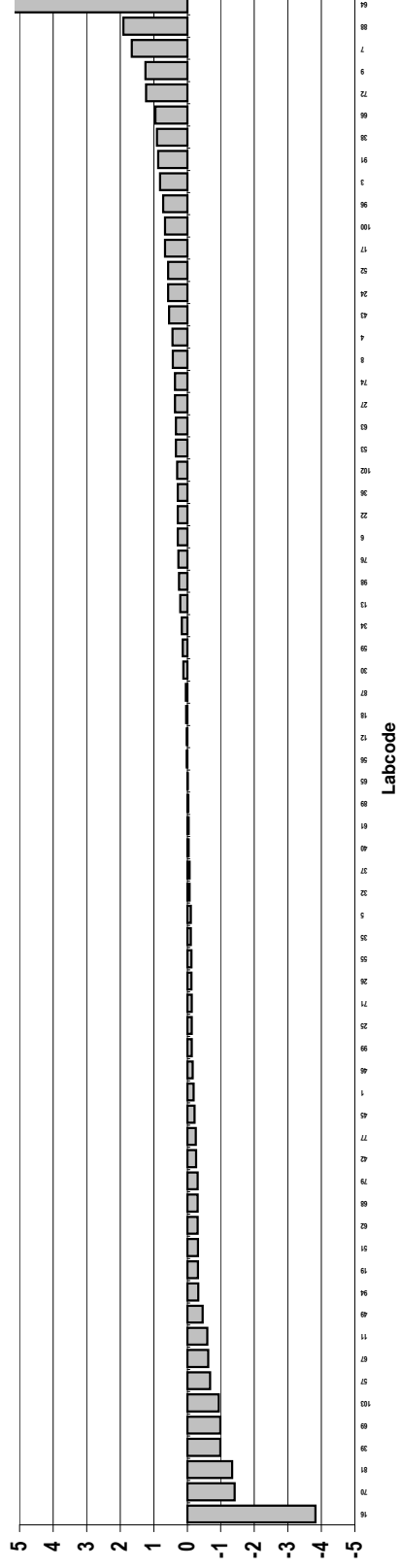
Consensus statistics

Consensus median, pg/g	171
Median all values pg/g	171
Consensus mean, pg/g	171
Standard deviation, pg/g	26
Relative standard deviation, %	15
No. of values reported	69
No. of values removed	1
No. of reported non-detects	0

PCB 167



Z-score: PCB 167



Butteroil
Congener: PCB 189

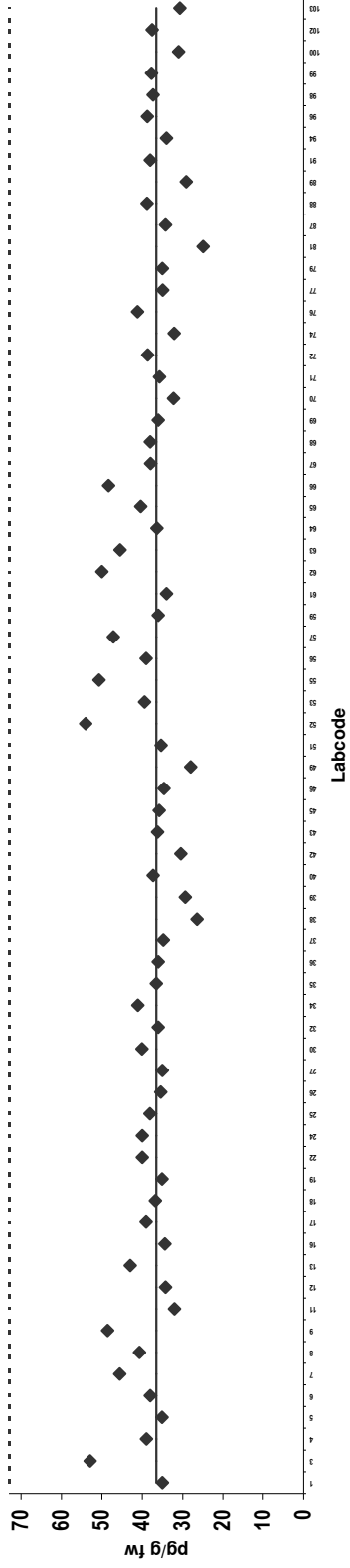
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	35		65	40	
3	53		66	48	
4	39		67	38	
5	35		68	38	
6	38		69	36	
7	46		70	32	
8	41		71	36	
9	49		72	39	
11	32		74	32	
12	34		76	41	
13	43		77	35	
16	34		79	35	
17	39		81	25	
18	37		87	34	
19	35		88	39	
22	40		89	29	
24	40		91	38	
25	38		94	34	
26	35		96	39	
27	35		98	37	
30	40		99	38	
32	36		100	31	
34	41		102	38	
35	37		103	31	
36	36				
37	35				
38	26				
39	29				
40	37				
42	30				
43	36				
44	36				
45	36				
46	35				
49	28				
51	35				
52	54				
53	39				
55	51				
56	39				
57	47				
59	36				
61	34				
62	50				
63	46				
64	36				

ND

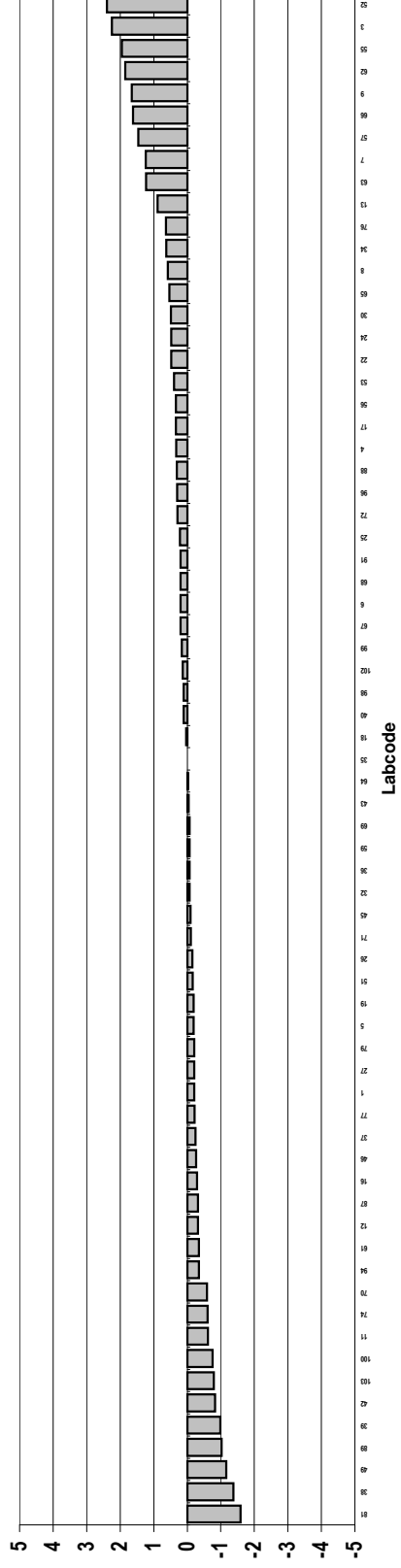
Consensus statistics

Consensus median, pg/g	37
Median all values pg/g	37
Consensus mean, pg/g	38
Standard deviation, pg/g	5.8
Relative standard deviation, %	15
No. of values reported	69
No. of values removed	0
No. of reported non-detects	1

PCB 189



Z-score: PCB 189



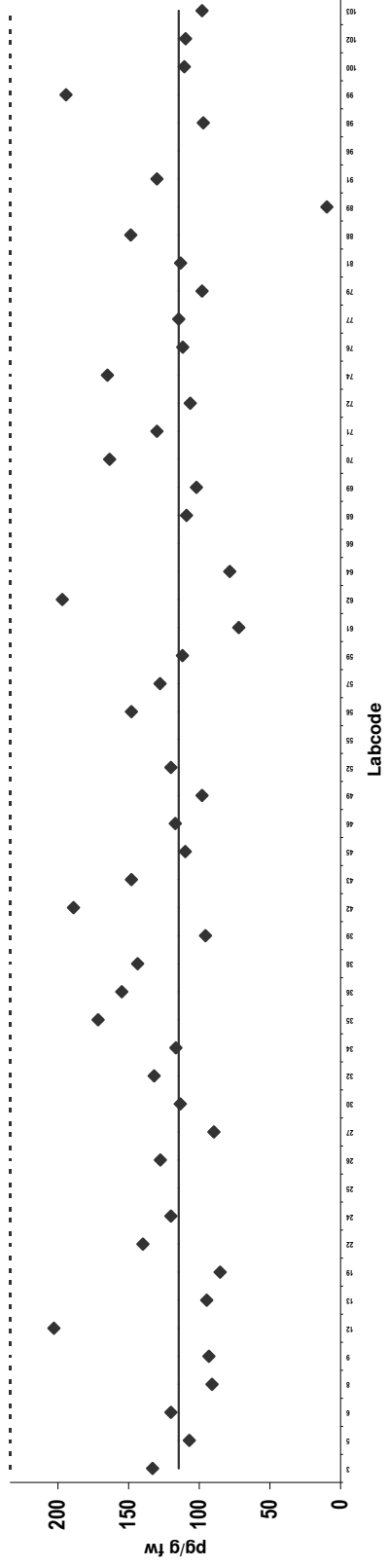
Butteroil
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	133		89	9,6	
5	107		91	130	
6	120		96	2000	Outlier,ND
8	91		98	97	
9	93		99	194	
12	203		100	111	
13	95		102	110	
19	85		103	98	
22	140				
24	120				
25	1360	Outlier			
26	128				
27	90				
30	114				
32	132				
34	116				
35	172				
36	155				
38	144				
39	96				
42	189				
43	148				
45	110				
46	117				
49	98				
52	120				
55	236	Outlier			
56	148				
57	128				
59	112				
61	72				
62	197				
64	78				
66	278	Outlier			
68	109				
69	102				
70	164				
71	130				
72	106				
74	165				
76	112				
77	115				
79	98				
81	113				
88	149				

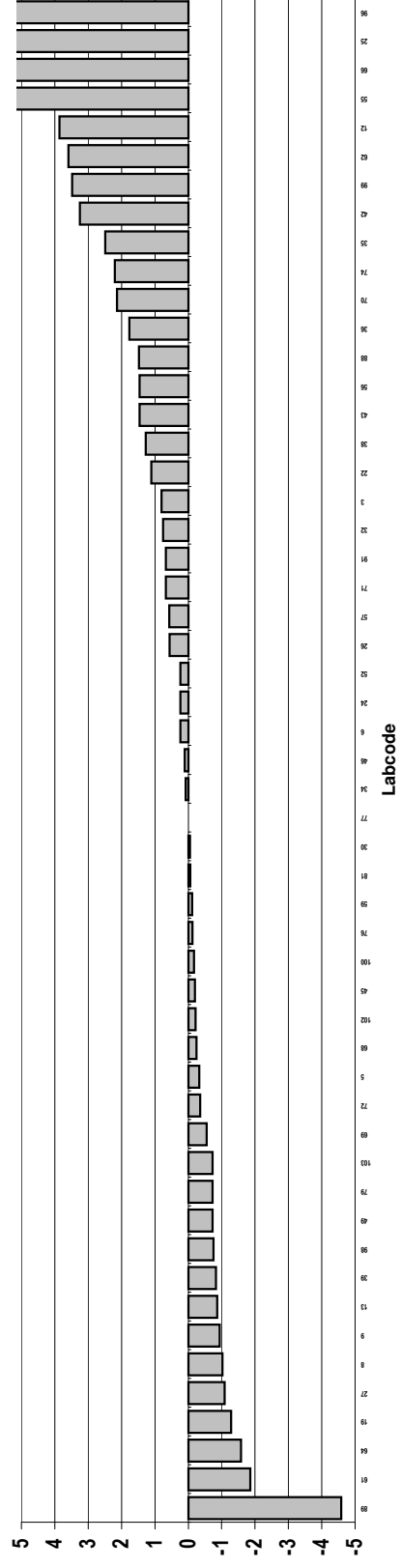
Consensus statistics

Consensus median, pg/g	115
Median all values pg/g	117
Consensus mean, pg/g	122
Standard deviation, pg/g	35
Relative standard deviation, %	29
No. of values reported	53
No. of values removed	4
No. of reported non-detects	1

CB 28



Z-score: CB 28



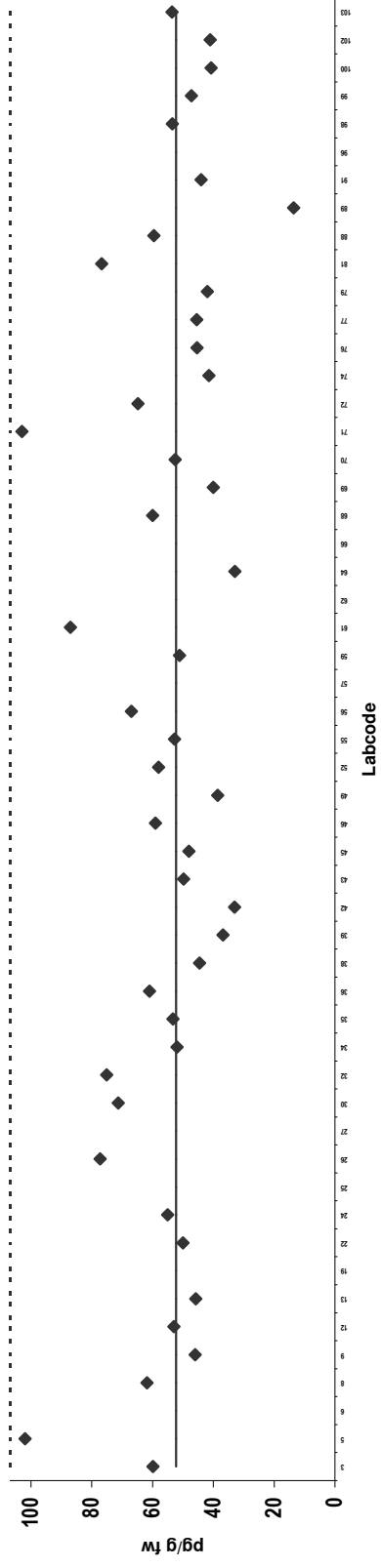
Butteroil
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	60		89	14	
5	102		91	44	
6	130		96	2000	Outlier,ND
8	62	Outlier	98	54	
9	46		99	47	
12	53		100	41	
13	46		102	41	
19	206	Outlier	103	54	
22	50				
24	55				
25	500	Outlier,ND			
26	77				
27	160	Outlier			
30	71				
32	75				
34	52				
35	53				
36	61				
38	45				
39	37				
42	33				
43	50				
45	48				
46	59				
49	39				
52	58				
55	53				
56	67				
57	157	Outlier			
59	51				
61	87				
62	130	Outlier			
64	33				
66	436	Outlier			
68	60				
69	40				
70	53				
71	103	ND			
72	65				
74	42				
76	45				
77	46				
79	42				
81	77				
88	60				

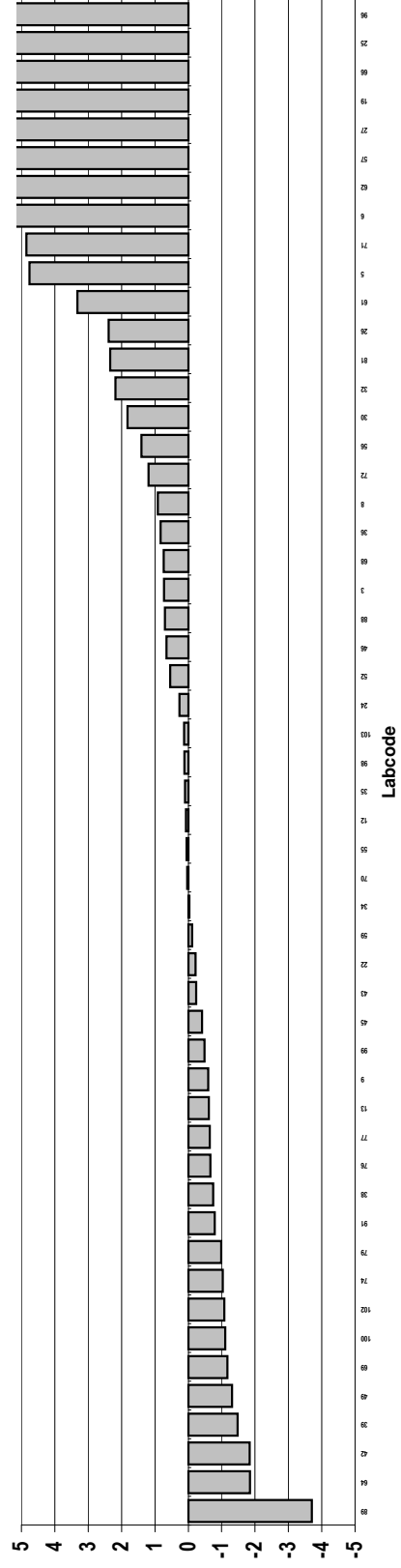
Consensus statistics

Consensus median, pg/g	52
Median all values pg/g	54
Consensus mean, pg/g	54
Standard deviation, pg/g	17
Relative standard deviation, %	31
No. of values reported	53
No. of values removed	8
No. of reported non-detects	3

CB 52



Z-score: CB 52



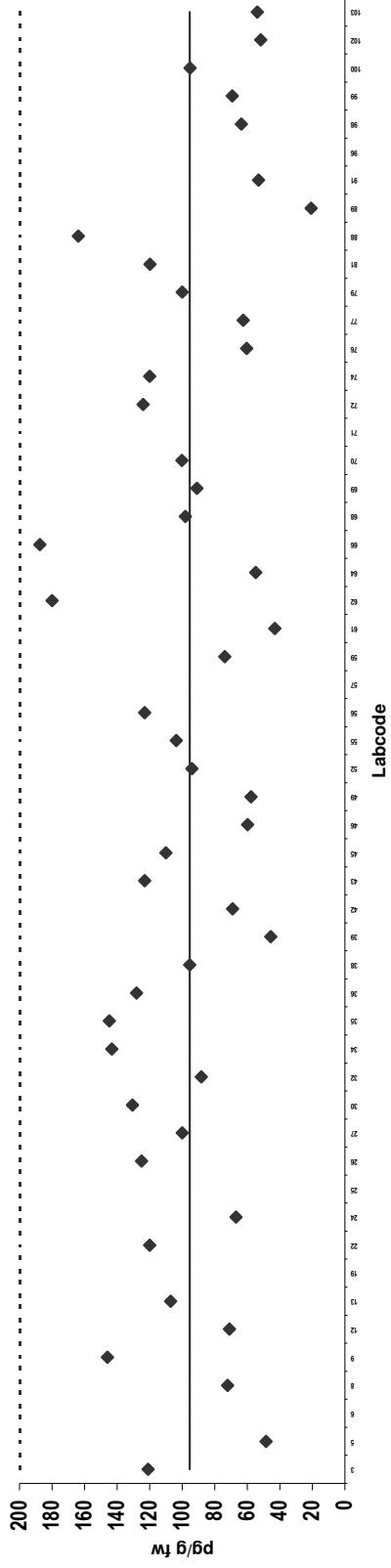
Butteroil
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	121		89	21	
5	48		91	53	
6	450	Outlier	96	2000	Outlier,ND
8	72		98	64	
9	146		99	69	
12	71		100	95	
13	107		102	52	
19	330	Outlier	103	54	
22	120				
24	67				
25	500	Outlier,ND			
26	125				
27	100				
30	131				
32	88				
34	143				
35	145				
36	128				
38	95				
39	46				
42	69				
43	123				
45	110				
46	60				
49	58				
52	94				
55	104				
56	123				
57	226	Outlier			
59	74				
61	43				
62	180				
64	55				
66	188				
68	98				
69	91				
70	100				
71	219				
72	124				
74	120				
76	60				
77	63				
79	100	Outlier,ND			
81	120				
88	164				

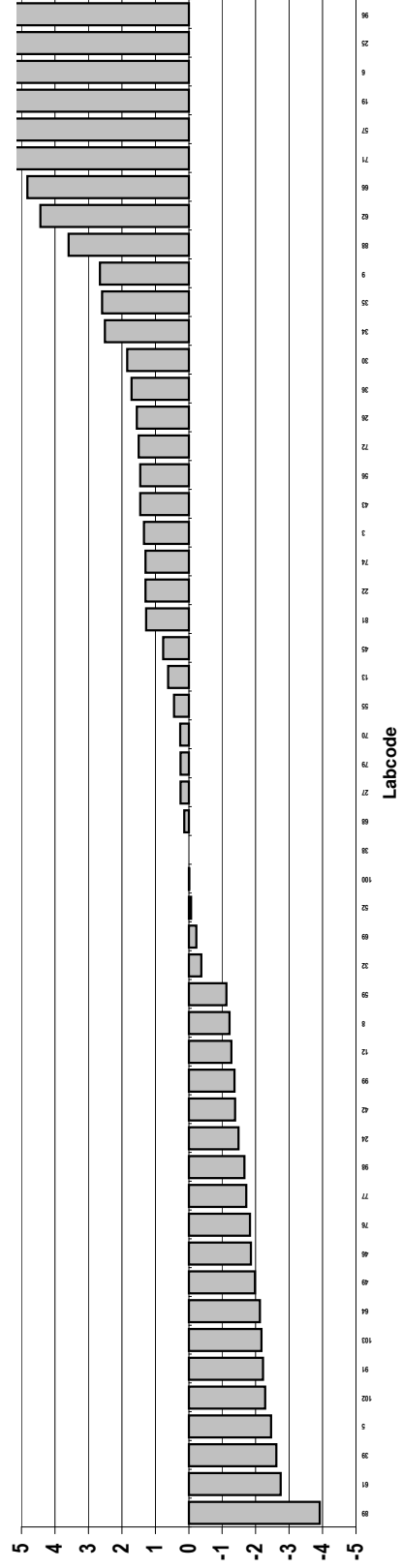
Consensus statistics

Consensus median, pg/g	95
Median all values pg/g	100
Consensus mean, pg/g	95
Standard deviation, pg/g	38
Relative standard deviation, %	40
No. of values reported	53
No. of values removed	6
No. of reported non-detects	3

CB 101



Z-score: CB 101



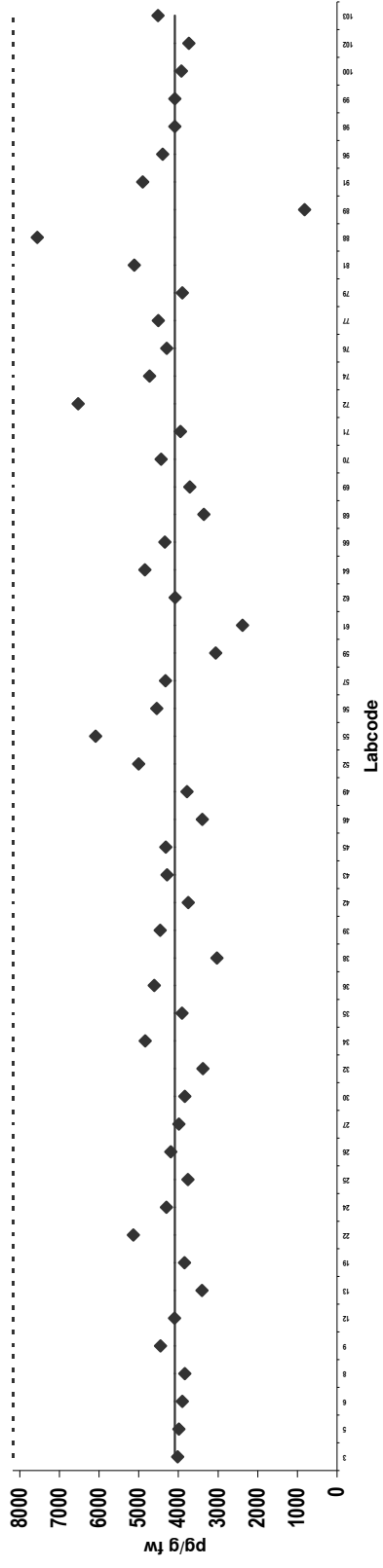
Butteroil
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	4021		89	821	
5	3989		91	4900	
6	3900		96	4400	
8	3841		98	4090	
9	4448		99	4088	
12	4097		100	3926	
13	3405		102	3736	
19	3848		103	4516	
22	5140				
24	4300				
25	3760				
26	4192				
27	3985				
30	3835				
32	3382				
34	4838				
35	3913				
36	4610				
38	3028				
39	4460				
42	3755				
43	4290				
45	4320				
46	3400				
49	3780				
52	5000				
55	6089				
56	4550				
57	4322				
59	3060				
61	2385				
62	4080				
64	4844				
66	4345				
68	3360				
69	3710				
70	4433				
71	3950				
72	6532				
74	4729				
76	4298				
77	4505				
79	3900				
81	5116				
88	7560				

Consensus statistics

Consensus median, pg/g	4090
Median all values pg/g	4090
Consensus mean, pg/g	4185
Standard deviation, pg/g	951
Relative standard deviation, %	23
No. of values reported	53
No. of values removed	0
No. of reported non-detects	0

CB 138



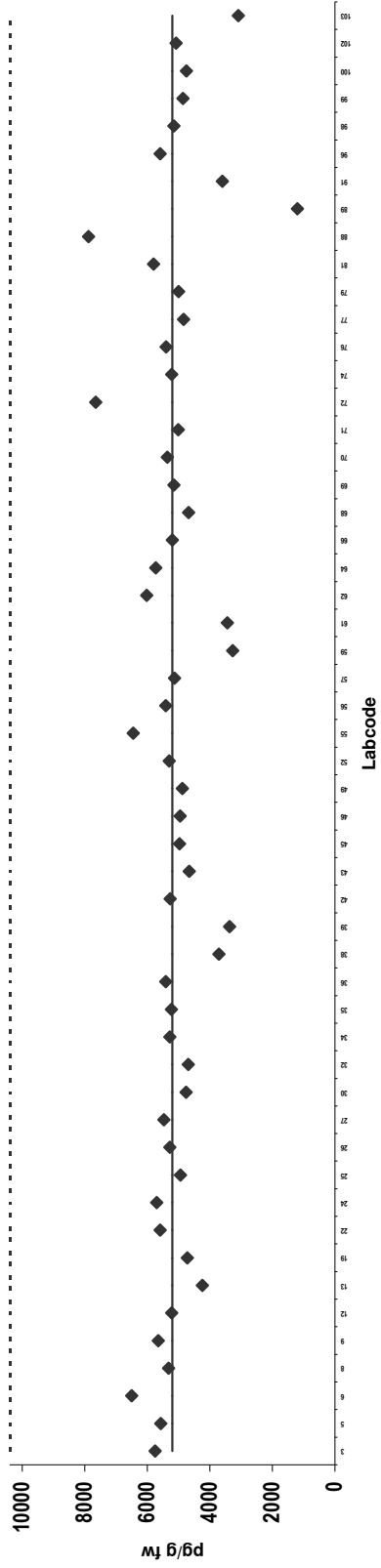
Butteroil
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	5747		89	1201	
5	5570		91	3600	
6	6500		96	5590	
8	5322		98	5150	
9	5648		99	4862	
12	5222		100	4753	
13	4238		102	5082	
19	4720		103	3089	
22	5590				
24	5700				
25	4940				
26	5279				
27	5468				
30	4759				
32	4687				
34	5277				
35	5229				
36	5410				
38	3710				
39	3370				
42	5274				
43	4660				
45	4970				
46	4950				
49	4880				
52	5300				
55	6446				
56	5410				
57	5128				
59	3270				
61	3443				
62	6020				
64	5731				
66	5201				
68	4680				
69	5150				
70	5358				
71	5010				
72	7646				
74	5222				
76	5399				
77	4845				
79	5000				
81	5800				
88	7878				

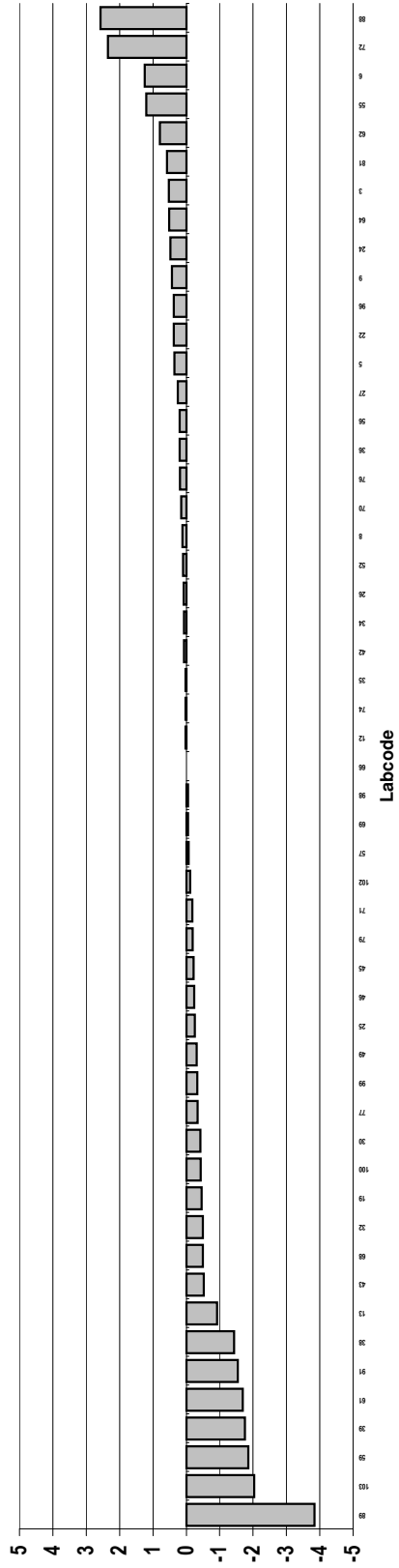
Consensus statistics

Consensus median, pg/g	5201
Median all values pg/g	5201
Consensus mean, pg/g	5064
Standard deviation, pg/g	1043
Relative standard deviation, %	21
No. of values reported	53
No. of values removed	0
No. of reported non-detects	0

CB 153



Z-score: CB 153



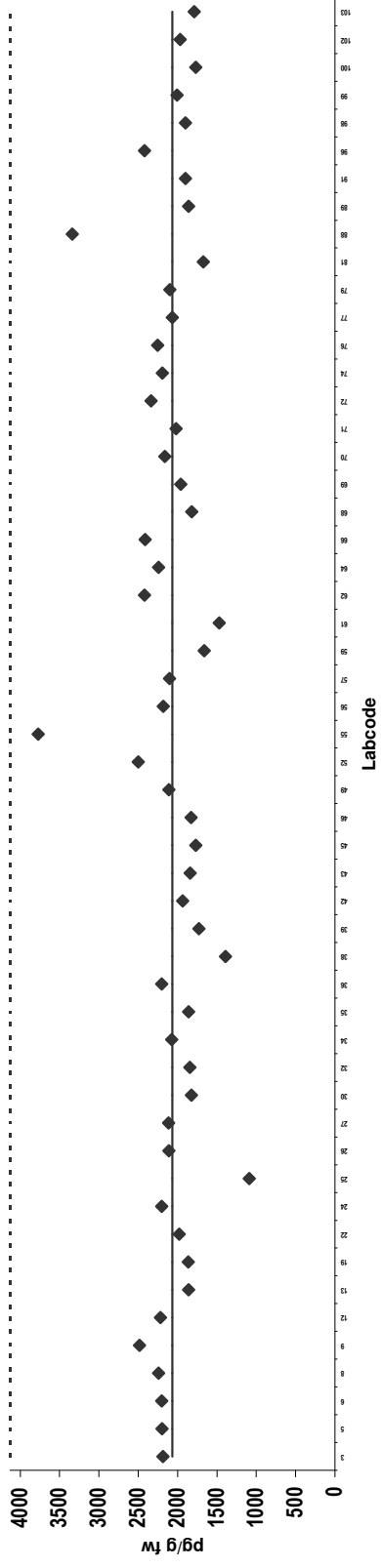
Butteroil
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	2184		89	1859	
5	2198		91	1900	
6	2200		96	2420	
8	2240		98	1900	
9	2484		99	2006	
12	2219		100	1769	
13	1859		102	1968	
19	1864		103	1788	
22	1980				
24	2200				
25	1090				
26	2109				
27	2116				
30	1822				
32	1845				
34	2074				
35	1858				
36	2200				
38	1390				
39	1730				
42	1936				
43	1840				
45	1770				
46	1830				
49	2110				
52	2500				
55	3773				
56	2180				
57	2102				
59	1660				
61	1471				
62	2420				
64	2243				
66	2413				
68	1820				
69	1960				
70	2160				
71	2020				
72	2337				
74	2192				
76	2254				
77	2067				
79	2100				
81	1674				
88	3339				

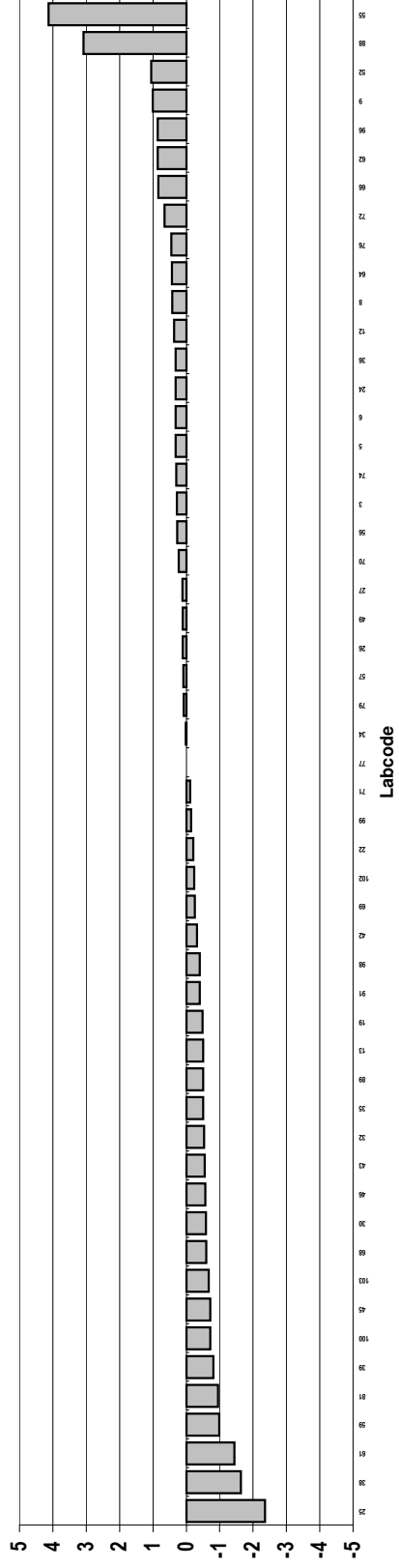
Consensus statistics

Consensus median, pg/g	2067
Median all values pg/g	2067
Consensus mean, pg/g	2065
Standard deviation, pg/g	407
Relative standard deviation, %	20
No. of values reported	53
No. of values removed	0
No. of reported non-detects	0

CB 180



Z-score: CB 180



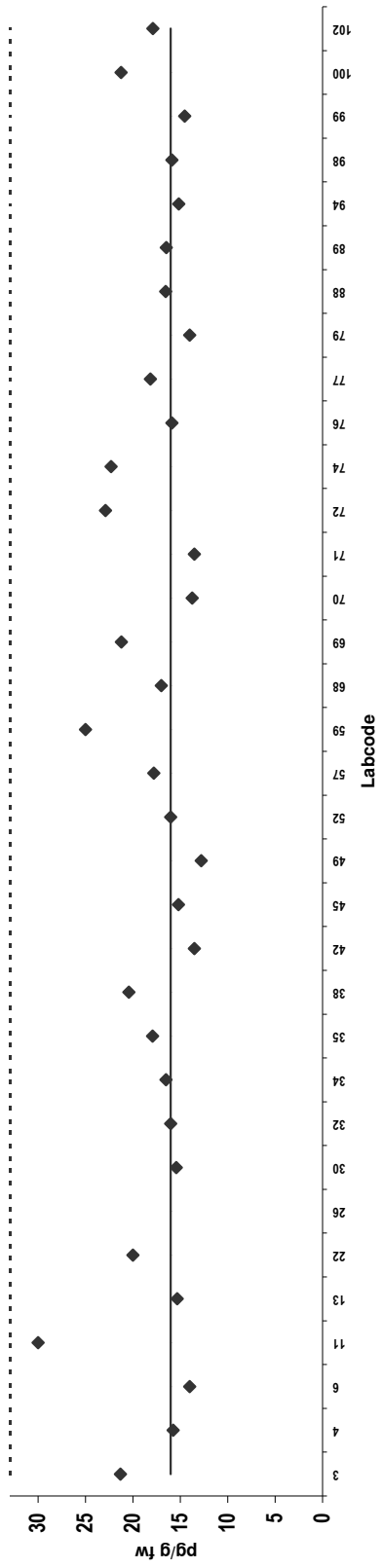
Butteroil
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	21				
4	16				
6	14				
11	30	ND			
13	15				
22	20				
26	35				
30	15	Outlier,ND			
32	16				
34	17				
35	18				
38	20				
42	14				
45	15				
49	13				
52	16				
57	18				
59	25	ND			
68	17				
69	21				
70	14				
71	14				
72	23				
74	22				
76	16				
77	18				
79	14				
88	17				
89	16				
94	15				
98	16				
99	15				
100	21				
102	18				

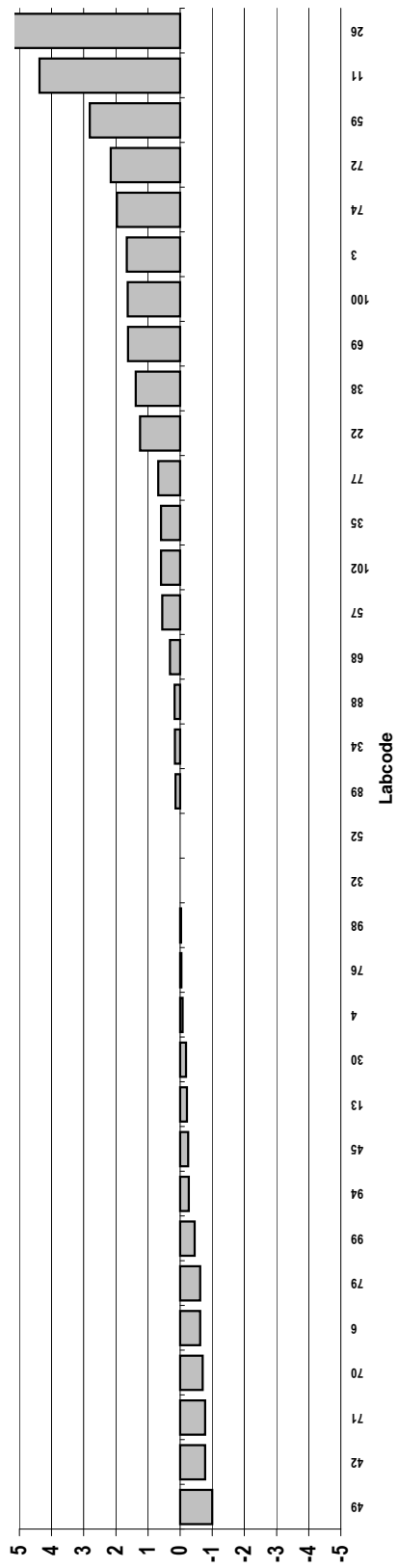
Consensus statistics

Consensus median, pg/g	16
Median all values pg/g	16
Consensus mean, pg/g	18
Standard deviation, pg/g	3.8
Relative standard deviation, %	22
No. of values reported	34
No. of values removed	1
No. of reported non-detects	3

BDE 28



Z-score: BDE 28



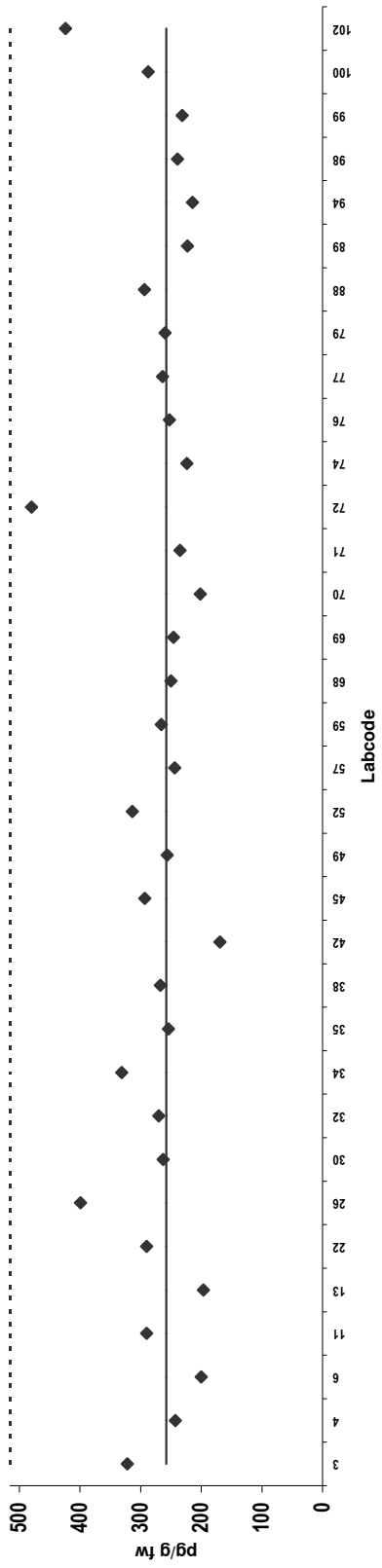
Butteroil
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	322				
4	243				
6	200				
11	290				
13	197				
22	290				
26	399				
30	263				
32	270				
34	331				
35	254				
38	268				
42	169				
45	293				
49	256				
52	314				
57	244				
59	266				
68	250				
69	246				
70	202				
71	235				
72	480				
74	224				
76	253				
77	264				
79	260				
88	294				
89	223				
94	214				
98	239				
99	232				
100	288				
102	424				

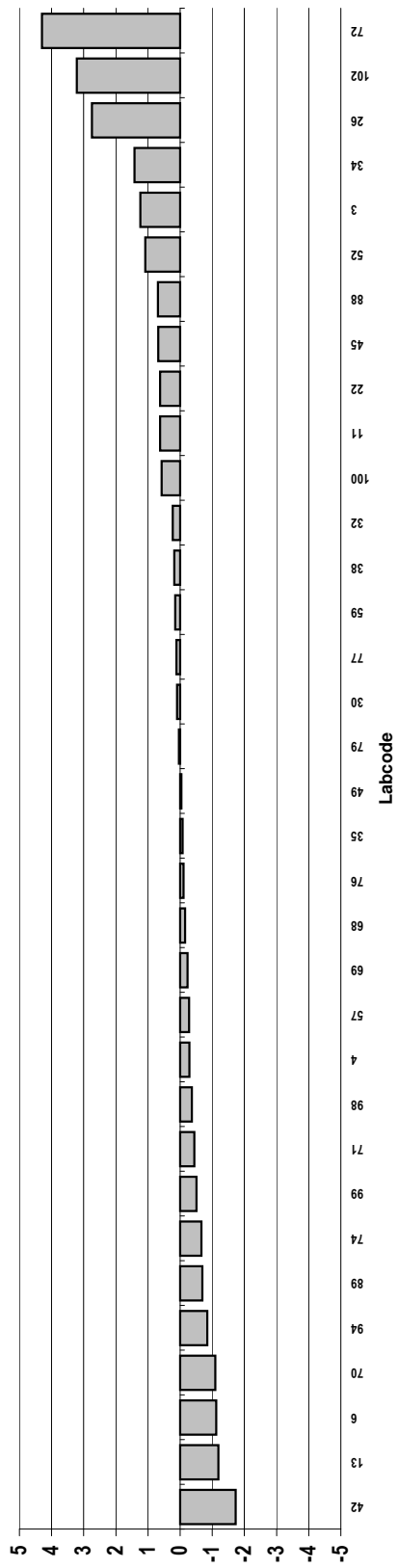
Consensus statistics

Consensus median, pg/g	258
Median all values pg/g	258
Consensus mean, pg/g	270
Standard deviation, pg/g	64
Relative standard deviation, %	24
No. of values reported	34
No. of values removed	0
No. of reported non-detects	0

BDE 47



Z-score: BDE 47



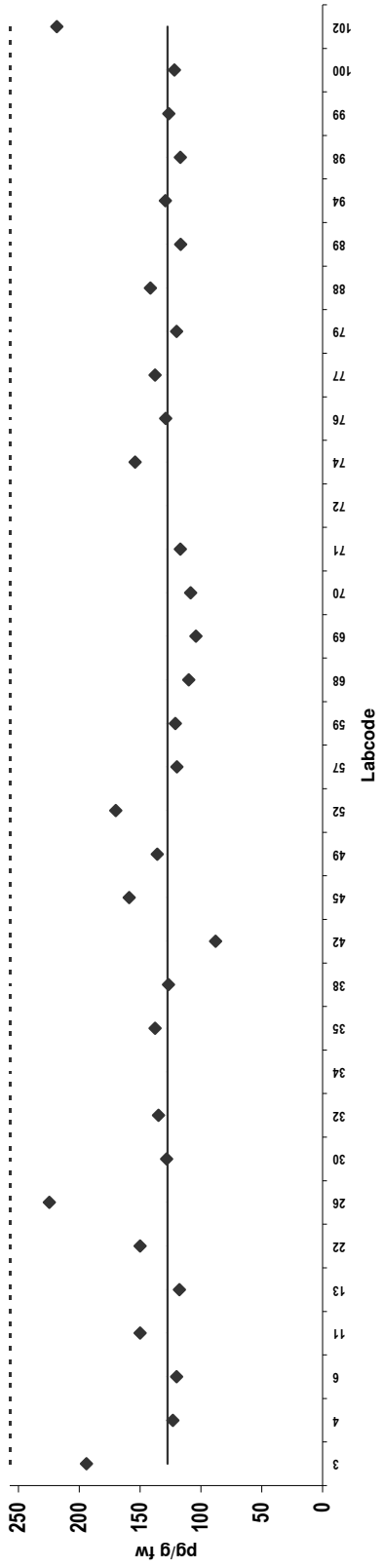
Butteroil
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	194				
4	123				
6	120				
11	150				
13	118				
22	150				
26	225				
30	128				
32	135				
34	324				
35	138				
38	127				
42	88				
45	159				
49	136				
52	170				
57	120				
59	121				
68	110				
69	104				
70	108				
71	117				
72	401	Outlier			
74	154				
76	129				
77	138				
79	120				
88	142				
89	117				
94	129				
98	117				
99	127				
100	122				
102	219				

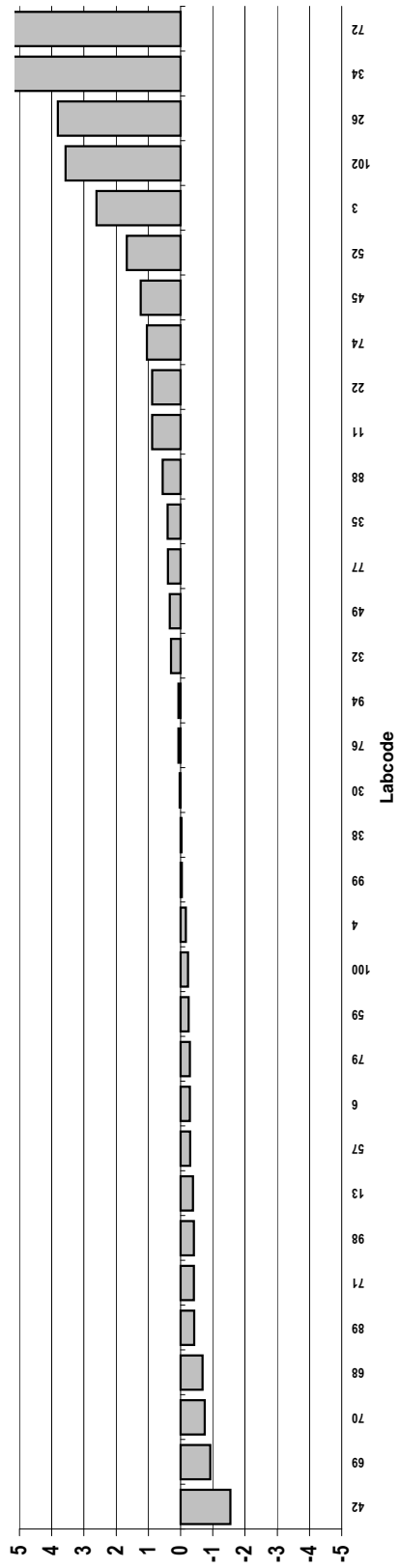
Consensus statistics

Consensus median, pg/g	127
Median all values pg/g	129
Consensus mean, pg/g	136
Standard deviation, pg/g	30
Relative standard deviation, %	22
No. of values reported	34
No. of values removed	2
No. of reported non-detects	0

BDE 99



Z-score: BDE 99



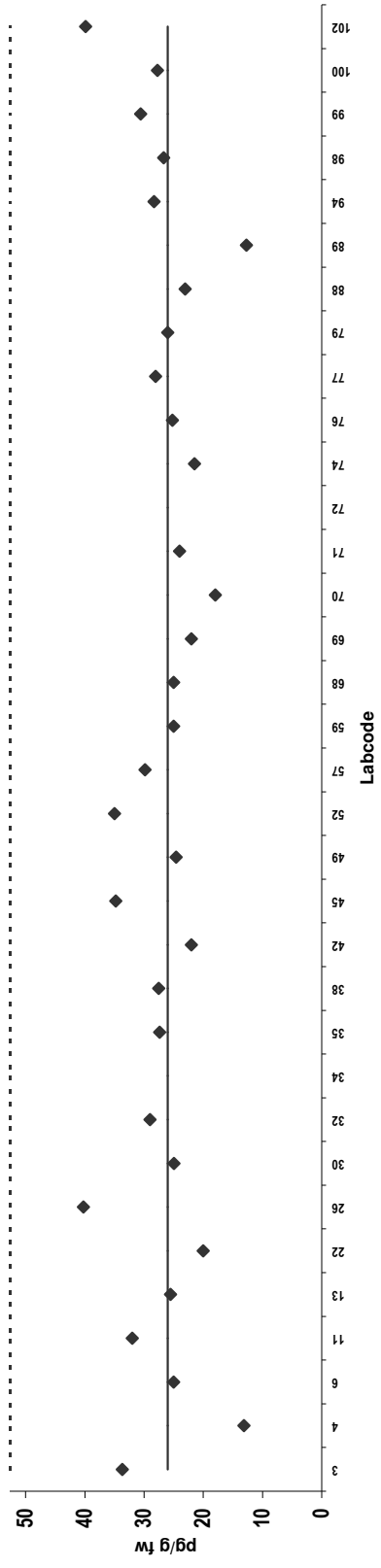
Butteroil
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	34				
4	13				
6	25				
11	32				
13	26				
22	20				
26	40				
30	25				
32	29				
34	78	Outlier			
35	27				
38	28				
42	22				
45	35				
49	25				
52	35				
57	30				
59	25	ND			
68	25				
69	22				
70	18				
71	24				
72	93	Outlier			
74	22				
76	25				
77	28				
79	26				
88	23				
89	13				
94	28				
98	27				
99	31				
100	28				
102	40				

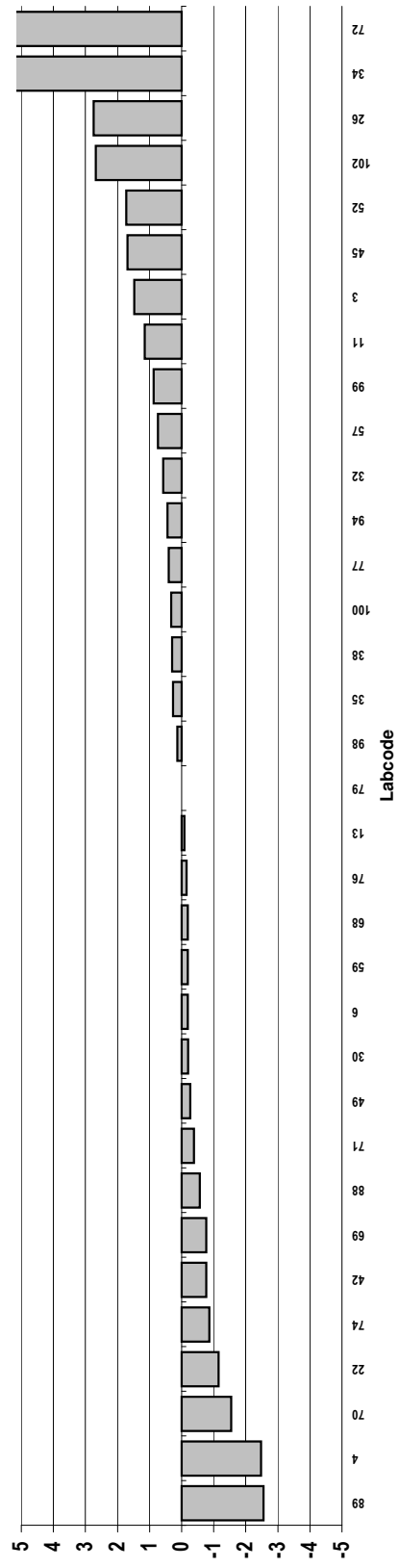
Consensus statistics

Consensus median, pg/g	26
Median all values pg/g	26
Consensus mean, pg/g	27
Standard deviation, pg/g	6.3
Relative standard deviation, %	24
No. of values reported	34
No. of values removed	2
No. of reported non-detects	1

BDE 100



Z-score: BDE 100



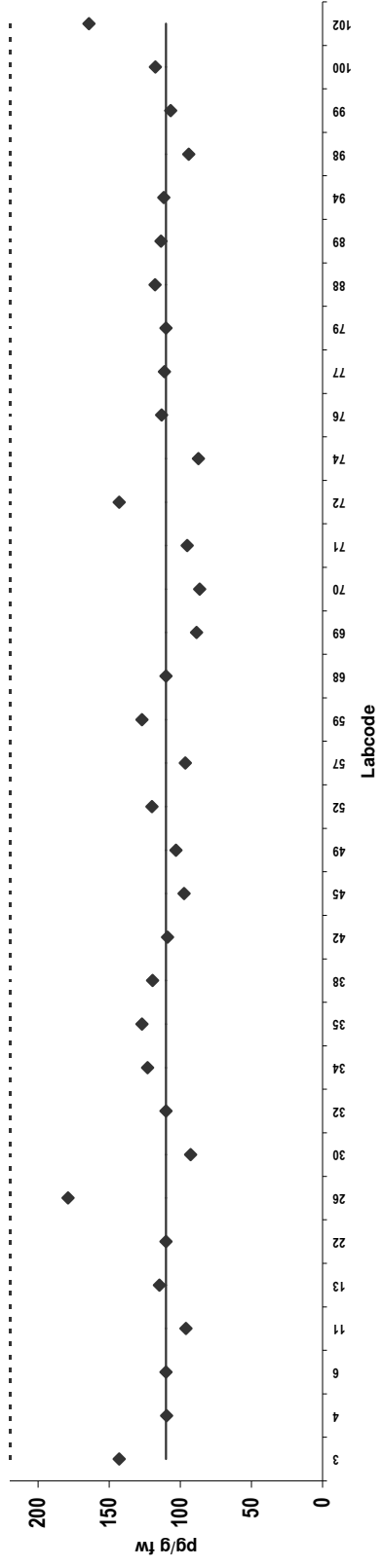
Butteroil
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	143				
4	110				
6	110				
11	96				
13	115				
22	110				
26	179				
30	93				
32	110				
34	123				
35	127				
38	120				
42	109				
45	97				
49	103				
52	120				
57	97				
59	127				
68	110				
69	89				
70	86				
71	95				
72	143				
74	87				
76	113				
77	111				
79	110				
88	118				
89	114				
94	112				
98	94				
99	107				
100	118				
102	164				

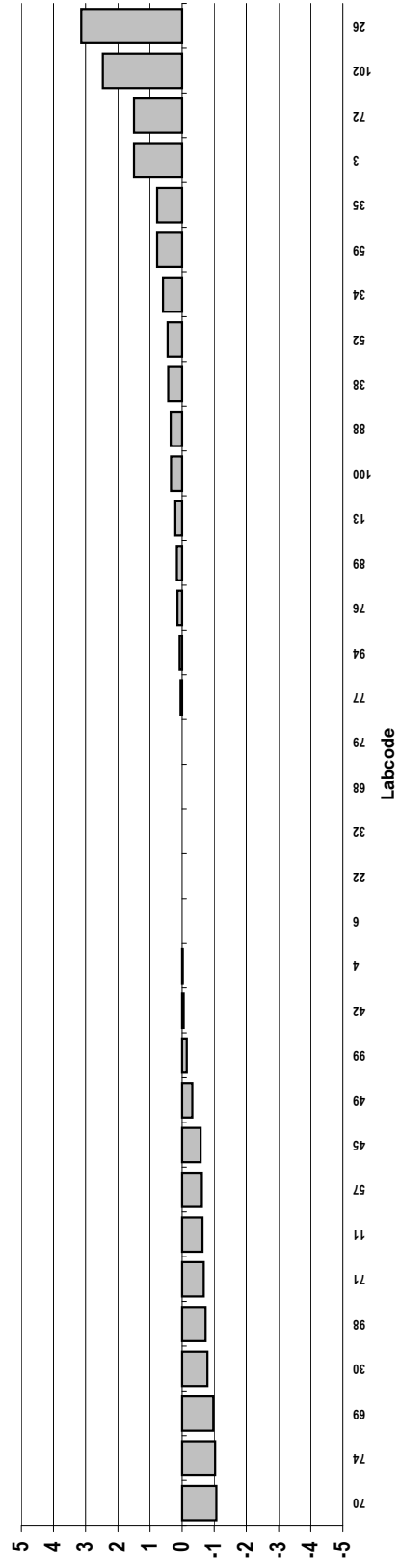
Consensus statistics

Consensus median, pg/g	110
Median all values pg/g	110
Consensus mean, pg/g	113
Standard deviation, pg/g	20
Relative standard deviation, %	18
No. of values reported	34
No. of values removed	0
No. of reported non-detects	0

BDE 153



Z-score: BDE 153



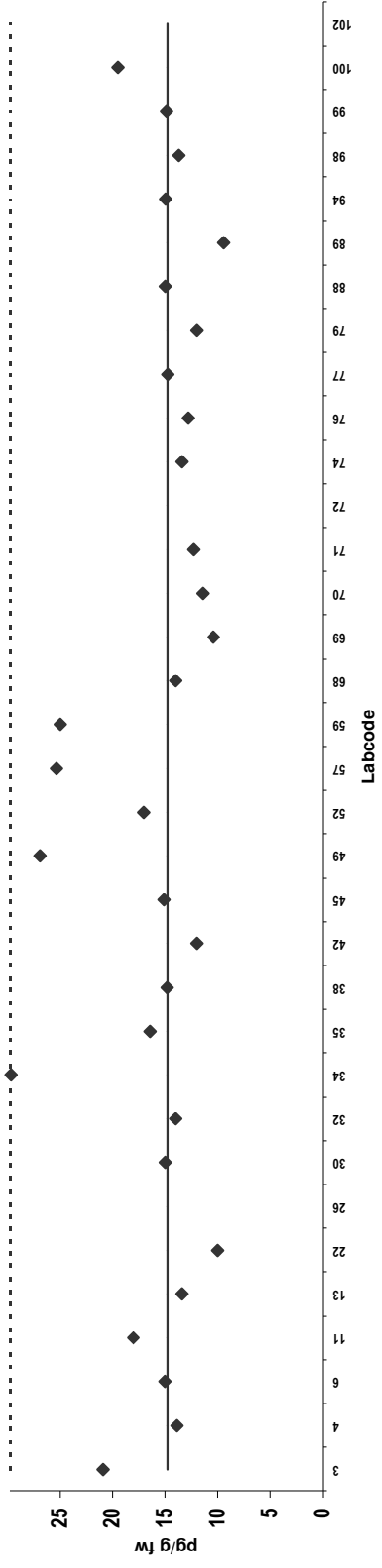
Butteroil
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	21				
4	14				
6	15				
11	18				
13	13				
22	10				
26	100	Outlier,ND			
30	15				
32	14				
34	30				
35	16				
38	15				
42	12				
45	15				
49	27				
52	17				
57	25				
59	25	ND			
68	14				
69	10				
70	11				
71	12				
72	40	Outlier			
74	13				
76	13				
77	15				
79	12				
88	15				
89	9.4				
94	15				
98	14				
99	15				
100	20				
102	34	Outlier			

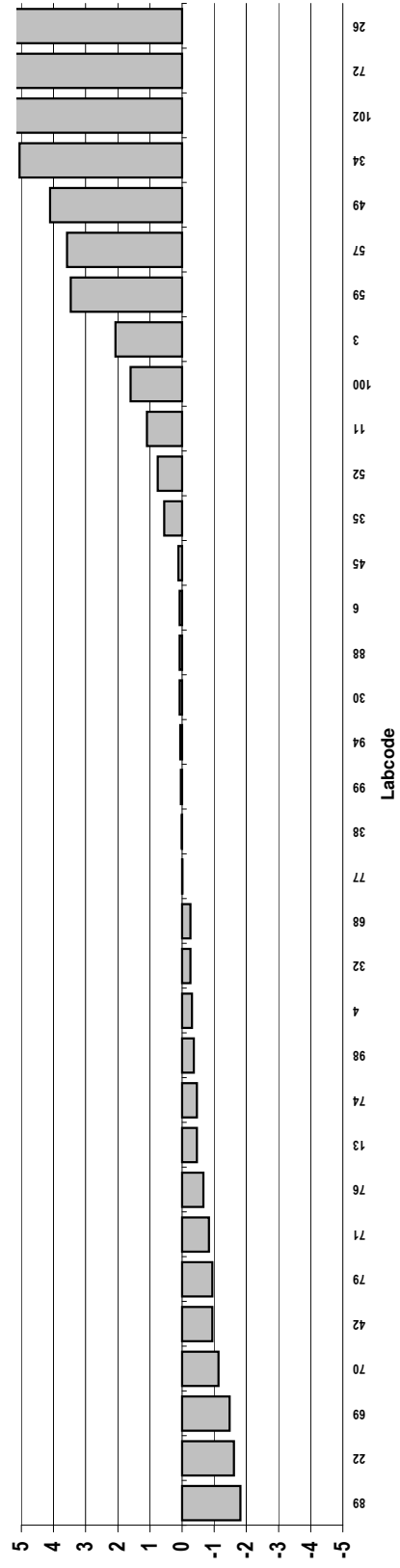
Consensus statistics

Consensus median, pg/g	15
Median all values pg/g	15
Consensus mean, pg/g	16
Standard deviation, pg/g	5.0
Relative standard deviation, %	31
No. of values reported	34
No. of values removed	3
No. of reported non-detects	2

BDE 154



Z-score: BDE 154



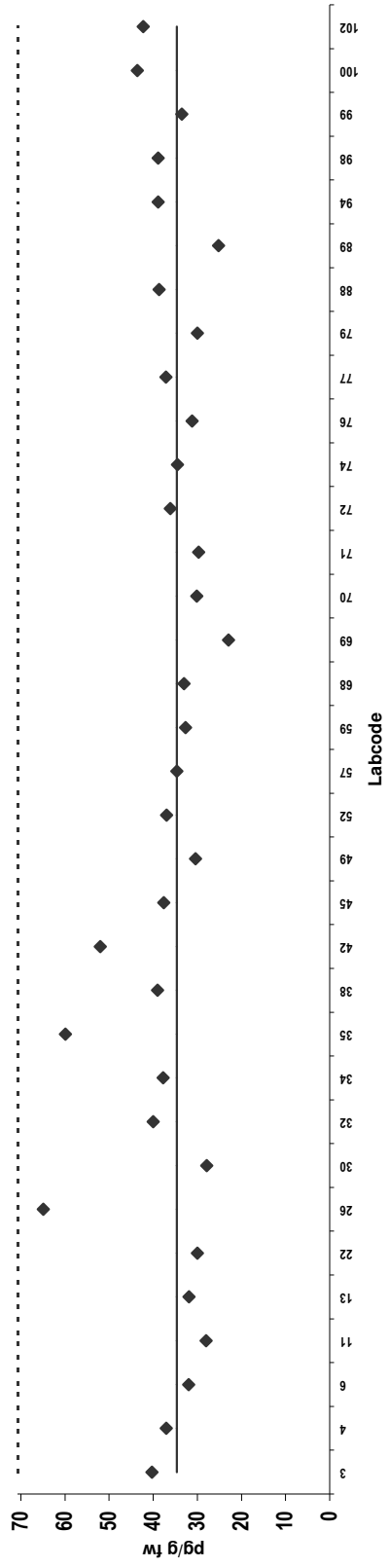
Butteroil
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	40				
4	37				
6	32				
11	28				
13	32				
22	30				
26	65				
30	28	ND			
32	40				
34	38				
35	60				
38	39				
42	52				
45	38				
49	30				
52	37				
57	35				
59	33				
68	33				
69	23				
70	30				
71	30				
72	36				
74	35				
76	31				
77	37				
79	30				
88	39				
89	25				
94	39				
98	39				
99	34				
100	44				
102	42				

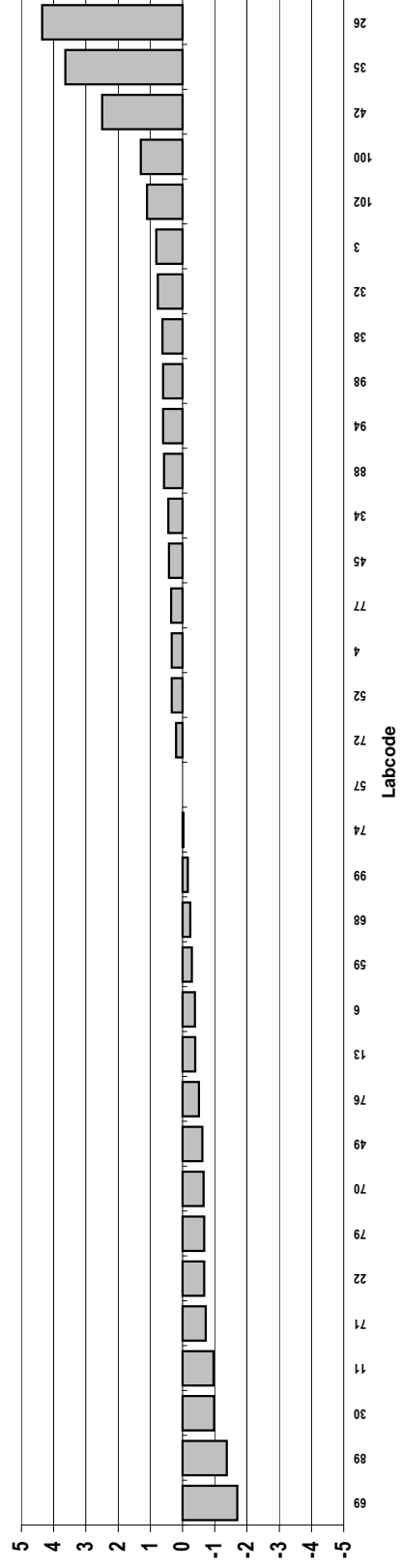
Consensus statistics

Consensus median, pg/g	35
Median all values pg/g	35
Consensus mean, pg/g	36
Standard deviation, pg/g	8.7
Relative standard deviation, %	24
No. of values reported	34
No. of values removed	0
No. of reported non-detects	1

BDE 183



Z-score: BDE 183



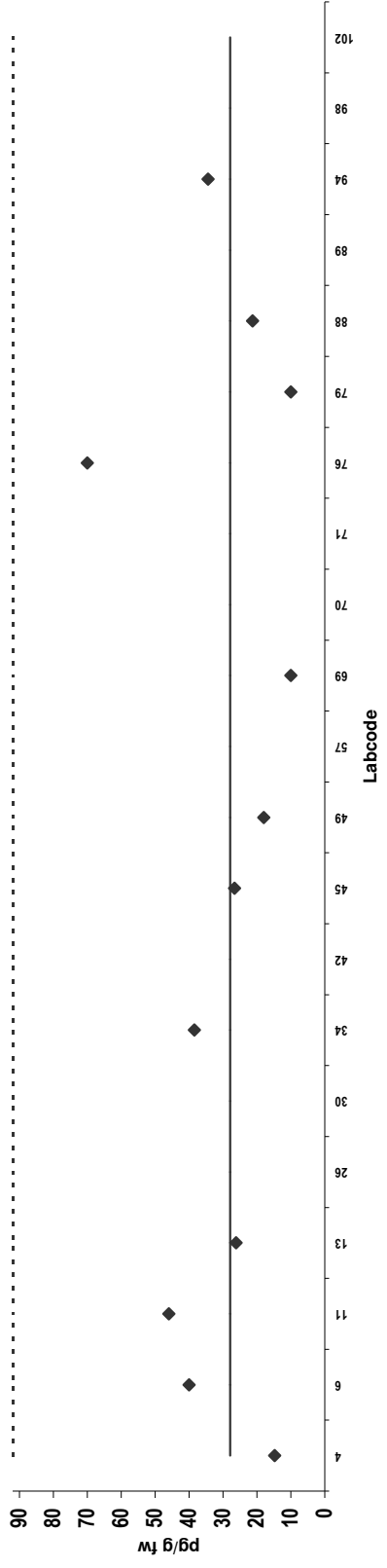
Butteroil
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	15				
6	40	ND			
11	46				
13	26	ND			
26	342	Outlier,ND			
30	447	Outlier,ND			
34	38				
42	356	Outlier			
45	27	ND			
49	18	ND			
57	999	Outlier			
69	10	ND			
70	223	Outlier			
71	100	Outlier,ND			
76	70	ND			
79	10				
88	21				
89	433	Outlier			
94	34				
98	3000	Outlier,ND			
102	400	Outlier,ND			

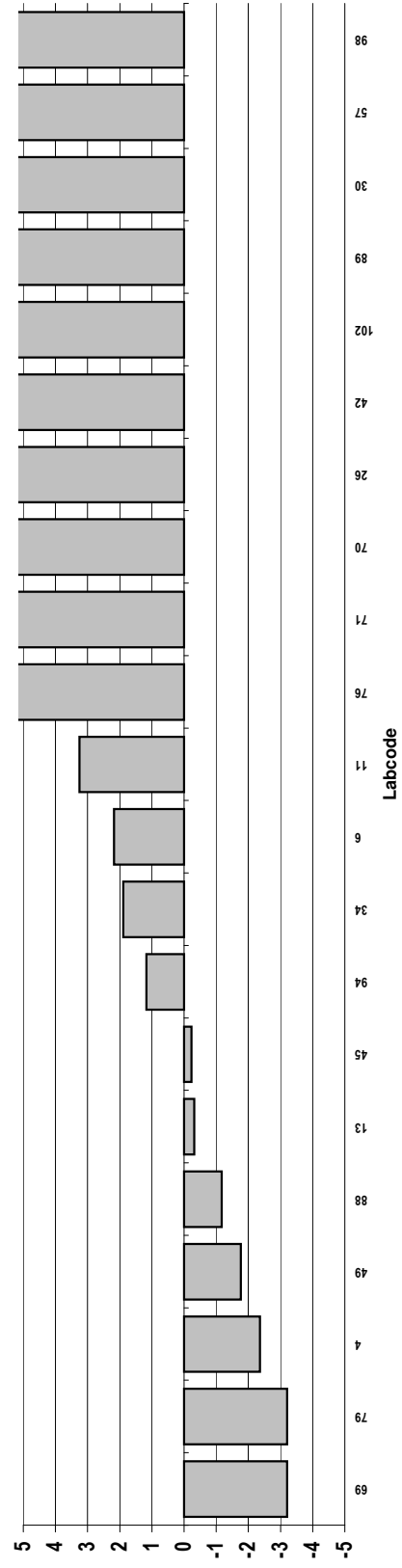
Consensus statistics

Consensus median, pg/g	28
Median all values pg/g	46
Consensus mean, pg/g	30
Standard deviation, pg/g	17
Relative standard deviation, %	59
No. of values reported	21
No. of values removed	9
No. of reported non-detects	11

BDE 209



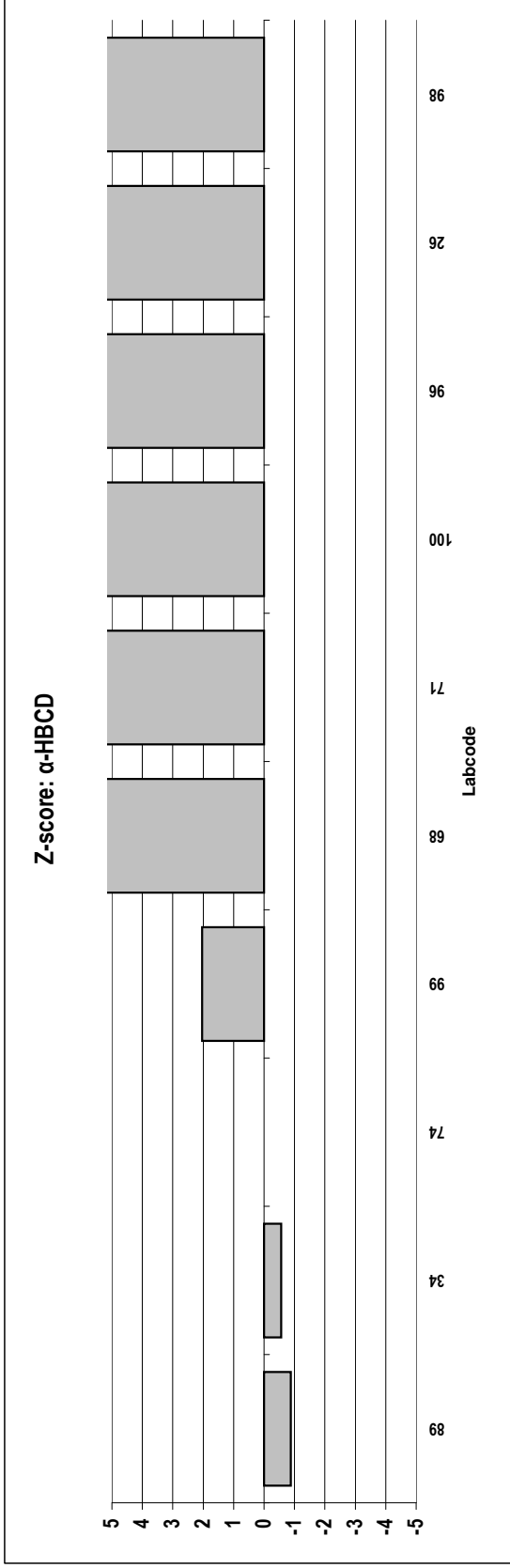
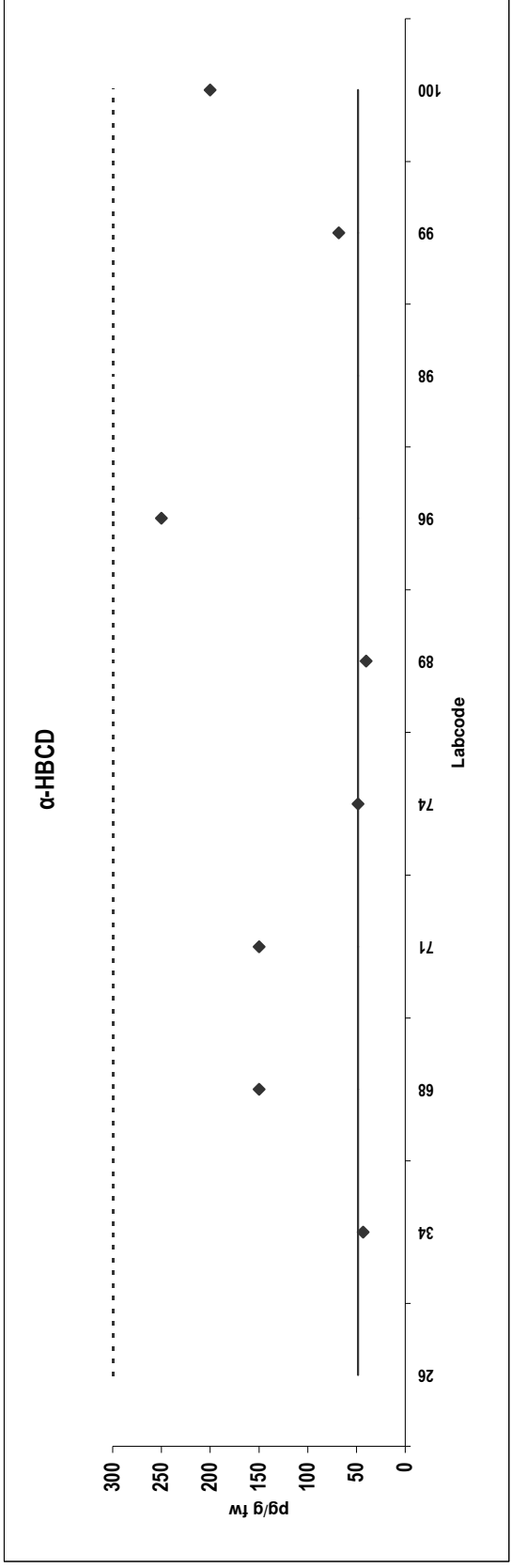
Z-score: BDE 209



Butteroil
Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	523	Outlier,ND			
34	43				
68	150	ND			
71	150	ND			
74	49				
89	40	ND			
96	250	ND			
98	800	Outlier,ND			
99	68				
100	200	ND			

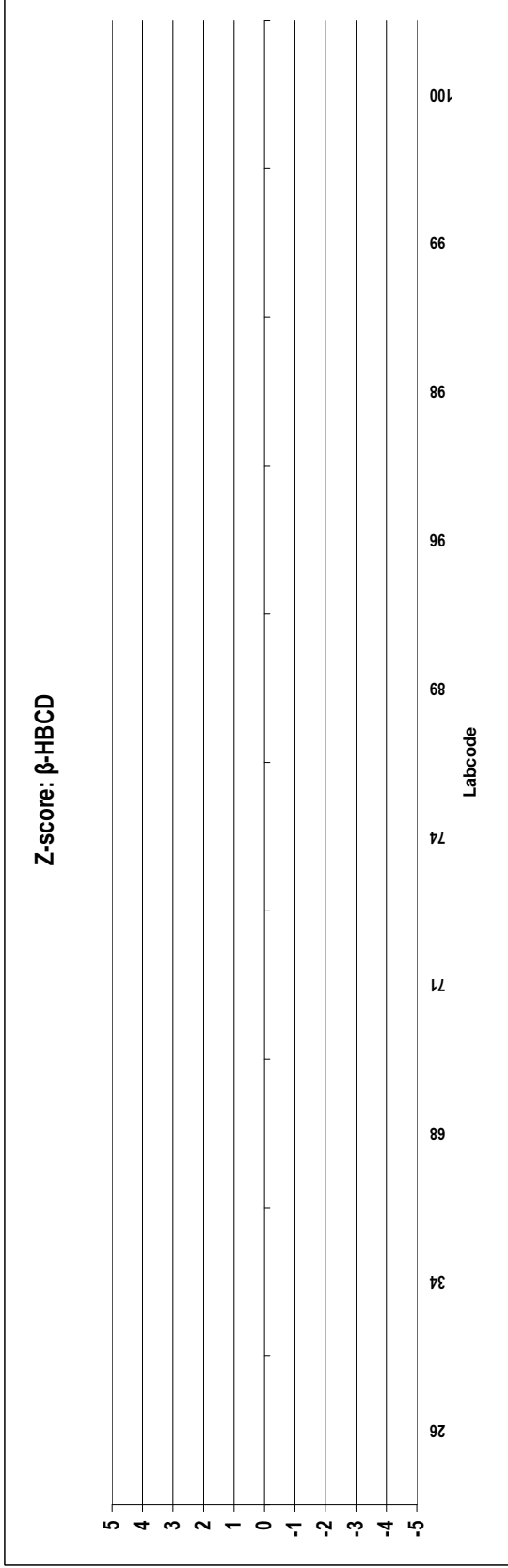
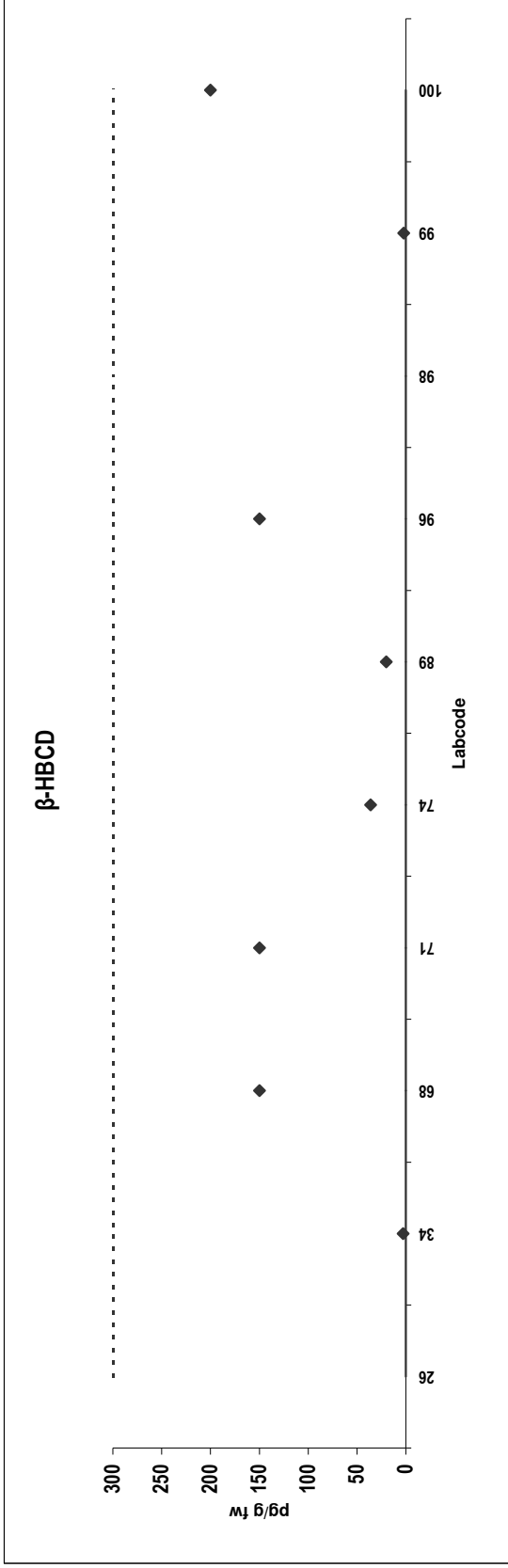
Consensus statistics	
Consensus median, pg/g	49
Median all values pg/g	150
Consensus mean, pg/g	119
Standard deviation, pg/g	80
Relative standard deviation, %	68
No. of values reported	10
No. of values removed	2
No. of reported non-detects	7



Butteroil
Congener: β -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	850	Outlier,ND			
34	2.6	ND			
68	150	ND			
71	150	ND			
74	36	ND			
89	20	ND			
96	150	ND			
98	700	Outlier,ND			
99	2.3	ND			
100	200	ND			

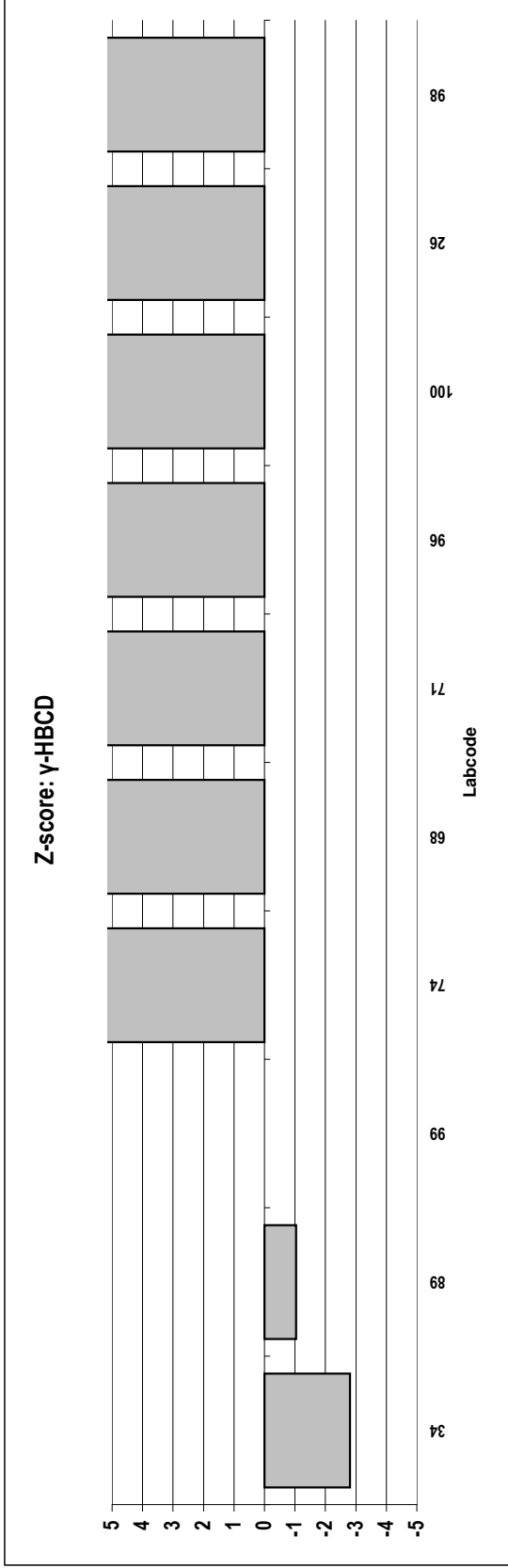
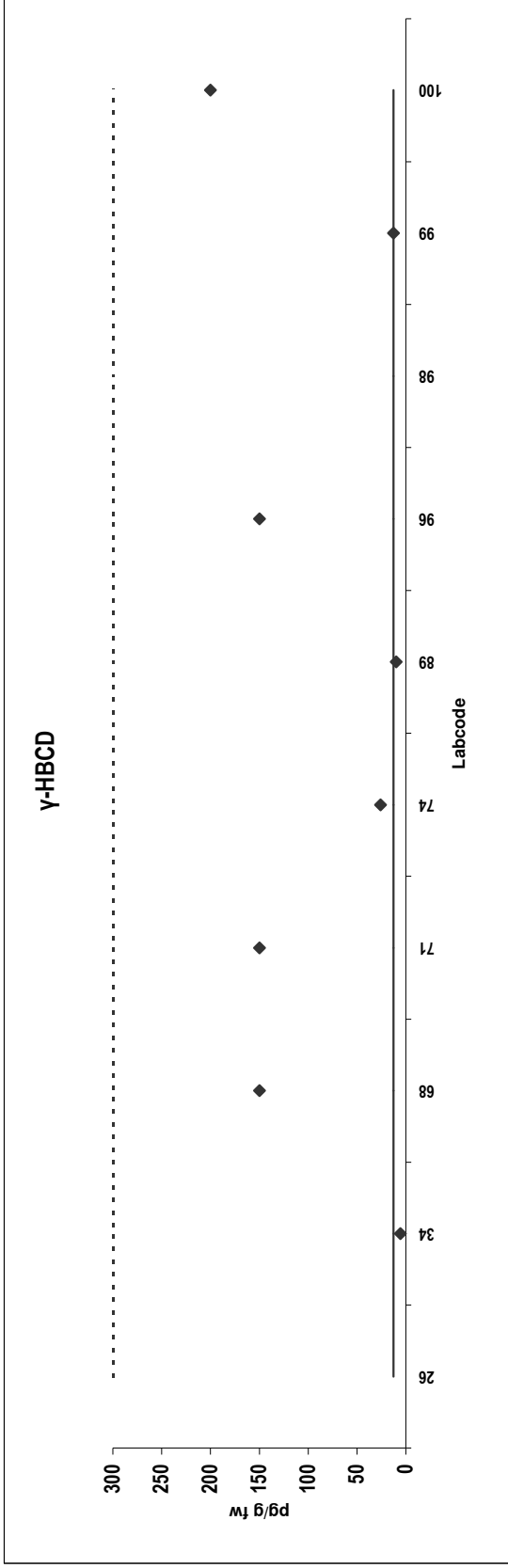
Consensus statistics	
Consensus median, pg/g	150
Median all values pg/g	89
Consensus mean, pg/g	81
Standard deviation, pg/g	91
Relative standard deviation, %	10
No. of values reported	2
No. of values removed	10
No. of reported non-detects	



Butteroil
Congener: γ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	578	Outlier,ND			
34	5.5				
68	150	ND			
71	150	ND			
74	26				
89	10	ND			
96	150	ND			
98	800	Outlier,ND			
99	13				
100	200	ND			

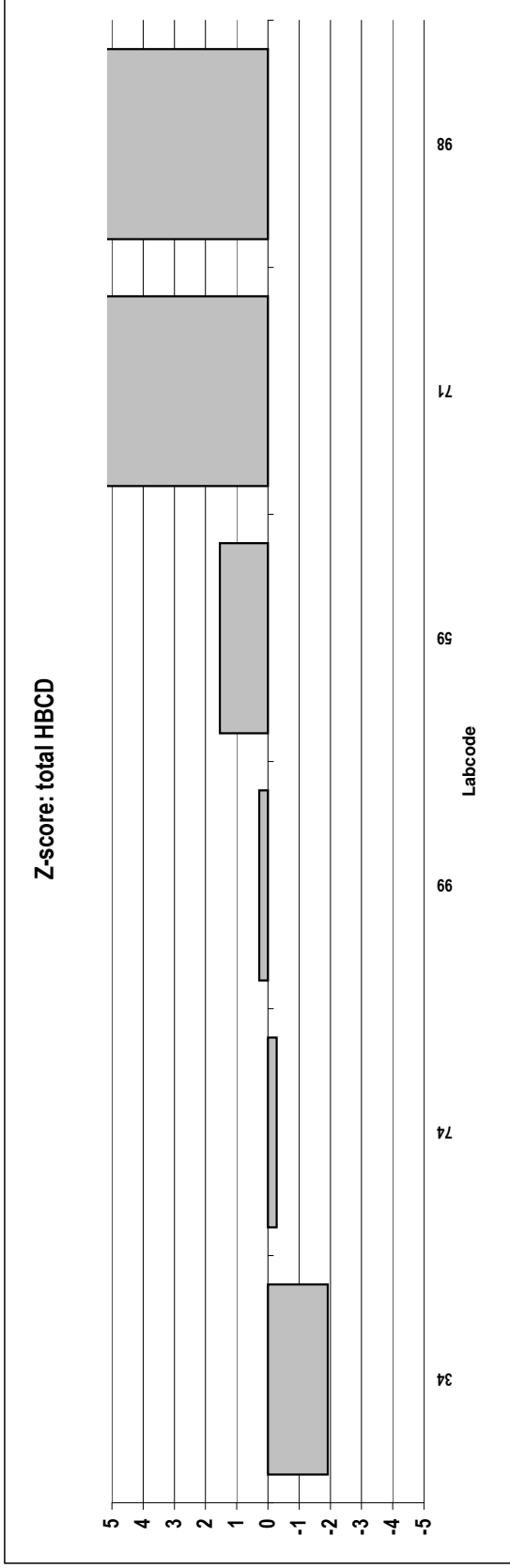
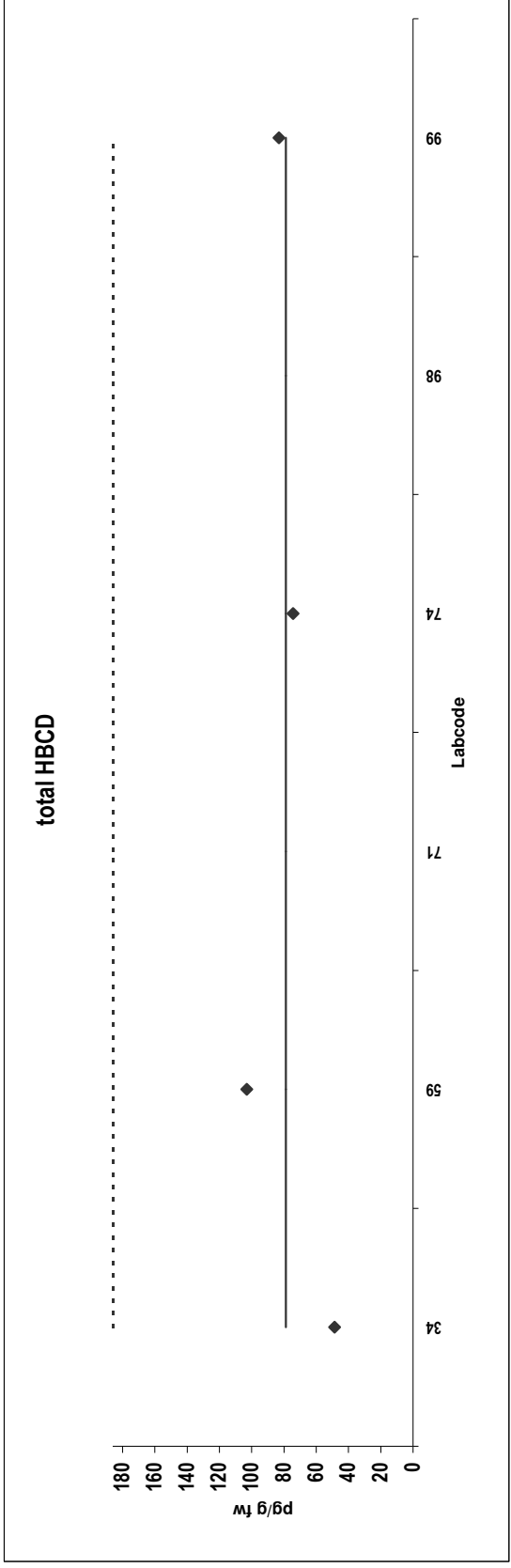
Consensus statistics	
Consensus median, pg/g	13
Median all values pg/g	150
Consensus mean, pg/g	88
Standard deviation, pg/g	82
Relative standard deviation, %	93
No. of values reported	10
No. of values removed	2
No. of reported non-detects	7



Butteroil
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
34	49				
59	103				
71	450	Outlier,ND			
74	74				
98	800	Outlier,ND			
99	83				

Consensus statistics	
Consensus median, pg/g	79
Median all values pg/g	93
Consensus mean, pg/g	77
Standard deviation, pg/g	23
Relative standard deviation, %	29
No. of values reported	6
No. of values removed	2
No. of reported non-detects	2



Appendix 4:

Presentation of results
for herring

Appendix 4: Presentation of results: Herring

Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

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

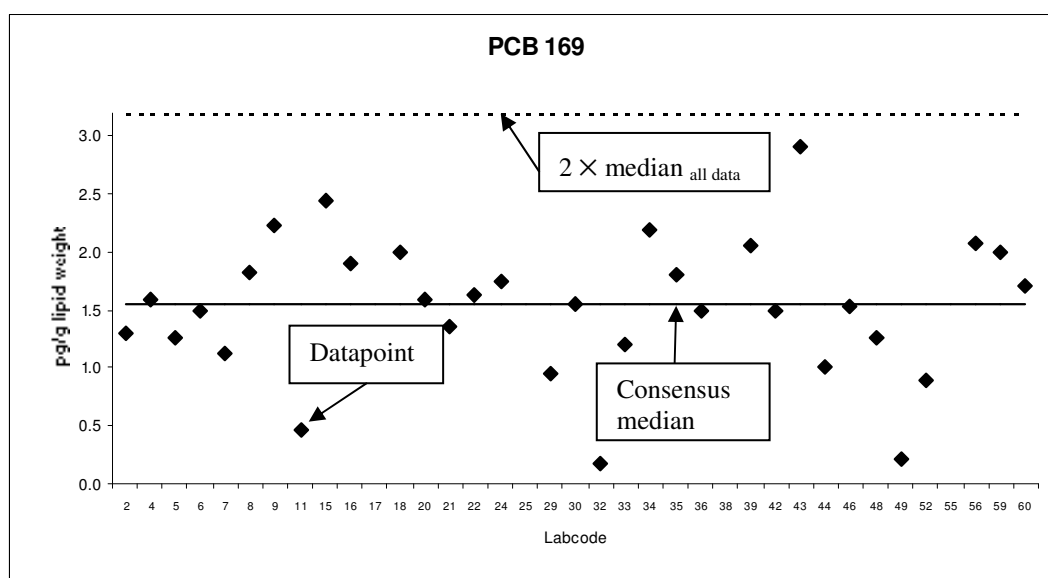
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding $2 \times$ this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

Statistic calculations for indicator PCBs, PBDEs and HBCD

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

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

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



Z-Scores of individual congeners

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

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

where x = reported value; X = assigned value (consensus); 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.

Herring

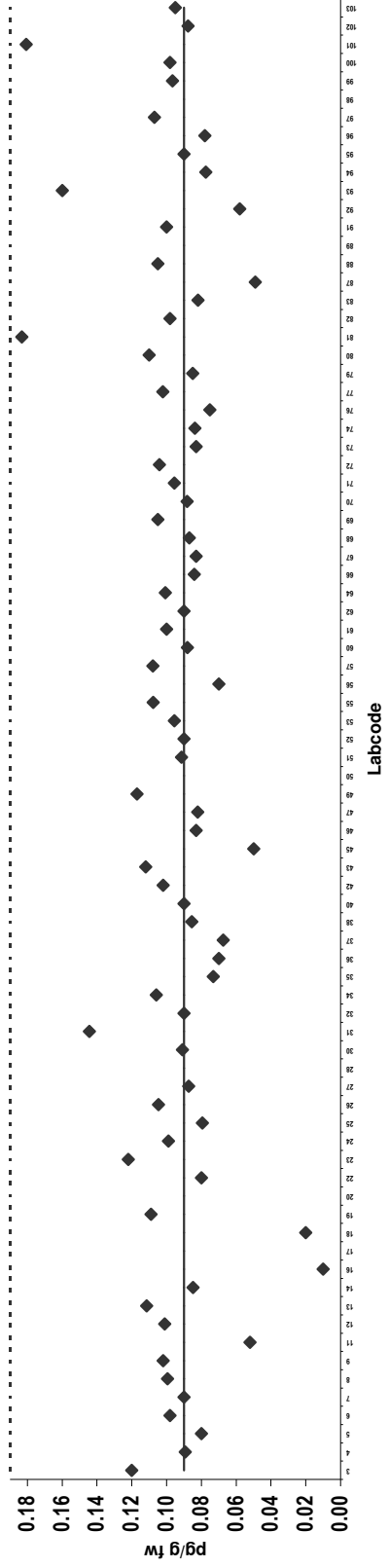
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.12		60	0.088	
4	0.089		61	0.10	
5	0.080		62	0.090	
6	0.098		64	0.10	
7	0.090		66	0.084	
8	0.10		67	0.083	
9	0.10		68	0.087	
11	0.052		69	0.11	
12	0.10		70	0.088	
13	0.11		71	0.096	
14	0.085		72	0.10	
16	0.010		73	0.083	
17	0.21	Outlier	74	0.084	
18	0.020	ND	76	0.075	
19	0.11		77	0.10	
20	0.50	Outlier,ND	79	0.085	
22	0.080		80	0.11	
23	0.12		81	0.18	
24	0.099		82	0.098	
25	0.080		83	0.082	
26	0.10		87	0.049	
27	0.087		88	0.11	
28	1.7	Outlier	89	0.20	Outlier
30	0.091		91	0.10	
31	0.14		92	0.058	
32	0.090		93	0.16	
34	0.11		94	0.078	
35	0.073		95	0.090	
36	0.070		96	0.078	
37	0.067		97	0.11	
38	0.086		98	0.30	Outlier,ND
40	0.090		99	0.097	
42	0.10		100	0.098	
43	0.11		101	0.18	
45	0.050		102	0.088	
46	0.083		103	0.095	
47	0.082				
49	0.12				
50	1.0	Outlier,ND			
51	0.091				
52	0.090				
53	0.096				
55	0.11				
56	0.070				
57	0.11				

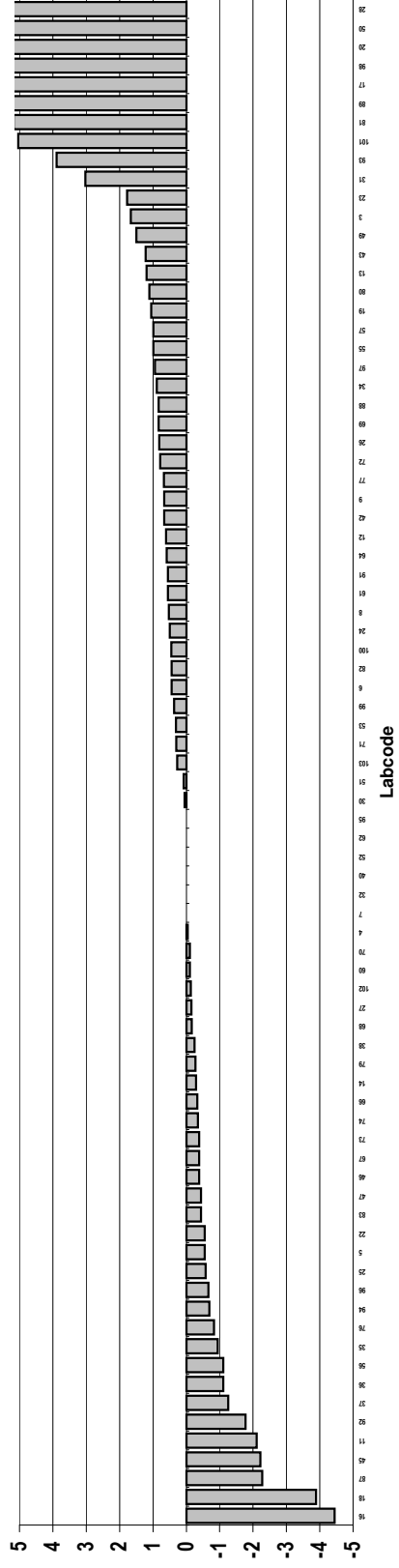
Consensus statistics

Consensus median, pg/g	0.090
Median all values pg/g	0.095
Consensus mean, pg/g	0.093
Standard deviation, pg/g	0.026
Relative standard deviation, %	28
No. of values reported	81
No. of values removed	6
No. of reported non-detects	4

2,3,7,8 TCDD



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



Herring

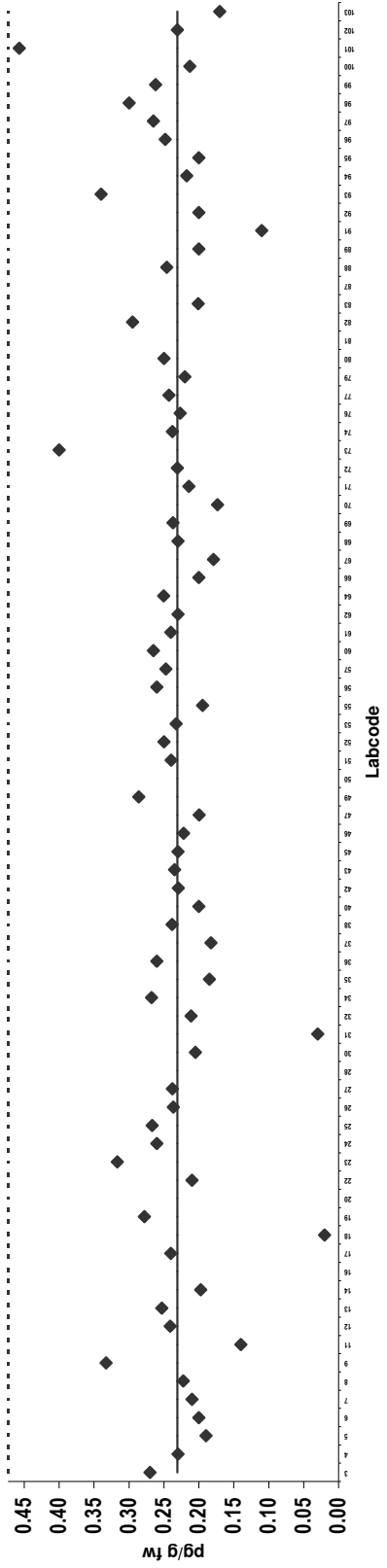
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.27		60	0.27	
4	0.23		61	0.24	
5	0.19		62	0.23	
6	0.20		64	0.25	
7	0.21		66	0.20	
8	0.22		67	0.18	
9	0.33		68	0.23	
11	0.14		69	0.24	
12	0.24		70	0.17	
13	0.25		71	0.21	
14	0.20		72	0.23	
16	1.8		73	0.40	
17	0.24	Outlier	74	0.24	
18	0.020	ND	76	0.23	
19	0.28		77	0.24	
20	0.50	Outlier,ND	79	0.22	
22	0.21		80	0.25	
23	0.32		81	0.69	Outlier
24	0.26		82	0.30	
25	0.27		83	0.20	
26	0.24		87	1.3	Outlier
27	0.24		88	0.25	
28	6.7	Outlier	89	0.20	
30	0.20		91	0.11	
31	0.030	ND	92	0.20	
32	0.21		93	0.34	
34	0.27		94	0.22	
35	0.19		95	0.20	
36	0.26		96	0.25	
37	0.18		97	0.27	
38	0.24		98	0.30	
40	0.20		99	0.26	
42	0.23		100	0.21	
43	0.24		101	0.46	
45	0.23		102	0.23	
46	0.22		103	0.17	
47	0.20				
49	0.29				
50	5.0	Outlier,ND			
51	0.24				
52	0.25				
53	0.23				
55	0.19				
56	0.26				
57	0.25				

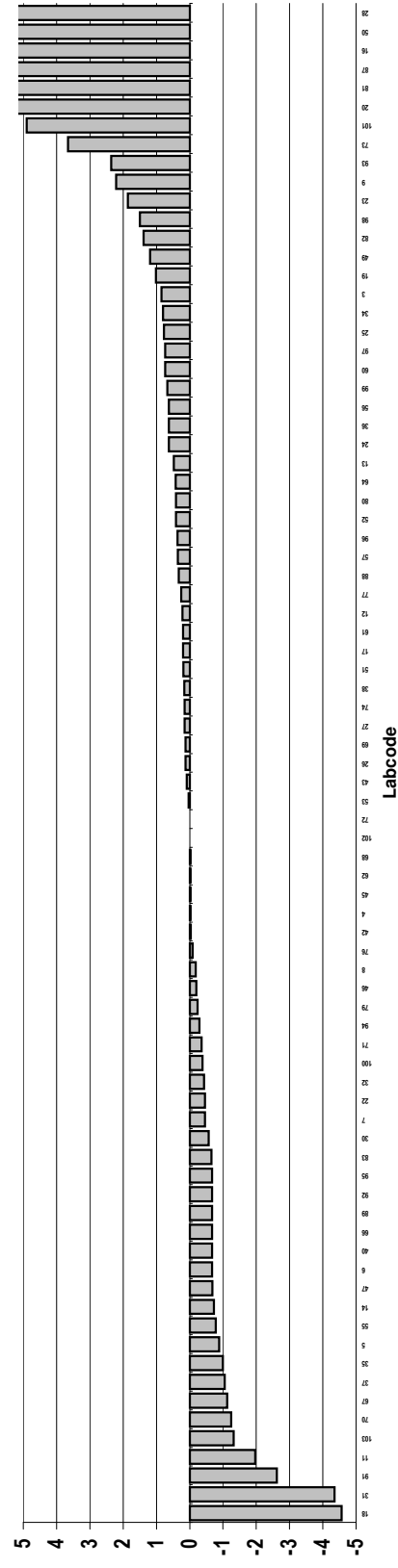
Consensus statistics

Consensus median, pg/g	0.23
Median all values pg/g	0.24
Consensus mean, pg/g	0.23
Standard deviation, pg/g	0.061
Relative standard deviation, %	26
No. of values reported	81
No. of values removed	6
No. of reported non-detects	5

1,2,3,7,8 PeCDD



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



Herring

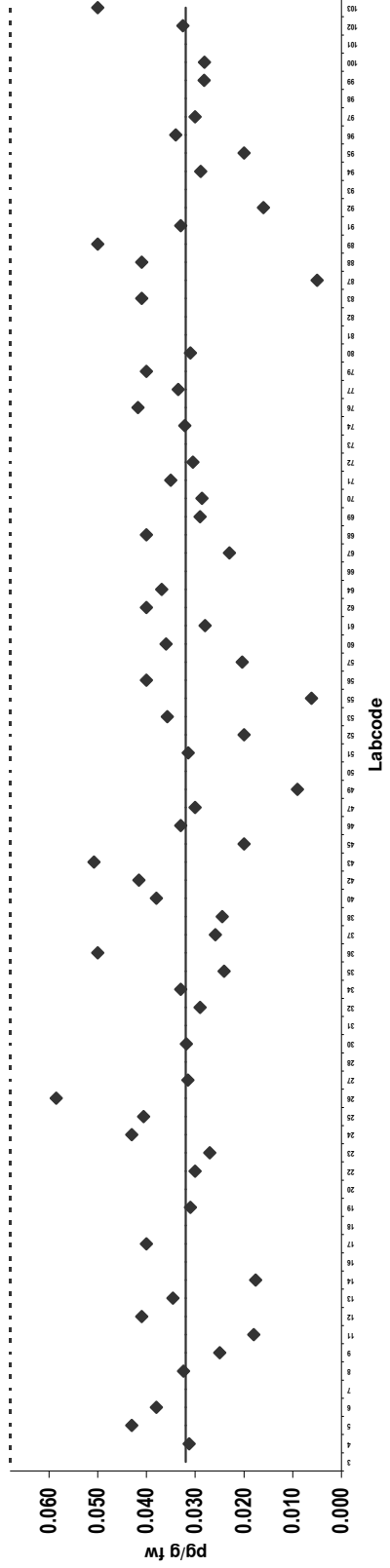
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.090		60	0.036	
4	0.031	Outlier	61	0.028	
5	0.043	ND	62	0.040	
6	0.038		64	0.037	
7	0.18	Outlier	66	0.12	Outlier
8	0.032		67	0.023	
9	0.025		68	0.040	
11	0.018		69	0.029	
12	0.041		70	0.029	
13	0.035		71	0.035	
14	0.018	ND	72	0.030	
16	0.69	Outlier	73	0.38	Outlier,ND
17	0.040		74	0.032	
18	0.14	Outlier	76	0.042	
19	0.031		77	0.034	
20	1.0	Outlier,ND	79	0.040	
22	0.030		80	0.031	ND
23	0.027		81	0.28	Outlier
24	0.043		82	0.11	Outlier
25	0.041		83	0.041	
26	0.059		87	0.0050	ND
27	0.032		88	0.041	
28	12	Outlier	89	0.050	
30	0.032		91	0.033	ND
31	0.11	Outlier	92	0.016	ND
32	0.029		93	0.22	Outlier
34	0.033		94	0.029	
35	0.024		95	0.020	
36	0.050		96	0.034	
37	0.026		97	0.030	
38	0.024		98	0.60	Outlier,ND
40	0.038		99	0.028	
42	0.042		100	0.028	
43	0.051	ND	101	0.13	Outlier
45	0.020		102	0.033	
46	0.033		103	0.050	
47	0.030	ND			
49	0.0090	Outlier,ND			
50	5.0				
51	0.031				
52	0.020				
53	0.036				
55	0.0061	ND			
56	0.040				
57	0.020				

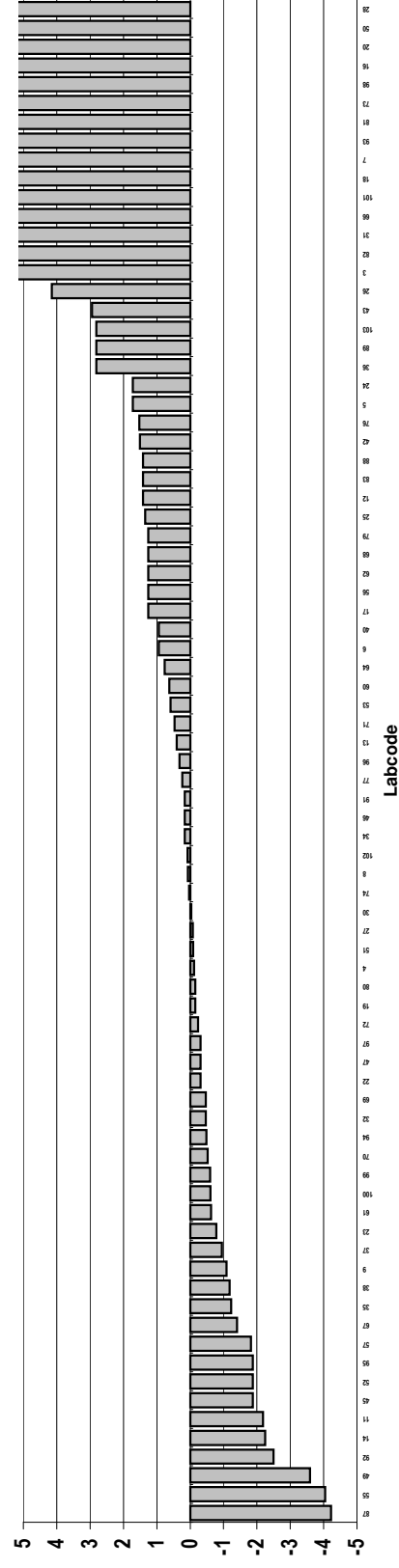
Consensus statistics

Consensus median, pg/g	0.032
Median all values pg/g	0.034
Consensus mean, pg/g	0.032
Standard deviation, pg/g	0.010
Relative standard deviation, %	32
No. of values reported	81
No. of values removed	15
No. of reported non-detects	15

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



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



Herring

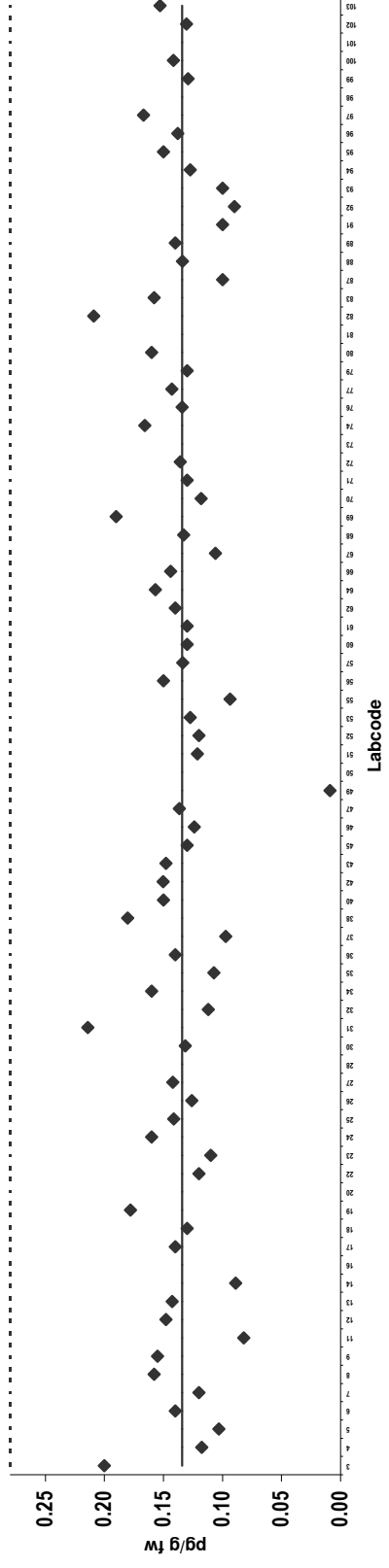
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.20		60	0.13	
4	0.12		61	0.13	
5	0.10		62	0.14	
6	0.14		64	0.16	
7	0.12		66	0.14	
8	0.16		67	0.11	
9	0.16		68	0.13	
11	0.082		69	0.19	
12	0.15		70	0.12	
13	0.14		71	0.13	
14	0.089		72	0.14	
16	0.30		73	0.37	Outlier,ND
17	0.14	Outlier	74	0.17	
18	0.13		76	0.13	
19	0.18		77	0.14	
20	1.0	Outlier,ND	79	0.13	
22	0.12		80	0.16	
23	0.11		81	0.37	Outlier
24	0.16		82	0.21	
25	0.14		83	0.16	
26	0.13		87	0.10	
27	0.14		88	0.13	
28	20	Outlier	89	0.14	
30	0.13		91	0.10	
31	0.21		92	0.090	
32	0.11		93	0.10	
34	0.16		94	0.13	
35	0.11		95	0.15	
36	0.14		96	0.14	
37	0.097		97	0.17	
38	0.18		98	0.60	Outlier,ND
40	0.15		99	0.13	
42	0.15		100	0.14	
43	0.15		101	0.30	Outlier
45	0.13		102	0.13	
46	0.12		103	0.15	
47	0.14				
49	0.0090	ND			
50	5.0	Outlier,ND			
51	0.12				
52	0.12				
53	0.13				
55	0.094				
56	0.15				
57	0.13				

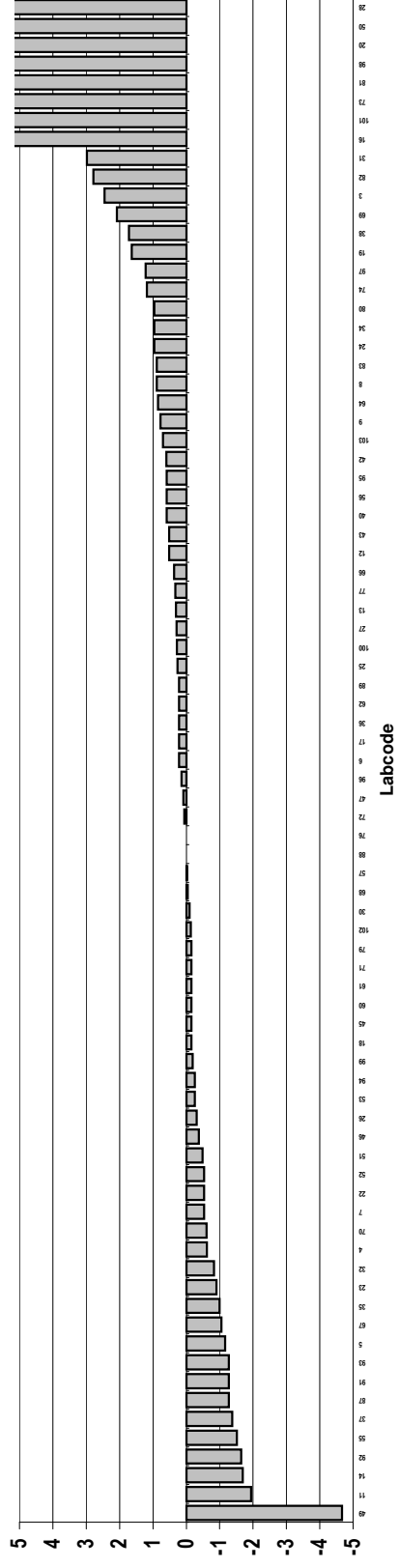
Consensus statistics

Consensus median, pg/g	0.13
Median all values pg/g	0.14
Consensus mean, pg/g	0.13
Standard deviation, pg/g	0.030
Relative standard deviation, %	22
No. of values reported	81
No. of values removed	8
No. of reported non-detects	5

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



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



Herring

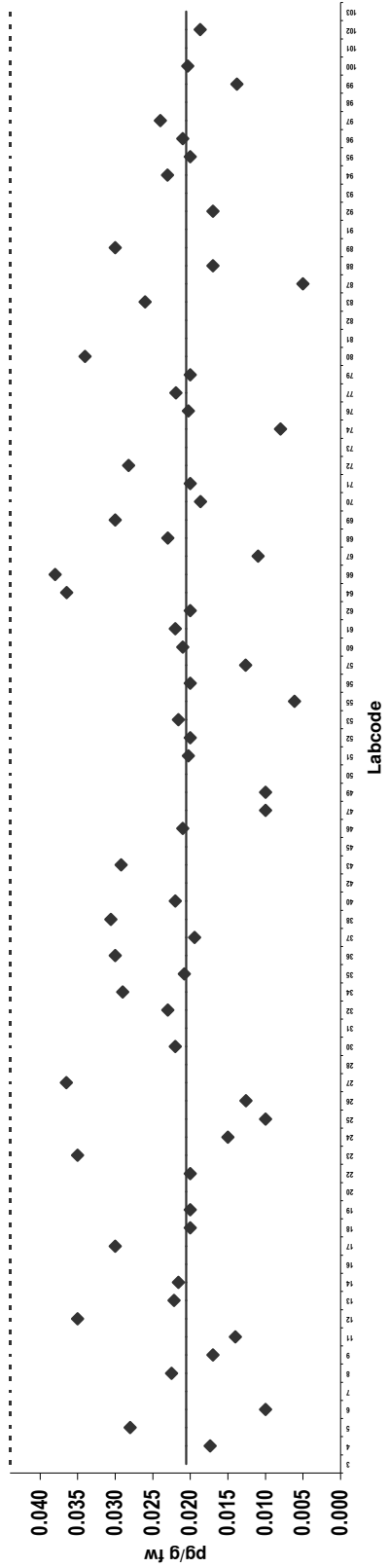
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.050	Outlier,ND	60	0.021	
4	0.017		61	0.022	
5	0.028	ND	62	0.020	
6	0.010	ND	64	0.036	
7	0.11	Outlier,ND	66	0.038	
8	0.023		67	0.011	
9	0.017		68	0.023	
11	0.014		69	0.030	
12	0.035		70	0.019	
13	0.022		71	0.020	
14	0.022		72	0.028	
16	0.079	ND	73	0.32	Outlier,ND
17	0.030	Outlier	74	0.0080	ND
18	0.020	ND	76	0.020	
19	0.020		77	0.022	
20	1.0	Outlier,ND	79	0.020	
22	0.020		80	0.034	ND
23	0.035		81	0.44	Outlier
24	0.015		82	0.15	Outlier
25	0.010	ND	83	0.026	
26	0.013		87	0.0050	ND
27	0.037		88	0.017	ND
28	14		89	0.030	
30	0.022	Outlier	91	0.045	Outlier
31	0.080		92	0.017	ND
32	0.023	Outlier	93	0.075	Outlier,ND
34	0.029		94	0.023	
35	0.021		95	0.020	
36	0.030		96	0.021	
37	0.019		97	0.024	
38	0.031		98	0.60	Outlier,ND
40	0.022		99	0.014	
42	0.055	Outlier,ND	100	0.020	
43	0.029		101	0.12	Outlier
45	0.070	Outlier	102	0.019	Outlier,ND
46	0.021		103	0.050	
47	0.010	ND			
49	0.010	ND			
50	5.0	Outlier,ND			
51	0.020				
52	0.020				
53	0.022				
55	0.0061	ND			
56	0.020				
57	0.013				

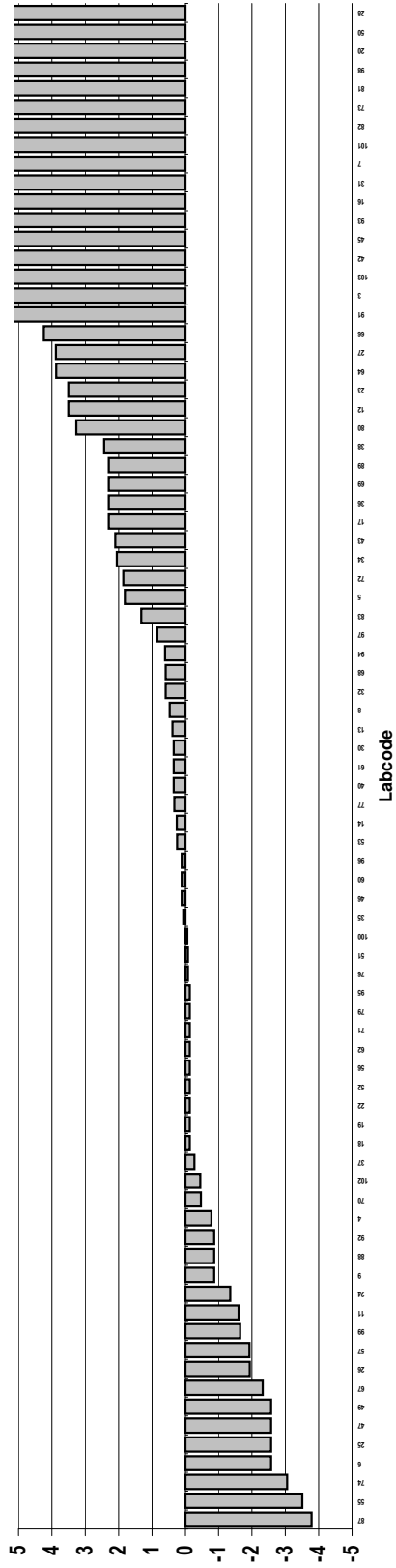
Consensus statistics

Consensus median, pg/g	0.021
Median all values pg/g	0.022
Consensus mean, pg/g	0.021
Standard deviation, pg/g	0.0076
Relative standard deviation, %	36
No. of values reported	81
No. of values removed	17
No. of reported non-detects	22

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



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



Herring

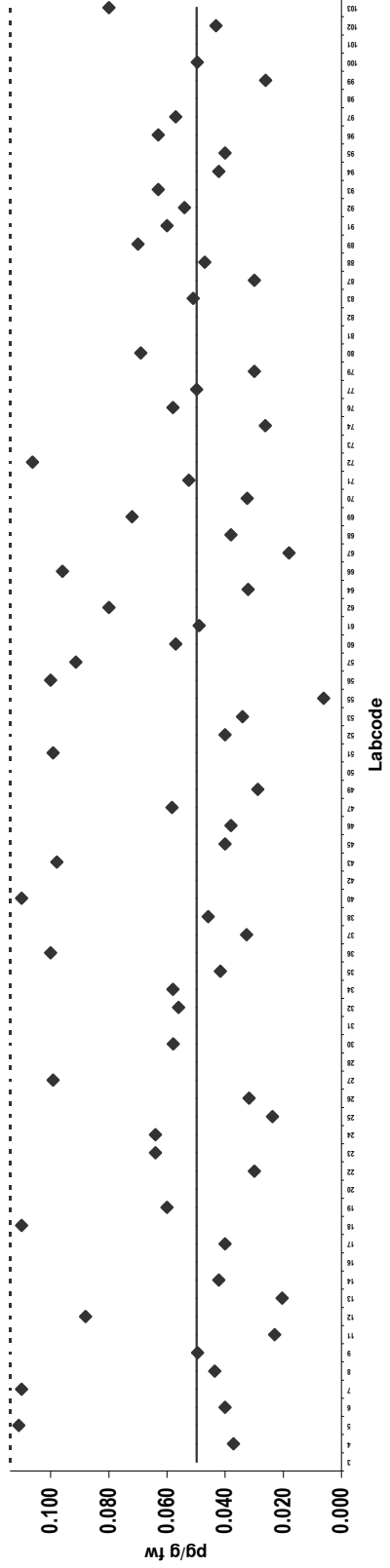
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.20		60	0.057	
4	0.037	Outlier	61	0.049	
5	0.11		62	0.080	
6	0.040		64	0.032	
7	0.11	ND	66	0.096	
8	0.044		67	0.018	
9	0.050		68	0.038	
11	0.023		69	0.072	
12	0.088		70	0.032	
13	0.020		71	0.053	
14	0.042		72	0.11	
16	0.35		73	0.16	
17	0.040	Outlier	74	0.026	Outlier,ND
18	0.11		76	0.058	
19	0.060		77	0.050	
20	1.0	Outlier,ND	79	0.030	
22	0.030		80	0.069	ND
23	0.064		81	0.43	Outlier
24	0.064		82	0.27	Outlier
25	0.024		83	0.051	
26	0.032		87	0.030	
27	0.099		88	0.047	
28	123		89	0.070	
30	0.058	Outlier	91	0.060	
31	0.14		92	0.054	
32	0.056	Outlier	93	0.063	
34	0.058		94	0.042	
35	0.042		95	0.040	
36	0.10	ND	96	0.063	
37	0.033		97	0.057	
38	0.046		98	0.60	Outlier,ND
40	0.11		99	0.026	
42	0.15		100	0.050	
43	0.098	Outlier	101	0.22	Outlier
45	0.040		102	0.043	
46	0.038		103	0.080	
47	0.058				
49	0.029				
50	5.0	Outlier,ND			
51	0.099				
52	0.040				
53	0.034				
55	0.0061	ND			
56	0.10	ND			
57	0.091				

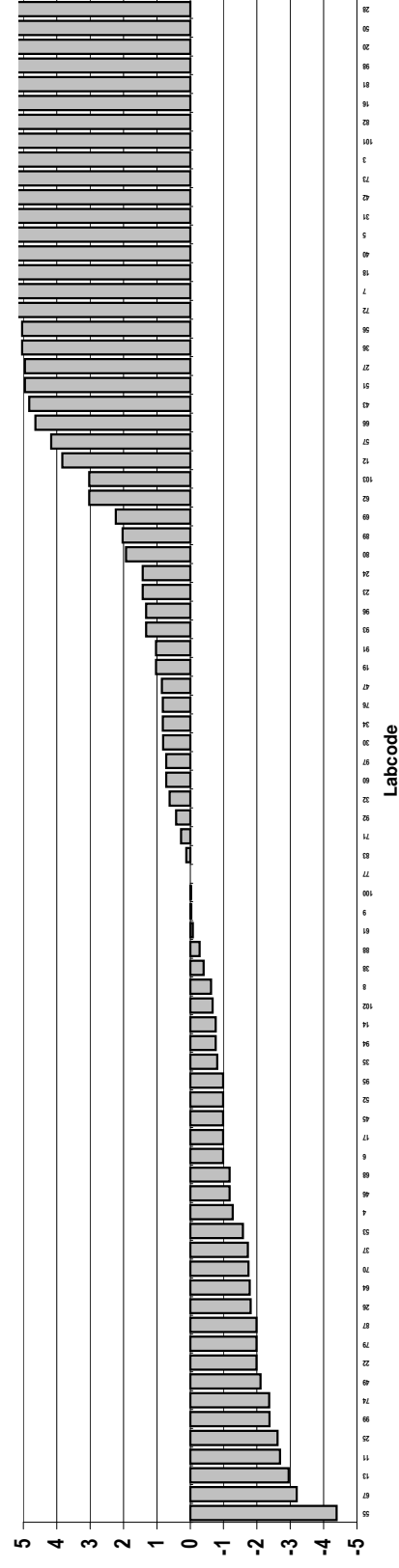
Consensus statistics

Consensus median, pg/g	0.050
Median all values pg/g	0.057
Consensus mean, pg/g	0.056
Standard deviation, pg/g	0.027
Relative standard deviation, %	47
No. of values reported	81
No. of values removed	12
No. of reported non-detects	9

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



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



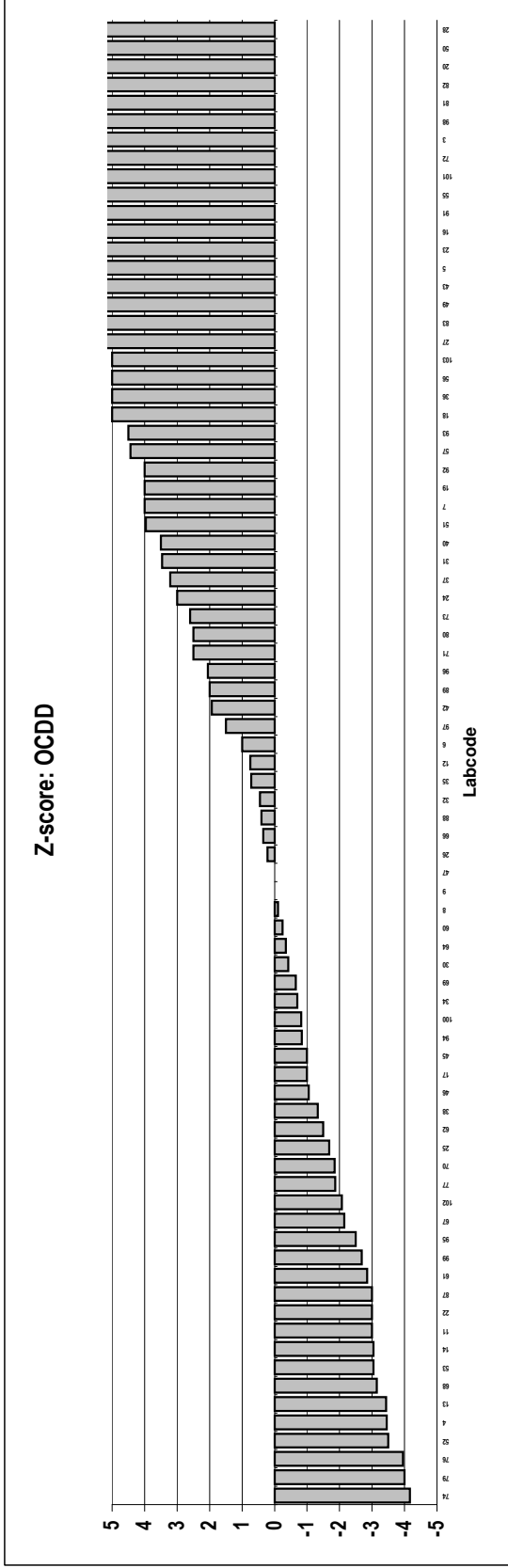
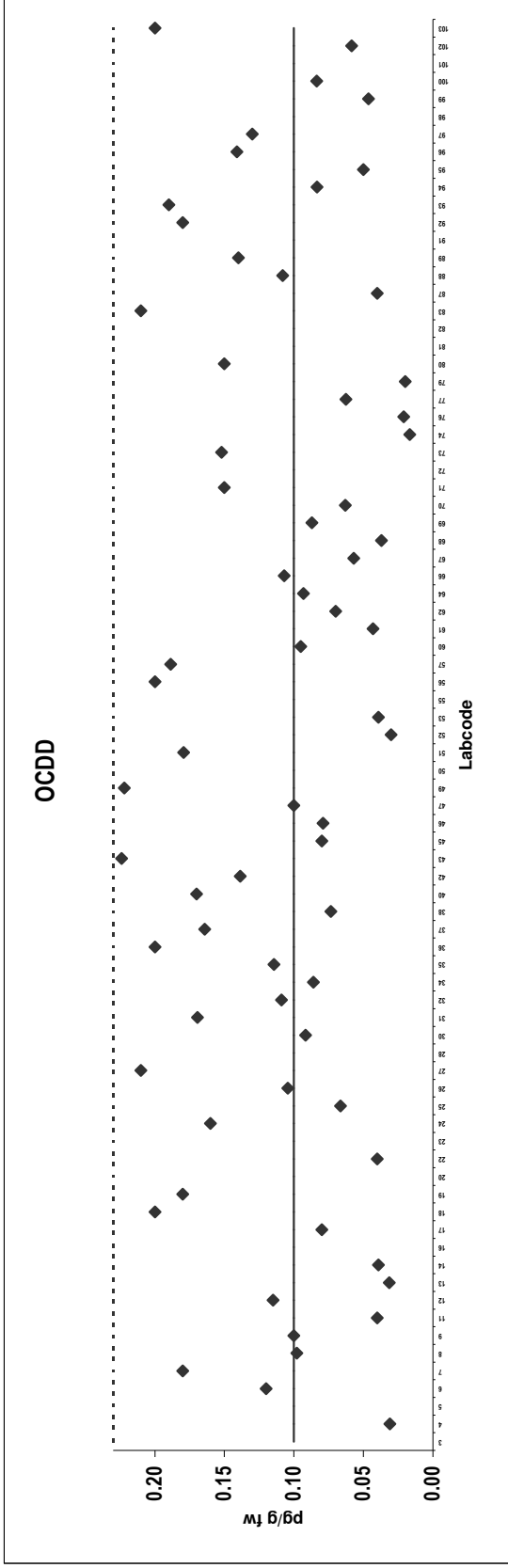
Herring

Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.71		60	0.095	
4	0.031	Outlier	61	0.043	
5	0.23		62	0.070	
6	0.12	Outlier	64	0.093	
7	0.18		66	0.11	
8	0.098	ND	67	0.057	
9	0.10		68	0.037	
11	0.040	ND	69	0.087	
12	0.12		70	0.063	ND
13	0.031		71	0.15	ND
14	0.039		72	0.46	Outlier
16	0.27	Outlier	73	0.15	ND
17	0.080		74	0.017	
18	0.20		76	0.021	
19	0.18		77	0.063	
20	2.0	Outlier,ND	79	0.020	
22	0.040		80	0.15	ND
23	0.25	Outlier	81	1.0	Outlier
24	0.16		82	1.4	Outlier
25	0.066		83	0.21	
26	0.10		87	0.040	
27	0.21		88	0.11	
28	258	Outlier	89	0.14	
30	0.092		91	0.33	Outlier,ND
31	0.17		92	0.18	
32	0.11		93	0.19	
34	0.086		94	0.083	
35	0.11		95	0.050	
36	0.20		96	0.14	ND
37	0.16		97	0.13	ND
38	0.073		98	1.0	Outlier,ND
40	0.17		99	0.046	
42	0.14		100	0.084	ND
43	0.22	ND	101	0.45	ND
45	0.080		102	0.059	Outlier
46	0.079		103	0.20	ND
47	0.10	ND			
49	0.22				
50	10	Outlier,ND			
51	0.18				
52	0.030				
53	0.039				
55	0.43	Outlier			
56	0.20	ND			
57	0.19				

Consensus statistics

Consensus median, pg/g	0.10
Median all values pg/g	0.12
Consensus mean, pg/g	0.11
Standard deviation, pg/g	0.060
Relative standard deviation, %	55
No. of values reported	81
No. of values removed	14
No. of reported non-detects	18



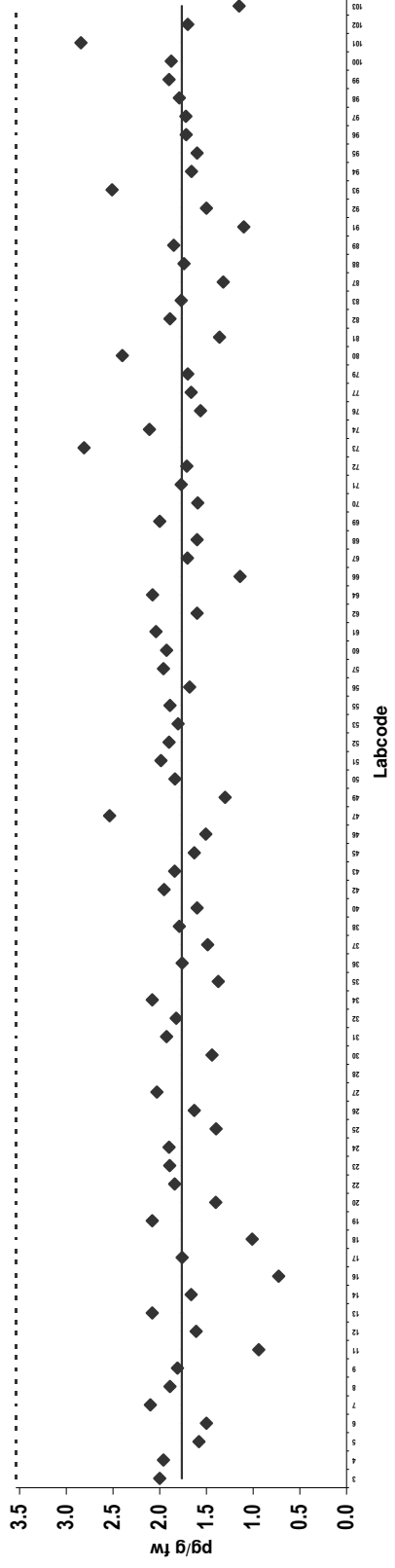
Herring
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	2.0		60	1.9	
4	2.0		61	2.0	
5	1.6		62	1.6	
6	1.5		64	2.1	
7	2.1		66	1.1	
8	1.9		67	1.7	
9	1.8		68	1.6	
11	0.94		69	2.0	
12	1.6		70	1.6	
13	2.1		71	1.8	
14	1.7		72	1.7	
16	0.73		73	2.8	
17	1.8		74	2.1	
18	1.0		76	1.6	
19	2.1		77	1.7	
20	1.4		79	1.7	
22	1.8		80	2.4	
23	1.9		81	1.4	
24	1.9		82	1.9	
25	1.4		83	1.8	
26	1.6		87	1.3	
27	2.0		88	1.7	
28	3.4	Outlier	89	1.9	
30	1.4		91	1.1	
31	1.9		92	1.5	
32	1.8		93	2.5	
34	2.1		94	1.7	
35	1.4		95	1.6	
36	1.8		96	1.7	
37	1.5		97	1.7	
38	1.8		98	1.8	
40	1.6		99	1.9	
42	2.0		100	1.9	
43	1.8		101	2.8	
45	1.6		102	1.7	
46	1.5		103	1.2	
47	2.5				
49	1.3				
50	1.8				
51	2.0				
52	1.9				
53	1.8				
55	1.9				
56	1.7				
57	2.0				

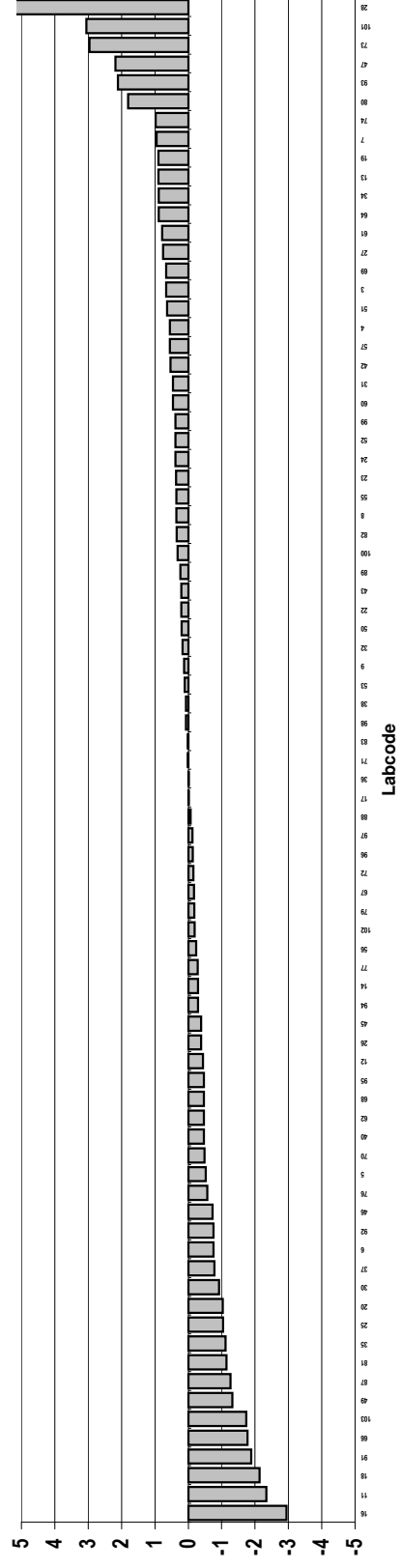
Consensus statistics

Consensus median, pg/g	1.8
Median all values pg/g	1.8
Consensus mean, pg/g	1.8
Standard deviation, pg/g	0.36
Relative standard deviation, %	21
No. of values reported	81
No. of values removed	1
No. of reported non-detects	0

2,3,7,8 TCDF



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



Herring

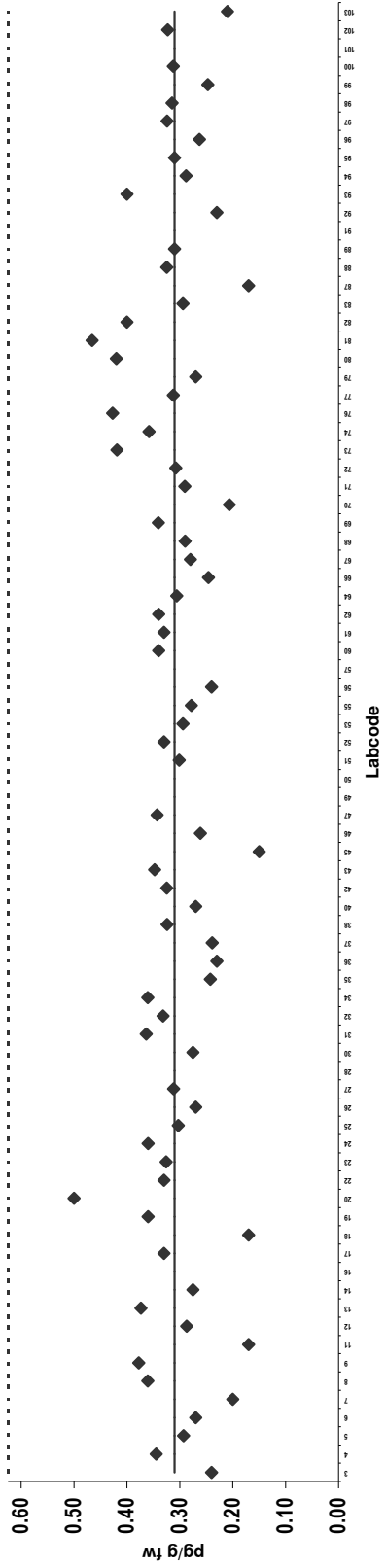
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.24		60	0.34	
4	0.34		61	0.33	
5	0.29		62	0.34	
6	0.27		64	0.31	
7	0.20		66	0.25	
8	0.36		67	0.28	
9	0.38		68	0.29	
11	0.17		69	0.34	
12	0.29		70	0.21	
13	0.37		71	0.29	
14	0.28		72	0.31	
16	0.79	Outlier	73	0.42	
17	0.33		74	0.36	
18	0.17		76	0.43	
19	0.36		77	0.31	
20	0.50	ND	79	0.27	
22	0.33		80	0.42	
23	0.33		81	0.47	
24	0.36		82	0.40	
25	0.30		83	0.29	
26	0.27		87	0.17	
27	0.31		88	0.33	
28	0.29		89	0.31	
30	0.28		91	0.79	Outlier
31	0.36		92	0.23	
32	0.33		93	0.40	
34	0.36		94	0.29	
35	0.24		95	0.31	
36	0.23		96	0.26	
37	0.24		97	0.32	
38	0.32		98	0.32	
40	0.27		99	0.25	
42	0.32		100	0.31	
43	0.35		101	0.91	Outlier
45	0.15		102	0.32	
46	0.26		103	0.21	
47	0.34				
49	1.5	Outlier			
50	5.0	Outlier,ND			
51	0.30				
52	0.33				
53	0.29				
55	0.28				
56	0.24				
57	1.1	Outlier			

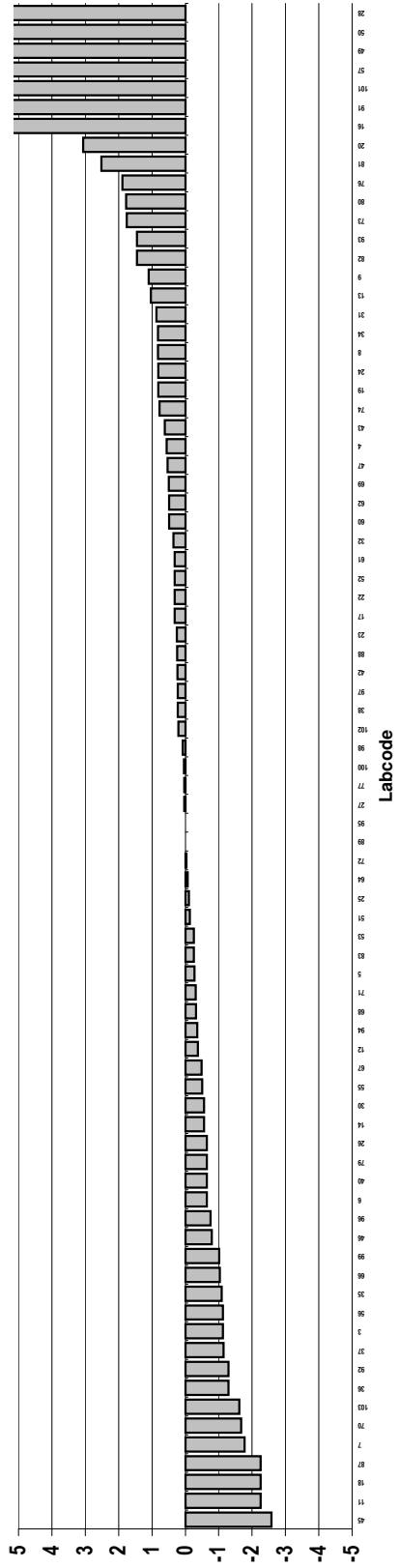
Consensus statistics

Consensus median, pg/g	0.31
Median all values pg/g	0.31
Consensus mean, pg/g	0.31
Standard deviation, pg/g	0.066
Relative standard deviation, %	22
No. of values reported	81
No. of values removed	7
No. of reported non-detects	2

1,2,3,7,8 PeCDF



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



Herring

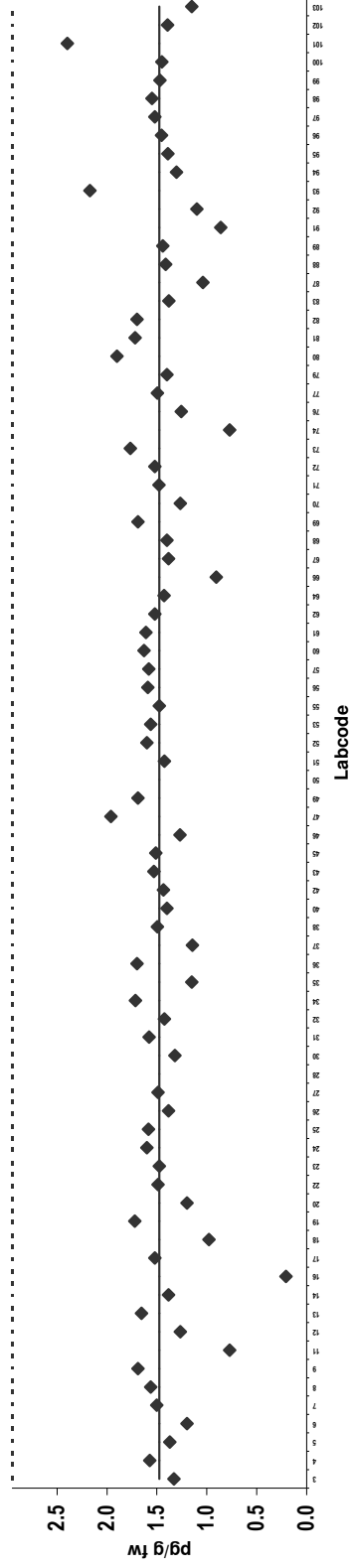
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	1.3		60	1.6	
4	1.6		61	1.6	
5	1.4		62	1.5	
6	1.2		64	1.4	
7	1.5		66	0.91	
8	1.6		67	1.4	
9	1.7		68	1.4	
11	0.77		69	1.7	
12	1.3		70	1.3	
13	1.7		71	1.5	
14	1.4		72	1.5	
16	0.21		73	1.8	
17	1.5		74	0.77	
18	0.98		76	1.3	
19	1.7		77	1.5	
20	1.2		79	1.4	
22	1.5		80	1.9	
23	1.5		81	1.7	
24	1.6		82	1.7	
25	1.6		83	1.4	
26	1.4		87	1.0	
27	1.5		88	1.4	
28	1.16		89	1.4	
30	1.3		91	0.86	
31	1.6		92	1.1	
32	1.4		93	2.2	
34	1.7		94	1.3	
35	1.2		95	1.4	
36	1.7		96	1.5	
37	1.1		97	1.5	
38	1.5		98	1.6	
40	1.4		99	1.5	
42	1.4		100	1.5	
43	1.5		101	2.4	
45	1.5		102	1.4	
46	1.3		103	1.2	
47	2.0				
49	1.7				
50	5.0				
51	1.4				
52	1.6				
53	1.6				
55	1.5				
56	1.6				
57	1.6				

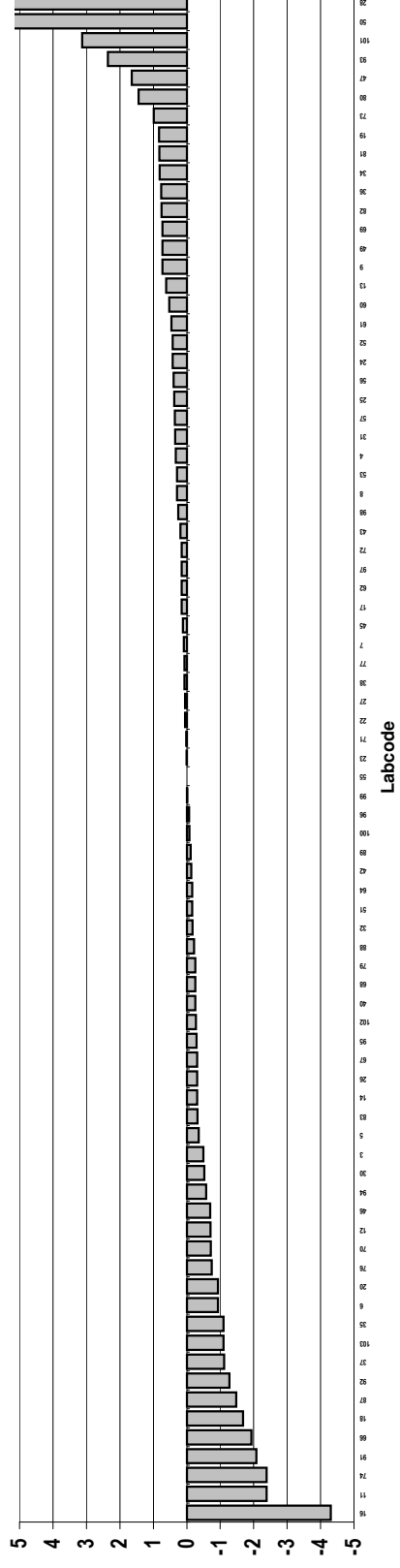
Consensus statistics

Consensus median, pg/g	1.5
Median all values pg/g	1.5
Consensus mean, pg/g	1.4
Standard deviation, pg/g	0.30
Relative standard deviation, %	21
No. of values reported	81
No. of values removed	2
No. of reported non-detects	1

2,3,4,7,8 PeCDF



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



Herring

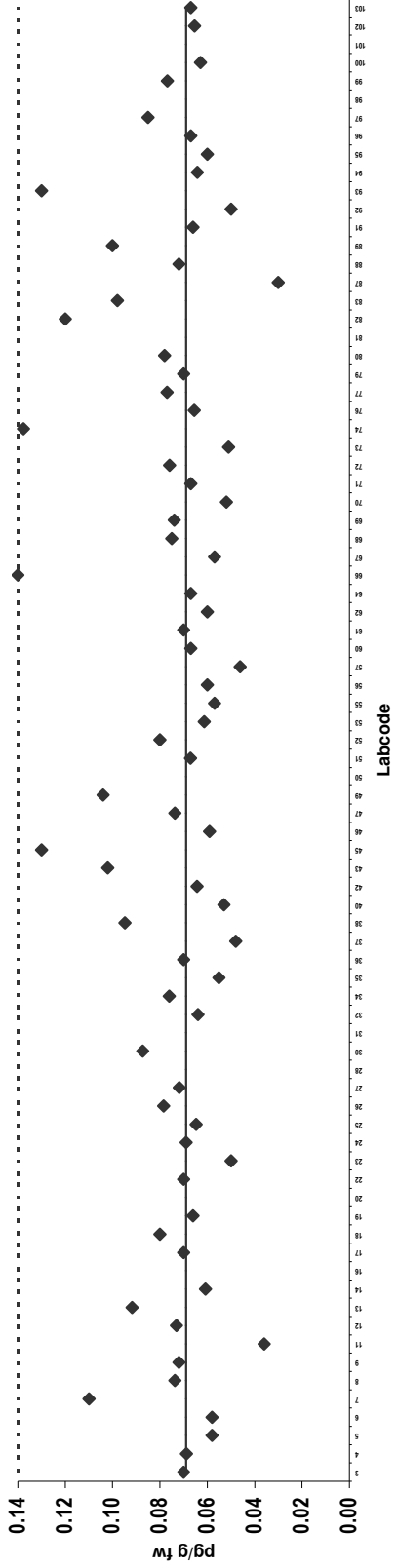
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.070		60	0.067	
4	0.069		61	0.070	
5	0.058		62	0.060	
6	0.058		64	0.067	
7	0.11		66	0.14	
8	0.074		67	0.057	
9	0.072		68	0.075	
11	0.036		69	0.074	
12	0.073		70	0.052	
13	0.092		71	0.067	
14	0.061		72	0.076	
16	0.15		73	0.051	ND
17	0.070	Outlier	74	0.14	
18	0.080		76	0.066	
19	0.066		77	0.077	
20	1.0	Outlier,ND	79	0.070	
22	0.070		80	0.078	Outlier
23	0.050		81	0.34	
24	0.069		82	0.12	
25	0.065		83	0.098	
26	0.079		87	0.030	
27	0.072		88	0.072	
28	73	Outlier	89	0.10	
30	0.087		91	0.066	
31	0.14	Outlier	92	0.050	
32	0.064		93	0.13	
34	0.076		94	0.064	
35	0.055		95	0.060	
36	0.070		96	0.067	
37	0.048		97	0.085	
38	0.095		98	0.60	Outlier,ND
40	0.053		99	0.077	
42	0.064		100	0.063	
43	0.10		101	0.18	Outlier
45	0.13		102	0.065	
46	0.059		103	0.067	
47	0.074				
49	0.10				
50	5.0	Outlier,ND			
51	0.067				
52	0.080				
53	0.061				
55	0.057				
56	0.060				
57	0.046				

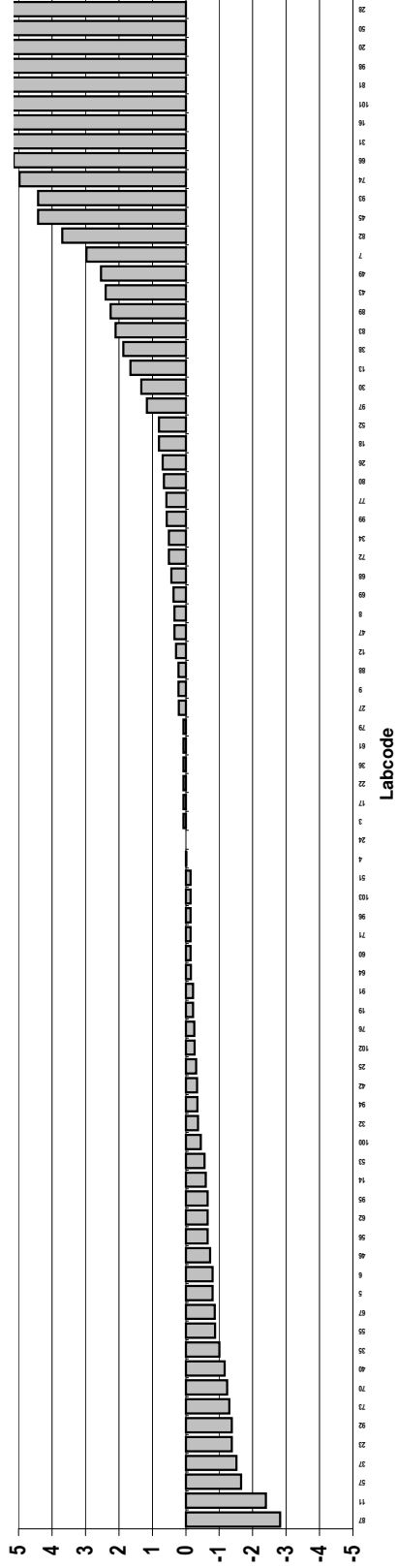
Consensus statistics

Consensus median, pg/g	0.069
Median all values pg/g	0.070
Consensus mean, pg/g	0.073
Standard deviation, pg/g	0.022
Relative standard deviation, %	29
No. of values reported	81
No. of values removed	8
No. of reported non-detects	4

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



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



Herring

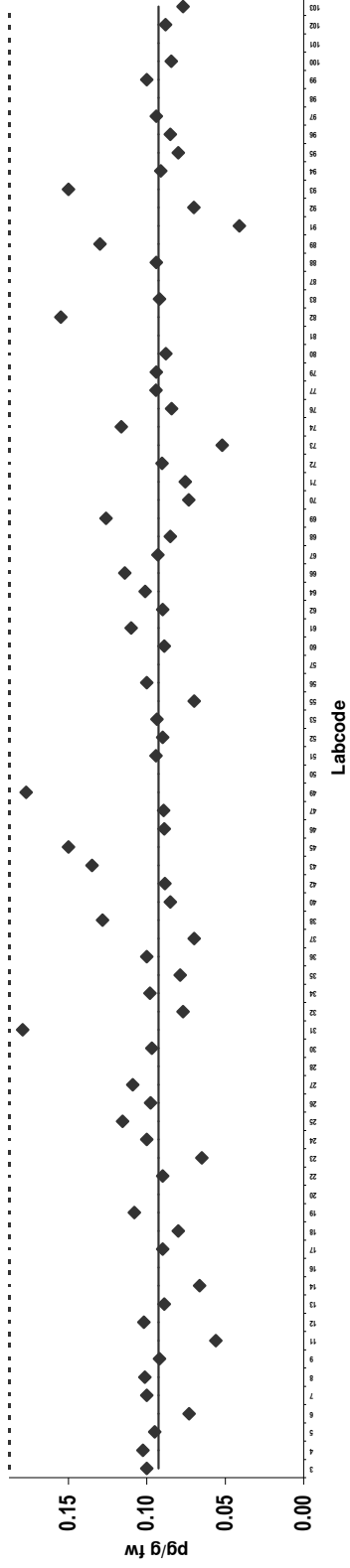
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.10		60	0.089	
4	0.10		61	0.11	
5	0.095		62	0.090	
6	0.073		64	0.10	
7	0.10	ND	66	0.11	
8	0.10		67	0.093	
9	0.092		68	0.085	
11	0.056		69	0.13	
12	0.10		70	0.073	
13	0.089		71	0.076	
14	0.066		72	0.090	
16	2.7		73	0.052	ND
17	0.090		74	0.12	
18	0.080		76	0.084	
19	0.11		77	0.094	
20	1.0		79	0.094	
22	0.090		80	0.088	
23	0.065		81	0.34	Outlier
24	0.10		82	0.16	
25	0.12		83	0.092	
26	0.098		87	0.19	Outlier
27	0.11		88	0.094	
28	63		89	0.13	
30	0.097		91	0.041	
31	0.18		92	0.070	
32	0.077		93	0.15	
34	0.098		94	0.091	
35	0.079		95	0.080	
36	0.10		96	0.085	
37	0.070		97	0.094	
38	0.13		98	0.60	Outlier,ND
40	0.085		99	0.10	
42	0.089		100	0.084	
43	0.14		101	0.32	
45	0.15		102	0.088	
46	0.089		103	0.077	
47	0.089				
49	0.18				
50	5.0				
51	0.094	Outlier,ND			
52	0.090				
53	0.094				
55	0.070				
56	0.10				
57	0.71	Outlier			

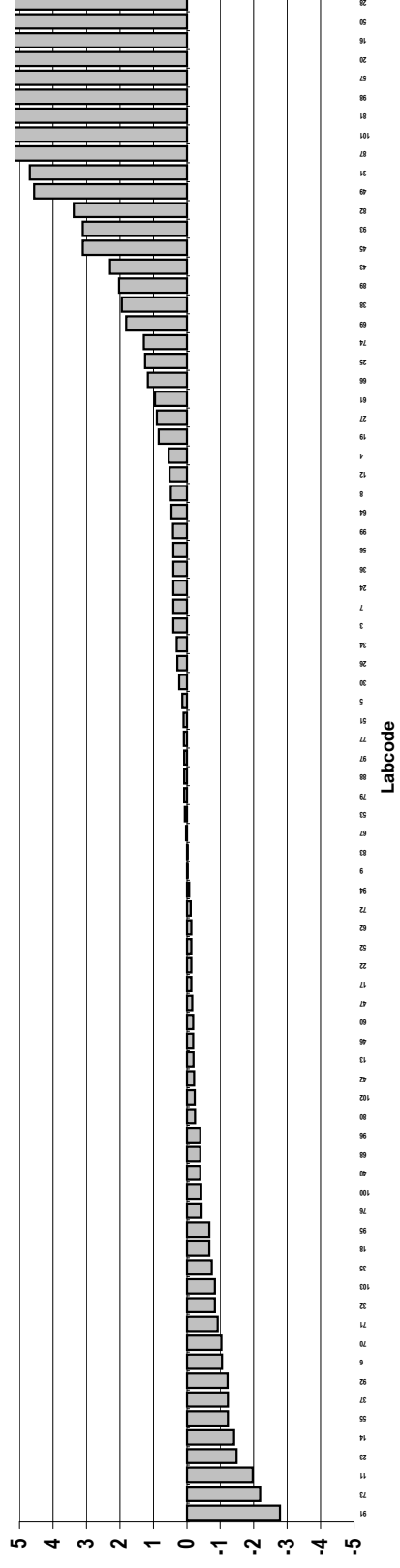
Consensus statistics

Consensus median, pg/g	0.093
Median all values pg/g	0.094
Consensus mean, pg/g	0.096
Standard deviation, pg/g	0.025
Relative standard deviation, %	26
No. of values reported	81
No. of values removed	9
No. of reported non-detects	5

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



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



Herring

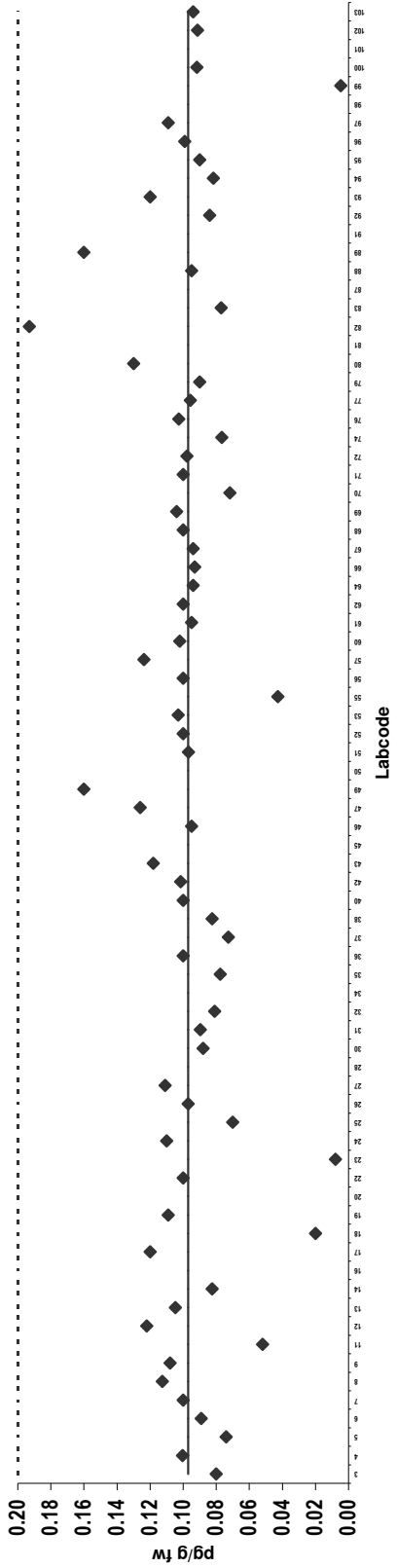
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.080		60	0.10	
4	0.10		61	0.095	
5	0.074		62	0.10	
6	0.089		64	0.094	
7	0.10	ND	66	0.093	
8	0.11		67	0.094	
9	0.11		68	0.10	
11	0.052		69	0.10	
12	0.12		70	0.072	
13	0.10		71	0.10	
14	0.082		72	0.098	
16	0.26	Outlier	74	0.077	
17	0.12		76	0.10	
18	0.020	ND	77	0.096	
19	0.11		79	0.090	
20	1.0	Outlier,ND	80	0.13	
22	0.10		81	0.47	Outlier
23	0.0080		82	0.19	
24	0.11		83	0.077	
25	0.070		87	1.6	Outlier
26	0.097		88	0.095	
27	0.11		89	0.16	
28	1.48		91	0.21	Outlier
30	0.088		92	0.084	
31	0.090		93	0.12	
32	0.081		94	0.082	
34	0.24	Outlier	95	0.090	
35	0.078		96	0.099	
36	0.10		97	0.11	
37	0.073		98	0.60	Outlier,ND
38	0.083		99	0.0048	ND
40	0.10		100	0.092	
42	0.10		101	0.25	Outlier
43	0.12		102	0.091	
45	0.51	Outlier	103	0.094	
46	0.095				
47	0.13				
49	0.16				
50	5.0	Outlier,ND			
51	0.097				
52	0.10				
53	0.10				
55	0.043				
56	0.10				
57	0.12				

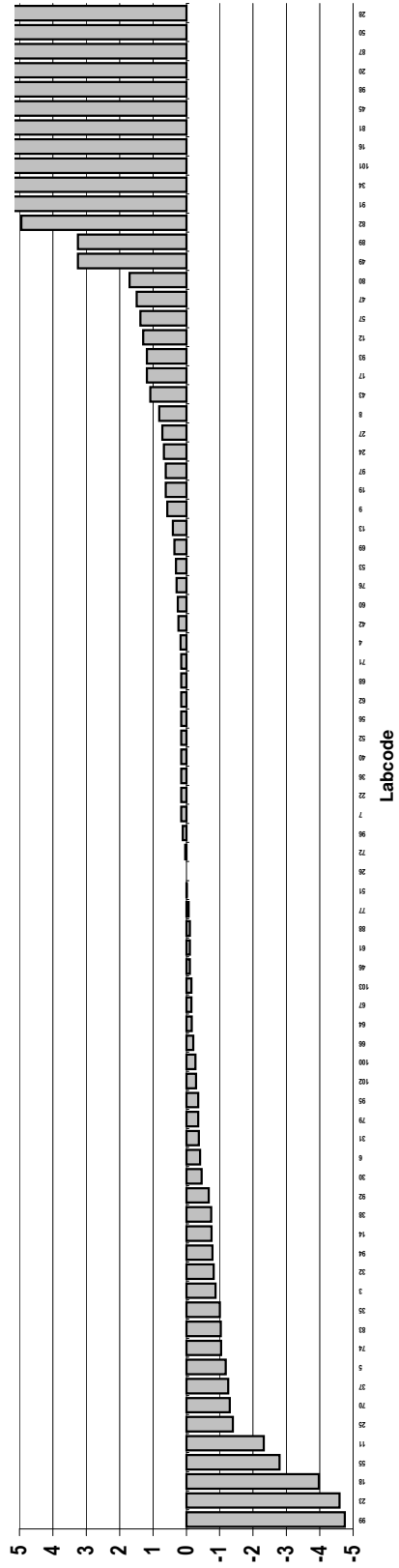
Consensus statistics

Consensus median, pg/g	0.097
Median all values pg/g	0.10
Consensus mean, pg/g	0.095
Standard deviation, pg/g	0.029
Relative standard deviation, %	30
No. of values reported	80
No. of values removed	11
No. of reported non-detects	6

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



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



Herring

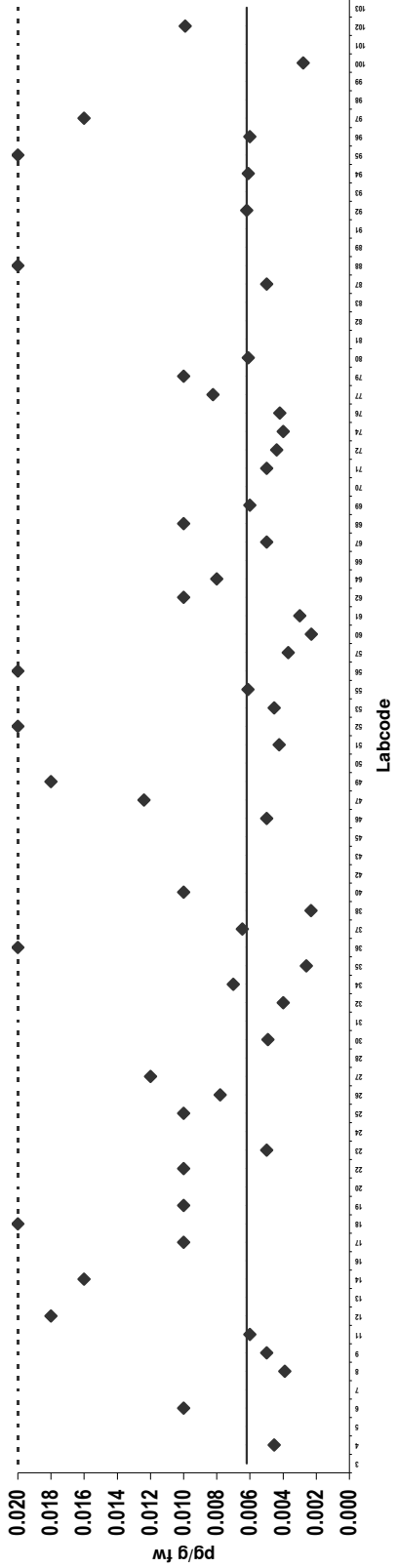
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.030	Outlier,ND	60	0.0023	ND
4	0.0045		61	0.0030	
5	0.026	Outlier,ND	62	0.010	ND
6	0.010	ND	64	0.0080	ND
7	0.10	Outlier,ND	66	0.029	Outlier
8	0.0039		67	0.0050	ND
9	0.0050	ND	68	0.010	ND
11	0.0060	ND	69	0.0060	
12	0.018		70	0.032	Outlier,ND
13	0.031	Outlier,ND	71	0.0050	ND
14	0.016		72	0.0044	ND
16	0.33	Outlier	74	0.0040	ND
17	0.010	ND	76	0.0042	ND
18	0.020	ND	77	0.0082	ND
19	0.010	ND	79	0.010	ND
20	1.0	Outlier,ND	80	0.0061	ND
22	0.010	ND	81	0.61	Outlier
23	0.0050		82	0.068	Outlier
24	0.029	Outlier	83	0.042	Outlier,ND
25	0.010	ND	87	0.0050	ND
26	0.0078		88	0.020	ND
27	0.012	ND	89	0.030	Outlier
28	0.18	Outlier,ND	91	0.060	Outlier
30	0.0049		92	0.0062	ND
31	0.19	Outlier	93	0.10	Outlier,ND
32	0.0040	ND	94	0.0061	
34	0.0070		95	0.020	ND
35	0.0026	ND	96	0.0060	ND
36	0.020	ND	97	0.016	ND
37	0.0065	ND	98	0.60	Outlier,ND
38	0.0023	ND	99	0.074	Outlier
40	0.010	ND	100	0.0028	
42	0.040	Outlier,ND	101	0.091	Outlier
43	0.026	Outlier,ND	102	0.0099	ND
45	0.58	Outlier	103	0.050	Outlier,ND
46	0.0050	ND			
47	0.012	ND			
49	0.018				
50	5.0	Outlier,ND			
51	0.0042	ND			
52	0.020	ND			
53	0.0045				
55	0.0061	ND			
56	0.020	ND			
57	0.0037				

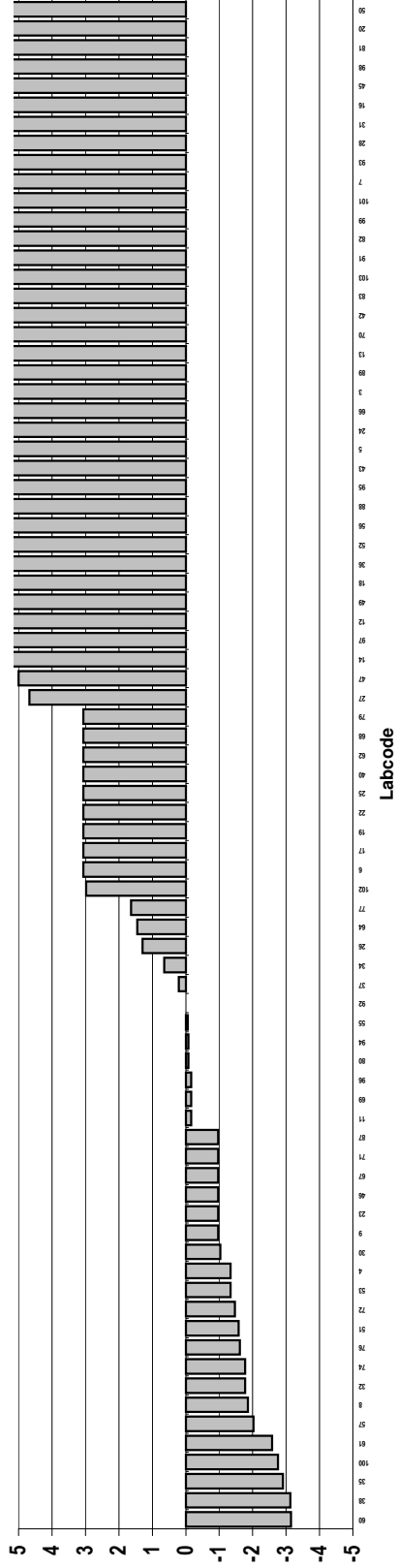
Consensus statistics

Consensus median, pg/g	0.0062
Median all values pg/g	0.010
Consensus mean, pg/g	0.0087
Standard deviation, pg/g	0.0055
Relative standard deviation, %	63
No. of values reported	80
No. of values removed	25
No. of reported non-detects	54

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



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



Herring

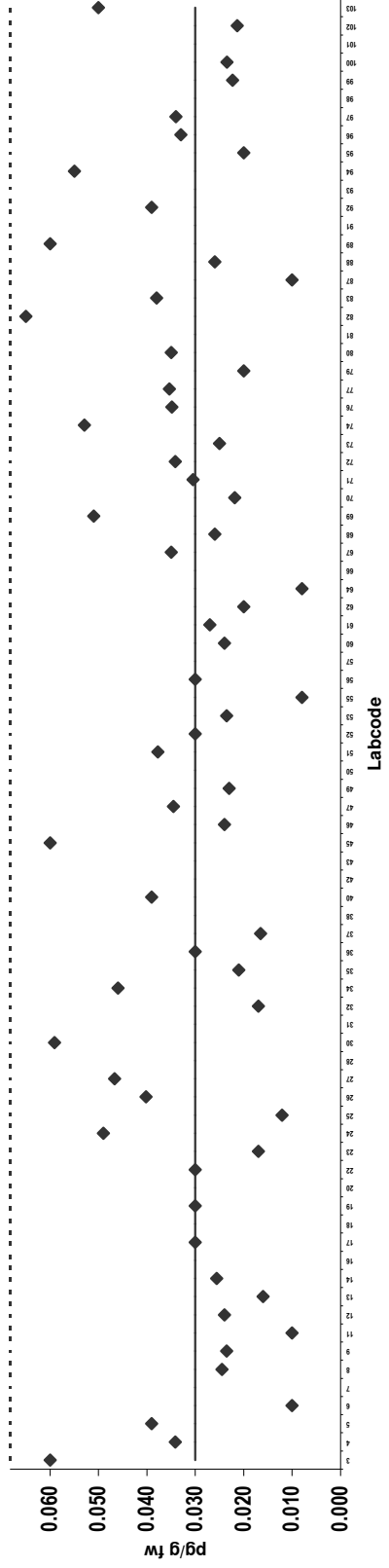
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.060		60	0.024	
4	0.034		61	0.027	
5	0.039		62	0.020	
6	0.010	ND	64	0.0080	ND
7	0.12	Outlier,ND	66	0.090	Outlier
8	0.025		67	0.035	
9	0.024		68	0.026	
11	0.010	ND	69	0.051	
12	0.024		70	0.022	
13	0.016		71	0.031	
14	0.026		72	0.034	
16	0.48	Outlier	73	0.025	ND
17	0.030	Outlier	74	0.053	
18	0.13	Outlier	76	0.035	
19	0.030	Outlier,ND	77	0.035	
20	1.0		79	0.020	
22	0.030		80	0.035	
23	0.017		81	0.25	Outlier
24	0.049		82	0.065	
25	0.012		83	0.038	
26	0.040		87	0.010	
27	0.047		88	0.026	
28	277	Outlier	89	0.060	
30	0.059		91	0.20	Outlier
31	0.11	Outlier	92	0.039	
32	0.017	ND	93	0.070	Outlier,ND
34	0.046		94	0.055	
35	0.021		95	0.020	
36	0.030		96	0.033	
37	0.017		97	0.034	
38	0.086	Outlier	98	0.60	ND
40	0.039		99	0.022	Outlier,ND
42	0.16	Outlier	100	0.023	
43	0.092	Outlier	101	0.45	Outlier
45	0.060		102	0.021	
46	0.024		103	0.050	
47	0.035	ND			
49	0.023	Outlier,ND			
50	5.0				
51	0.038				
52	0.030				
53	0.024				
55	0.0080				
56	0.030	Outlier			
57	0.40				

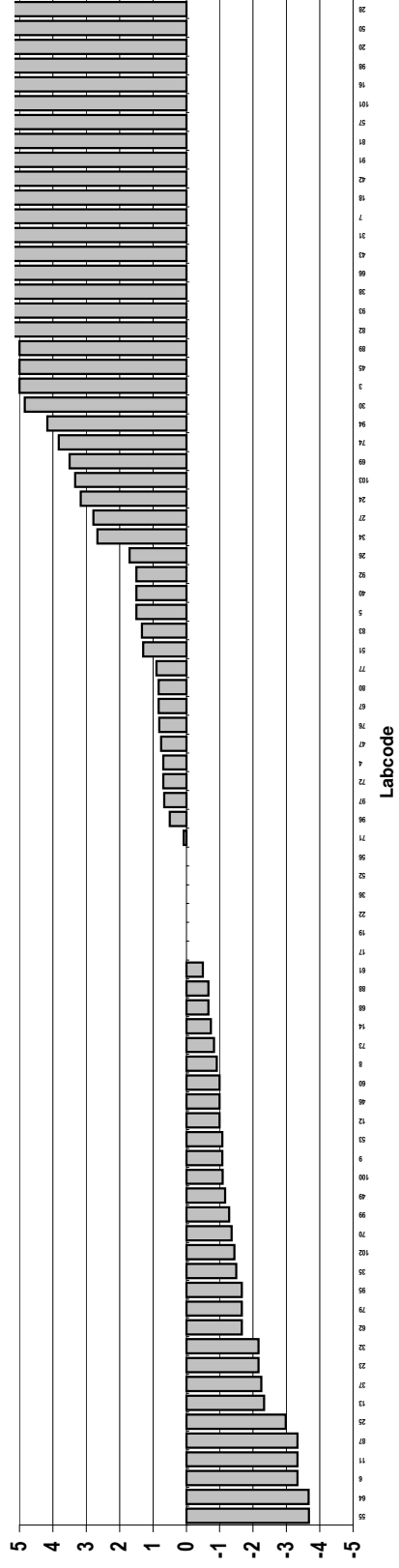
Consensus statistics

Consensus median, pg/g	0.030
Median all values pg/g	0.034
Consensus mean, pg/g	0.031
Standard deviation, pg/g	0.014
Relative standard deviation, %	45
No. of values reported	81
No. of values removed	17
No. of reported non-detects	12

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



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



Herring

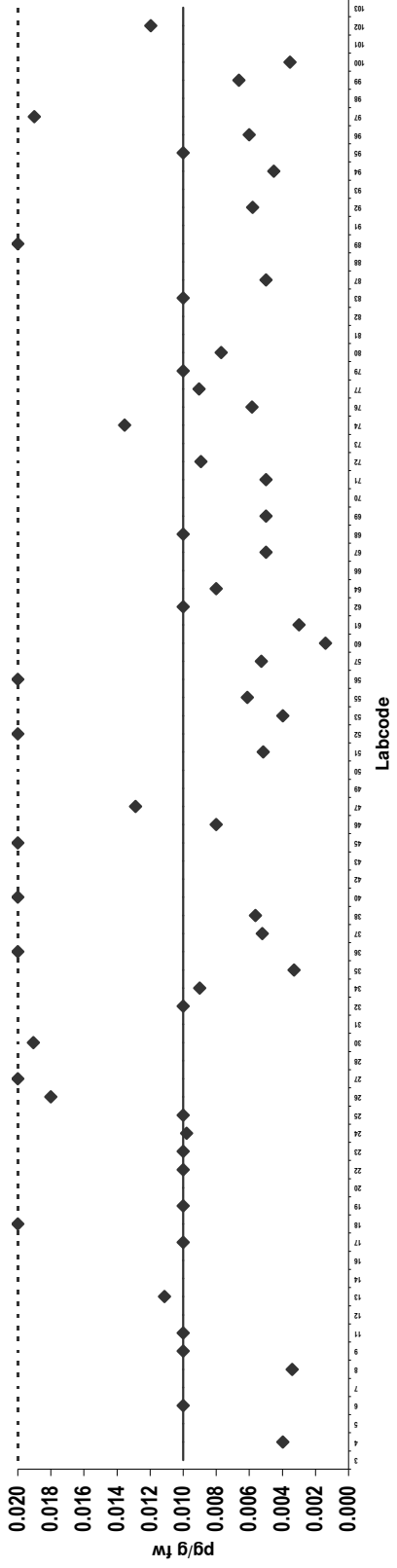
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.030	Outlier,ND	60	0.0014	ND
4	0.0040		61	0.0030	
5	0.026	Outlier,ND	62	0.010	ND
6	0.010	ND	64	0.0080	ND
7	0.12	Outlier,ND	66	0.062	Outlier
8	0.0034		67	0.0050	ND
9	0.010	ND	68	0.010	ND
11	0.010	ND	69	0.0050	
12	0.023	Outlier	70	0.053	Outlier,ND
13	0.011	ND	71	0.0050	ND
14	0.024	Outlier,ND	72	0.0089	ND
16	0.27	Outlier	73	0.17	Outlier,ND
17	0.010	ND	74	0.014	
18	0.020	ND	76	0.0058	
19	0.010	ND	77	0.0090	ND
20	1.0	Outlier,ND	79	0.010	ND
22	0.010	ND	80	0.0077	ND
23	0.010	ND	81	0.27	Outlier
24	0.0098	ND	82	0.073	Outlier
25	0.010	ND	83	0.010	
26	0.018	ND	87	0.0050	ND
27	0.020	ND	88	0.037	Outlier,ND
28	40	Outlier	89	0.020	
30	0.019		91	0.033	Outlier,ND
31	0.095	Outlier	92	0.0058	ND
32	0.010	ND	93	0.10	Outlier,ND
34	0.0090		94	0.0045	
35	0.0033		95	0.010	ND
36	0.020	ND	96	0.0060	ND
37	0.0052	ND	97	0.019	ND
38	0.0056	ND	98	0.60	Outlier,ND
40	0.020	ND	99	0.0066	
42	0.042	Outlier,ND	100	0.0035	
43	0.039	Outlier,ND	101	0.10	Outlier
45	0.020		102	0.012	ND
46	0.0080	ND	103	0.050	Outlier,ND
47	0.013	ND			
49	0.035	Outlier			
50	5.0	Outlier,ND			
51	0.0052				
52	0.020	ND			
53	0.0040				
55	0.0061	ND			
56	0.020	ND			
57	0.0053				

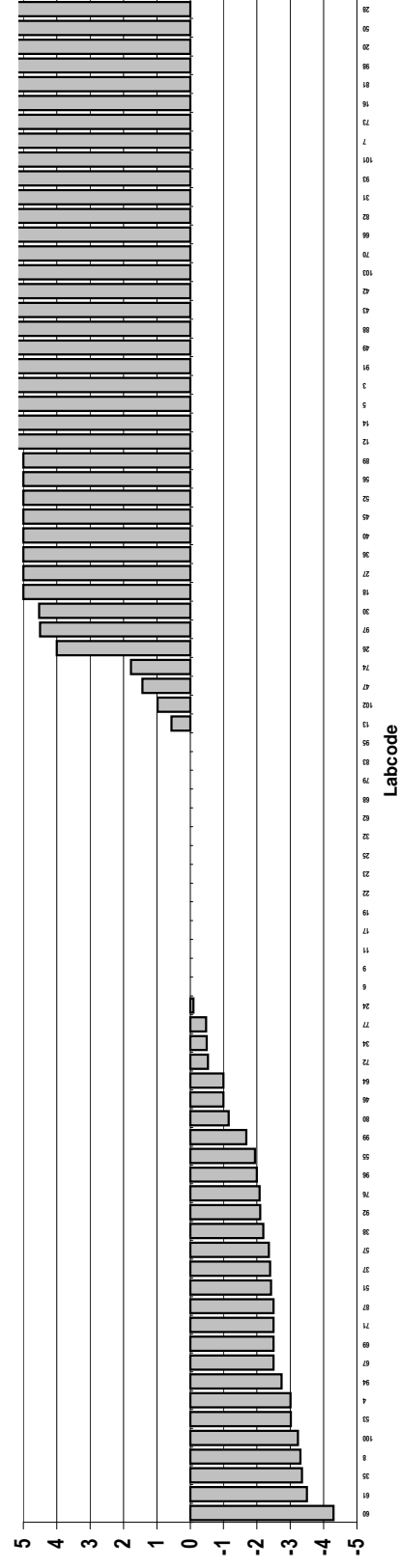
Consensus statistics

Consensus median, pg/g	0.010
Median all values pg/g	0.010
Consensus mean, pg/g	0.010
Standard deviation, pg/g	0.0055
Relative standard deviation, %	55
No. of values reported	81
No. of values removed	24
No. of reported non-detects	54

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



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



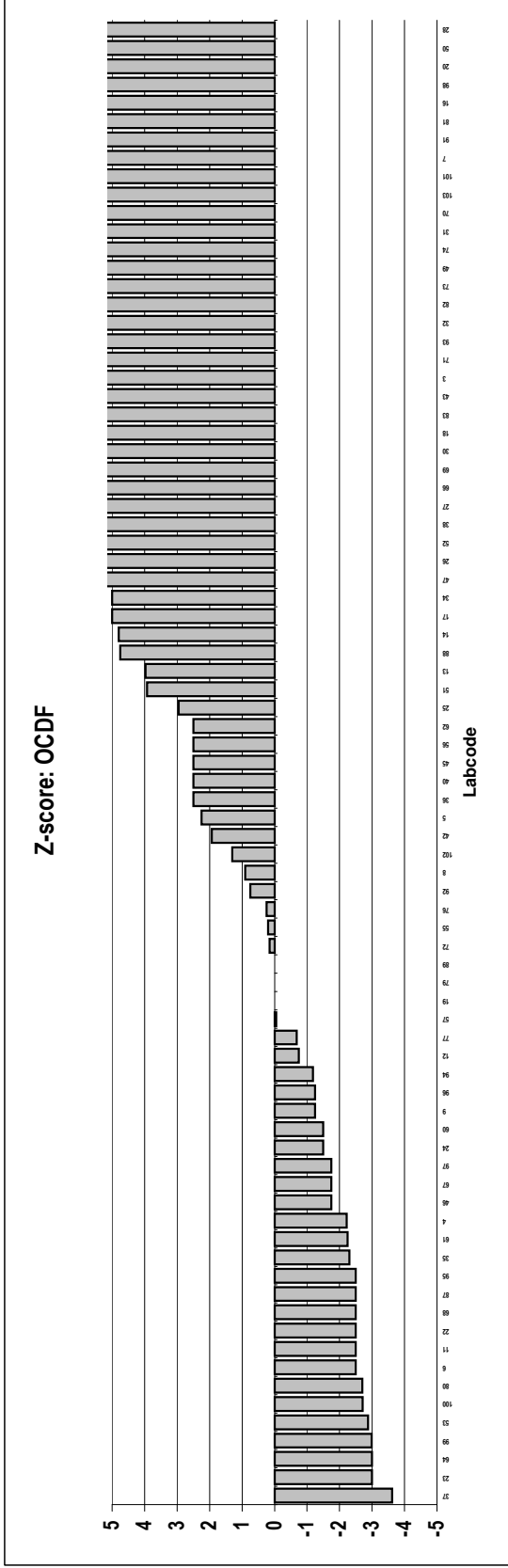
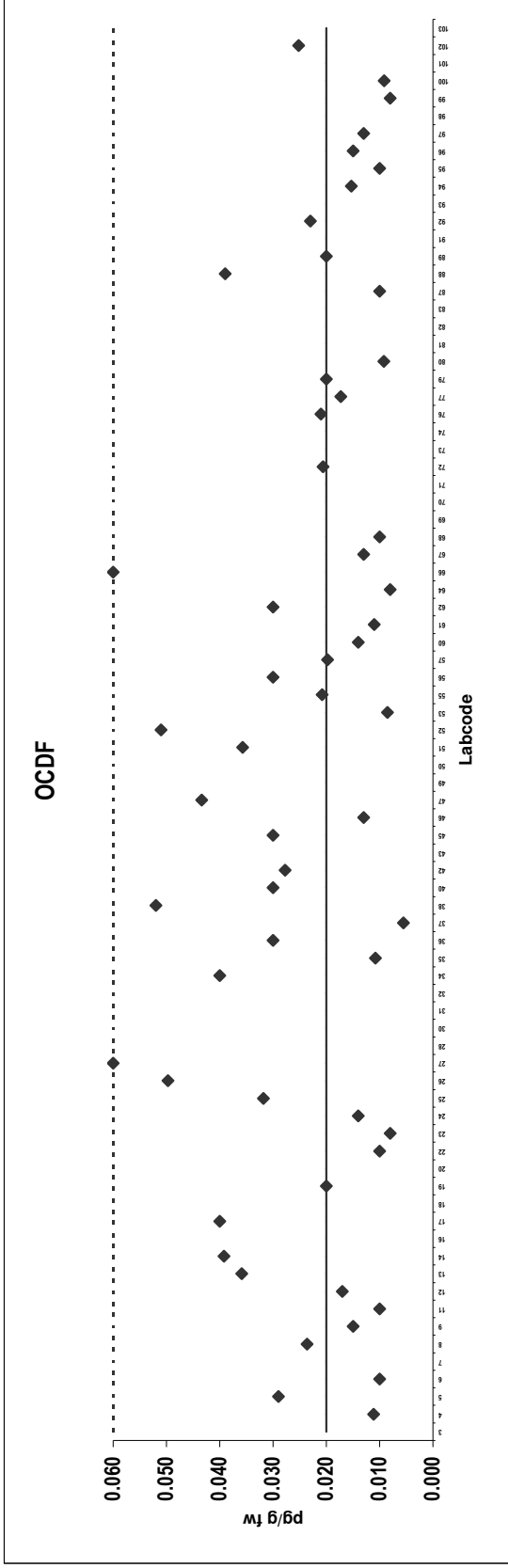
Herring

Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.090	Outlier	60	0.014	
4	0.011		61	0.011	
5	0.029	ND	62	0.030	ND
6	0.010	ND	64	0.0080	ND
7	0.30	Outlier,ND	66	0.060	
8	0.024		67	0.013	
9	0.015		68	0.010	ND
11	0.010	ND	69	0.061	Outlier
12	0.017	ND	70	0.20	Outlier,ND
13	0.036		71	0.10	Outlier,ND
14	0.039	ND	72	0.021	
16	0.59	Outlier	73	0.13	Outlier,ND
17	0.040		74	0.16	Outlier
18	0.070	Outlier	76	0.021	ND
19	0.020		77	0.017	
20	2.0	Outlier,ND	79	0.020	ND
22	0.010	ND	80	0.0092	ND
23	0.0080		81	0.44	Outlier
24	0.014	ND	82	0.12	Outlier
25	0.032		83	0.071	Outlier
26	0.050		87	0.010	Outlier
27	0.060		88	0.039	ND
28	1.26	ND	89	0.020	
30	0.061	Outlier	91	0.33	Outlier,ND
31	0.17	Outlier	92	0.023	
32	0.12	Outlier	93	0.10	Outlier,ND
34	0.040		94	0.015	
35	0.011		95	0.010	
36	0.030	ND	96	0.015	
37	0.0055	ND	97	0.013	
38	0.052		98	1.0	ND
40	0.030	ND	99	0.0080	Outlier,ND
42	0.028	ND	100	0.0092	
43	0.089	Outlier,ND	101	0.24	Outlier
45	0.030		102	0.025	ND
46	0.013		103	0.21	Outlier
47	0.043	ND			
49	0.15	Outlier			
50	10	Outlier,ND			
51	0.036				
52	0.051	ND			
53	0.0085				
55	0.021				
56	0.030	ND			
57	0.020				

Consensus statistics

Consensus median, pg/g	0.020
Median all values pg/g	0.030
Consensus mean, pg/g	0.023
Standard deviation, pg/g	0.014
Relative standard deviation, %	61
No. of values reported	81
No. of values removed	25
No. of reported non-detects	34



Herring

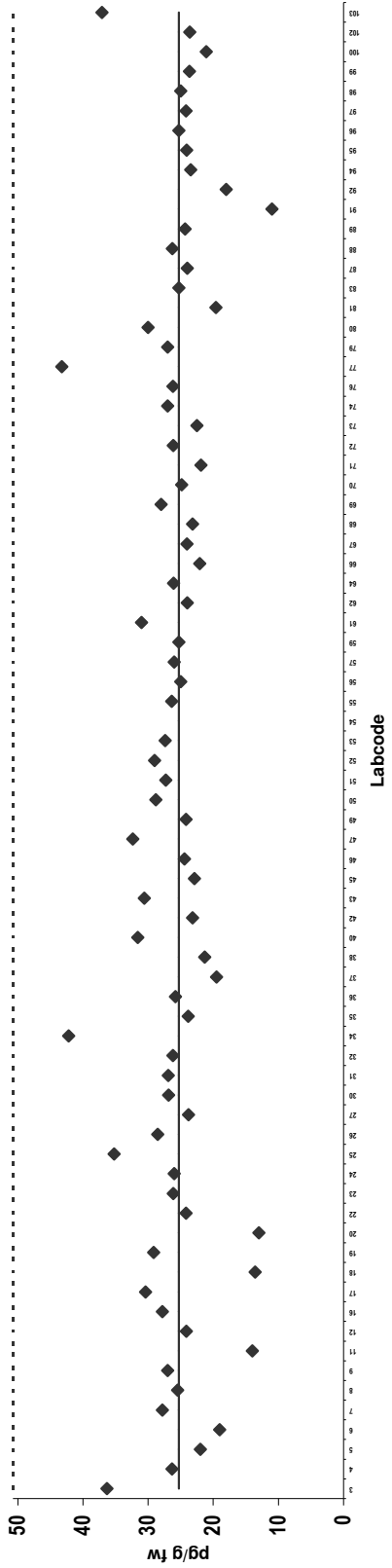
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	36		62	24	
4	26		64	26	
5	22		66	22	
6	19		67	24	
7	28		68	23	
8	25		69	28	
9	27		70	25	
11	14		71	22	
12	24		72	26	
16	28		73	23	
17	30		74	27	
18	14		76	26	
19	29		77	43	
20	13		79	27	
22	24		80	30	
23	26		81	20	
24	26		83	25	
25	35		87	24	
26	29		88	26	
27	24		89	24	
30	27		91	11	
31	27		92	18	
32	26		94	23	
34	42		95	24	
35	24		96	25	
36	26		97	24	
37	19		98	24	
38	21		99	24	
40	32		100	21	
42	23		102	24	
43	31		103	37	
45	23				
46	24				
47	32				
49	24				
50	29				
51	27				
52	29				
53	27				
54	87	Outlier			
55	26				
56	25				
57	26				
59	25				
61	31				

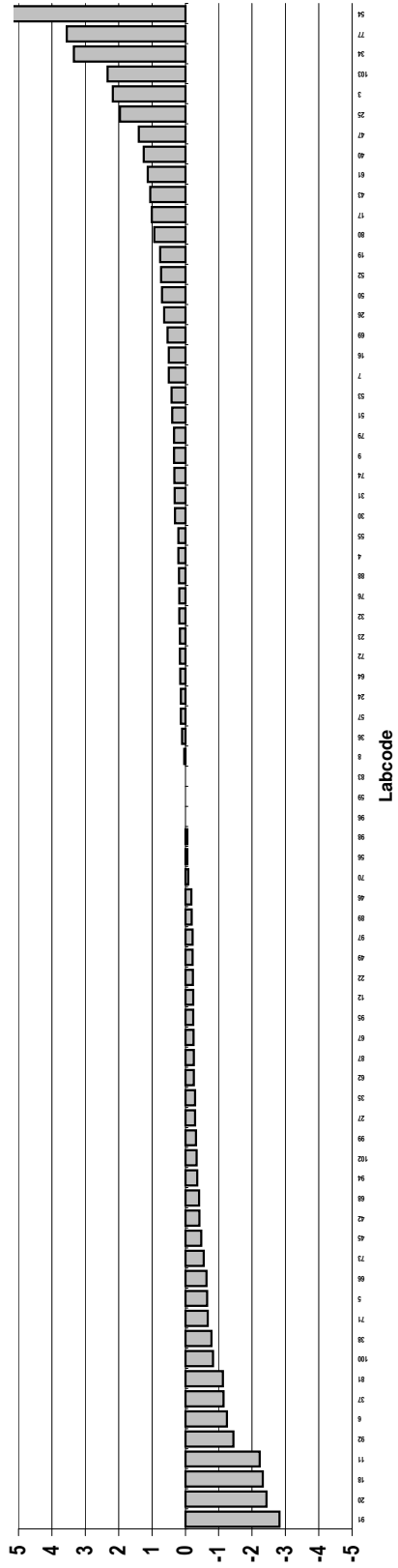
Consensus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	26
Standard deviation, pg/g	5.4
Relative standard deviation, %	21
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 77



Z-score: PCB 77



Herring

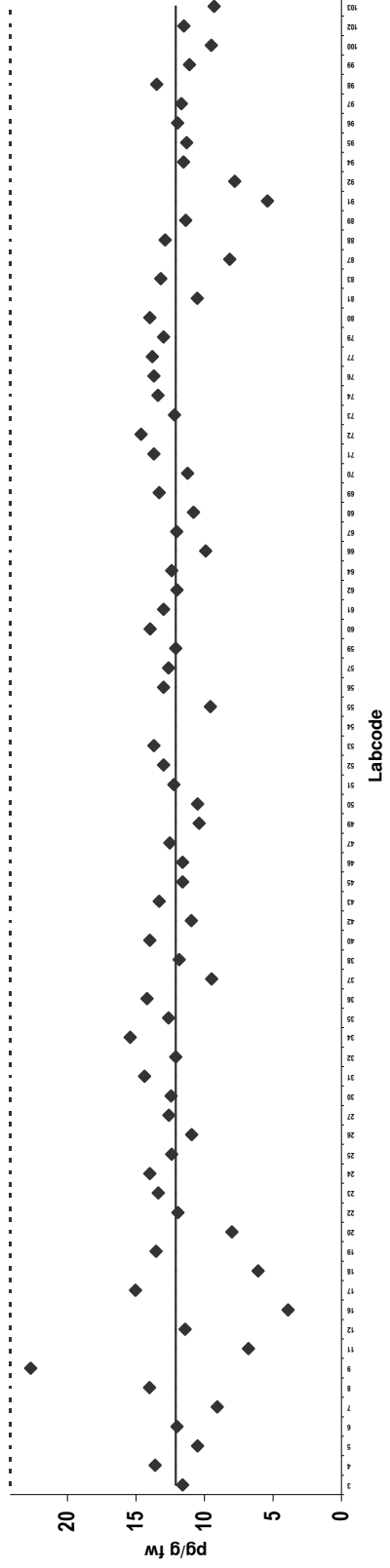
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	12		61	13	
4	14		62	12	
5	11		64	12	
6	12		66	9.9	
7	9.1		67	12	
8	14		68	11	
9	23		69	13	
11	6.8		70	11	
12	11		71	14	
16	3.9		72	15	
17	15		73	12	
18	6.1		74	13	
19	14		76	14	
20	8.0		77	14	
22	12		79	13	
23	13		80	14	
24	14		81	11	
25	12		83	13	
26	11		87	8.2	
27	13		88	13	
30	12		89	11	
31	14		91	5.4	
32	12		92	7.8	
34	15		94	12	
35	13		95	11	
36	14		96	12	
37	9.5		97	12	
38	12		98	14	
40	14		99	11	
42	11		100	9.5	
43	13		102	12	
45	12		103	9.3	
46	12				
47	13				
49	10				
50	10				
51	12				
52	13				
53	14				
54	42	Outlier			
55	9.6				
56	13				
57	13				
59	12				
60	14				

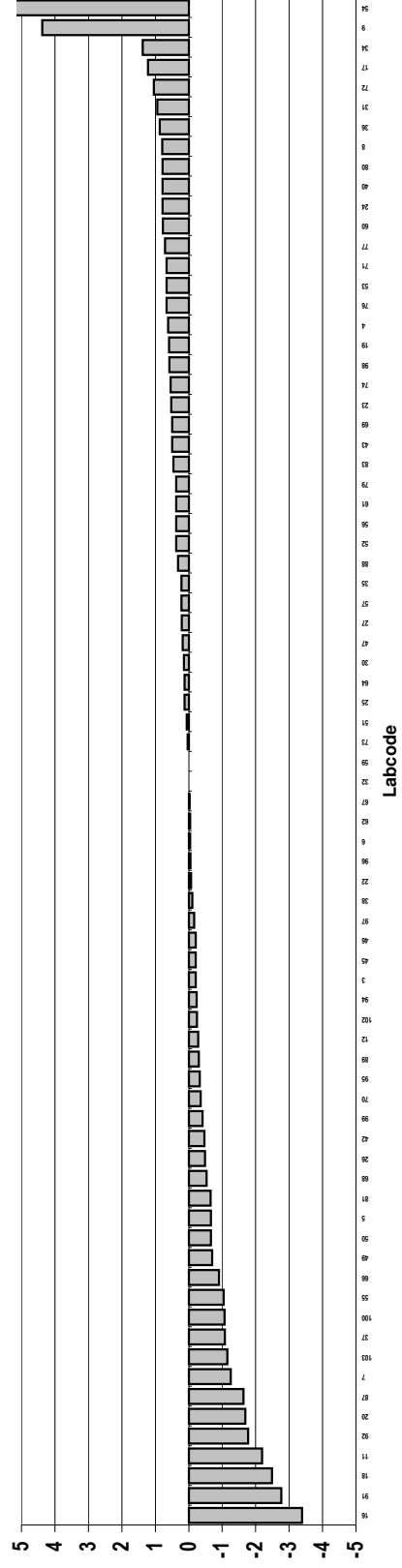
Consensus statistics

Consensus median, pg/g	12
Median all values pg/g	12
Consensus mean, pg/g	12
Standard deviation, pg/g	2.5
Relative standard deviation, %	21
No. of values reported	77
No. of values removed	1
No. of reported non-detects	0

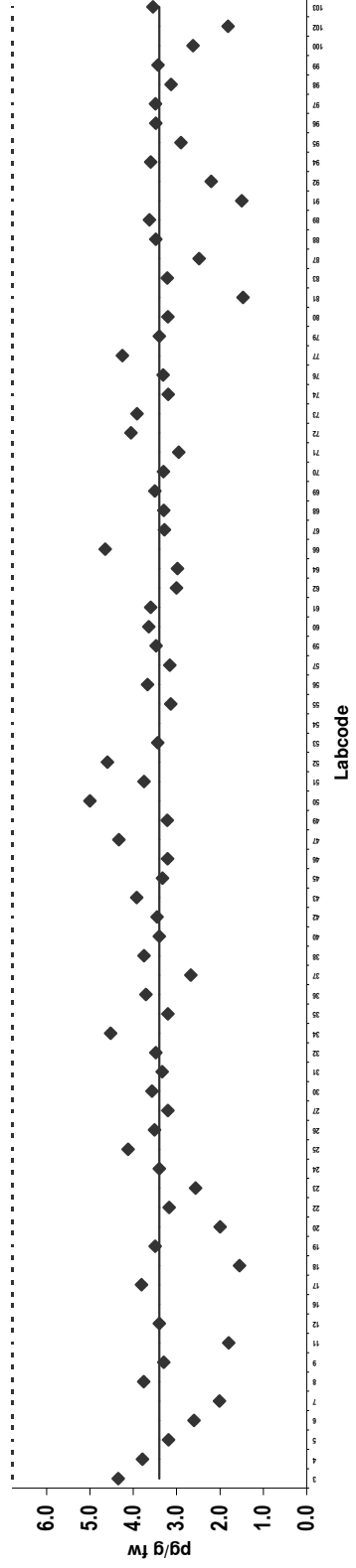
PCB 126



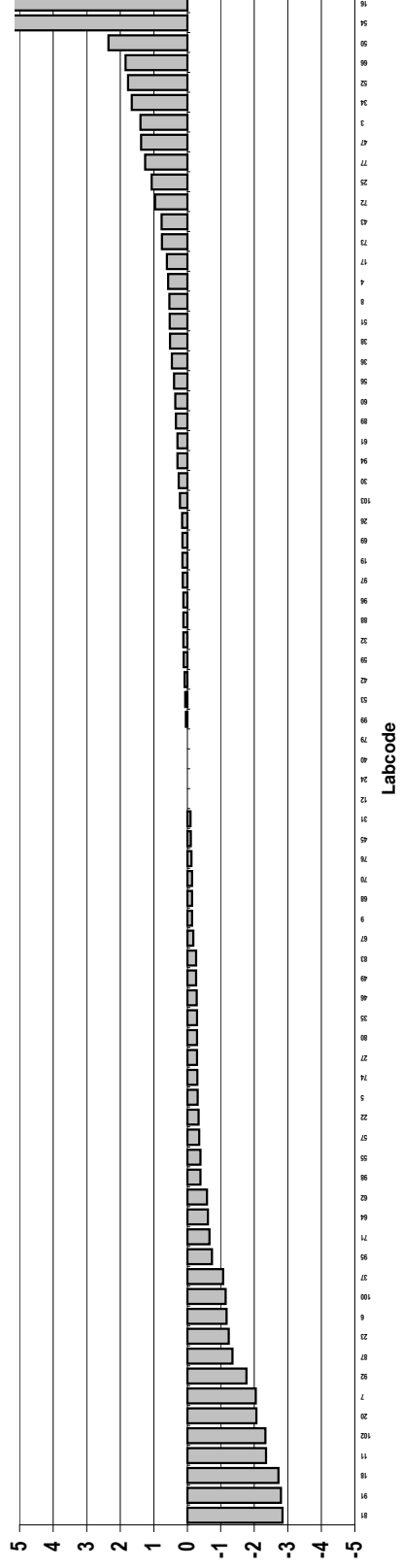
Z-score: PCB 126



PCB 169



Z-score: PCB 169



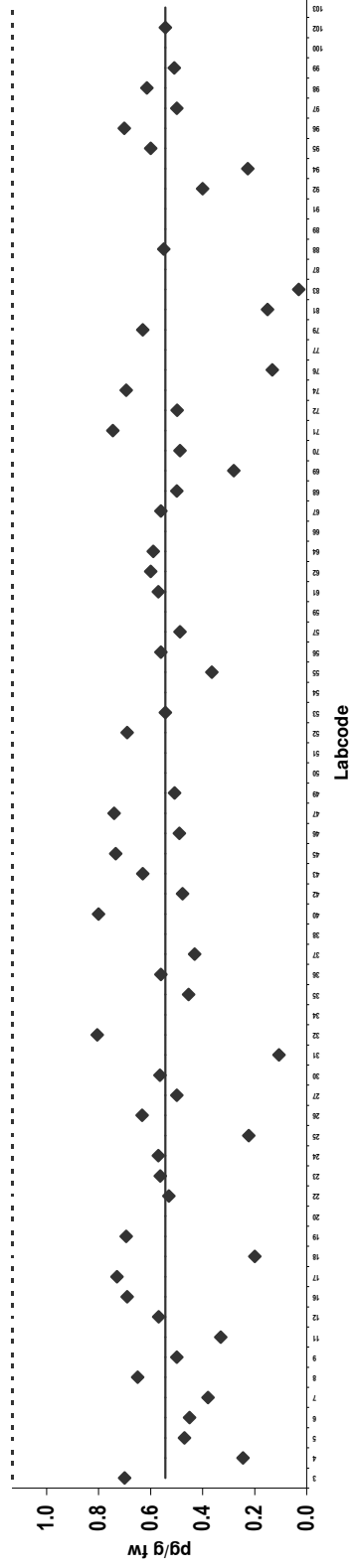
Herring Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.70		62	0.60	
4	0.25		64	0.59	Outlier
5	0.47		66	1.4	
6	0.45	ND	67	0.56	
7	0.38		68	0.50	
8	0.65		69	0.28	
9	0.50	ND	70	0.49	
11	0.33		71	0.75	
12	0.57		72	0.50	ND
16	0.69		74	0.69	
17	0.73		76	0.13	
18	0.20		77	1.7	Outlier
19	0.69		79	0.63	
20	2.0		81	0.15	ND
22	0.53	Outlier,ND	83	0.030	ND
23	0.56		87	4.5	Outlier
24	0.57		88	0.55	
25	0.22		89	2.4	Outlier
26	0.63		91	3.4	Outlier
27	0.50		92	0.40	
30	0.56		94	0.23	
31	0.11		95	0.60	
32	0.81		96	0.70	
34	28		97	0.50	
35	0.45	Outlier	98	0.62	
36	0.56		99	0.51	
37	0.43		100	2.0	Outlier,ND
38	5.6		102	0.54	
40	0.80		103	1.2	Outlier
42	0.48				
43	0.63				
45	0.74				
46	0.49				
47	0.74				
49	0.51	ND			
50	5.0	Outlier,ND			
51	3.8	Outlier			
52	0.69				
53	0.54				
54	3.4	Outlier			
55	0.36				
56	0.56				
57	0.49				
59	1.6	Outlier,ND			
61	0.57				

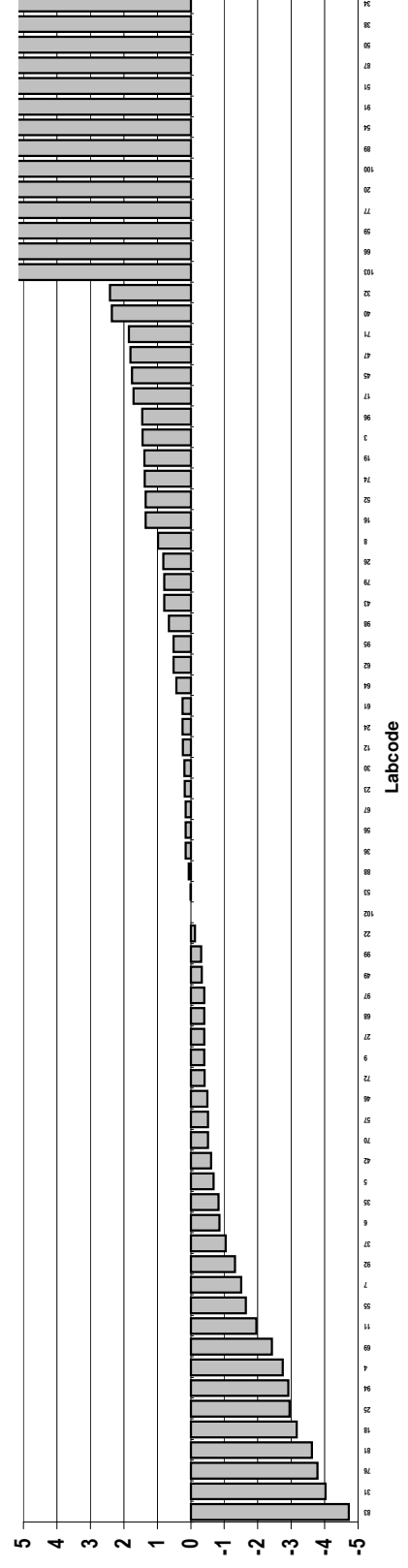
Consensus statistics

Consensus median, pg/g	0.54
Median all values pg/g	0.57
Consensus mean, pg/g	0.51
Standard deviation, pg/g	0.18
Relative standard deviation, %	35
No. of values reported	74
No. of values removed	14
No. of reported non-detects	13

PCB 81



Z-score: PCB 81



Herring

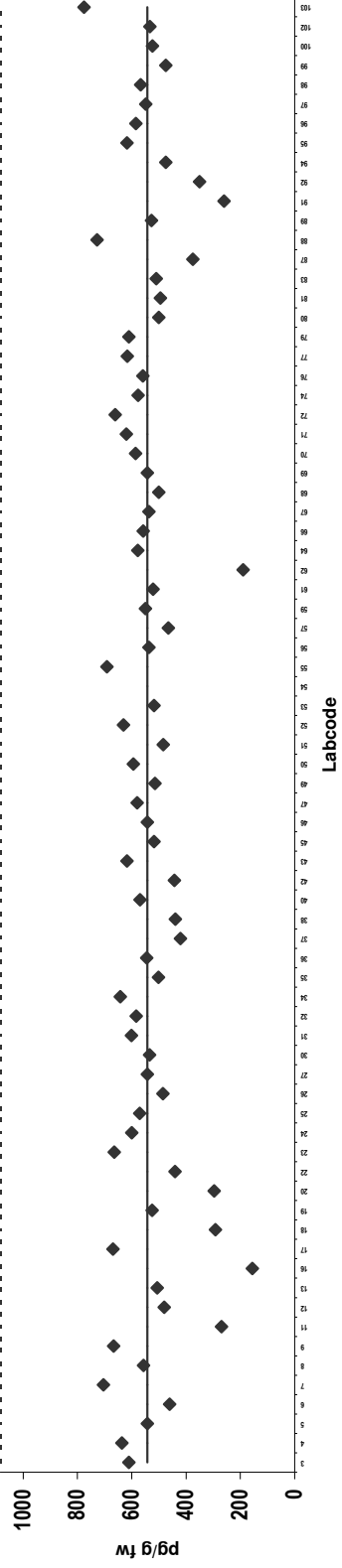
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	610		61	521	
4	637		62	190	
5	542		64	577	
6	460		66	558	
7	704		67	536	
8	556		68	500	
9	667		69	543	
11	270		70	586	
12	480		71	620	
13	506		72	661	
16	155		74	577	
17	669		76	559	
18	292		77	616	
19	525		79	610	
20	297		80	500	
22	440		81	495	
23	664		83	510	
24	600		87	375	
25	571		88	727	
26	485		89	527	
27	542		91	260	
30	534		92	350	
31	601		94	475	
32	583		95	617	
34	642		96	584	
35	501		97	548	
36	545		98	567	
37	421		99	475	
38	439		100	524	
40	569		102	533	
42	443		103	775	
43	618				
45	518				
46	543				
47	580				
49	514				
50	594				
51	484				
52	630				
53	518				
54	1810	Outlier			
55	691				
56	537				
57	465				
59	550				

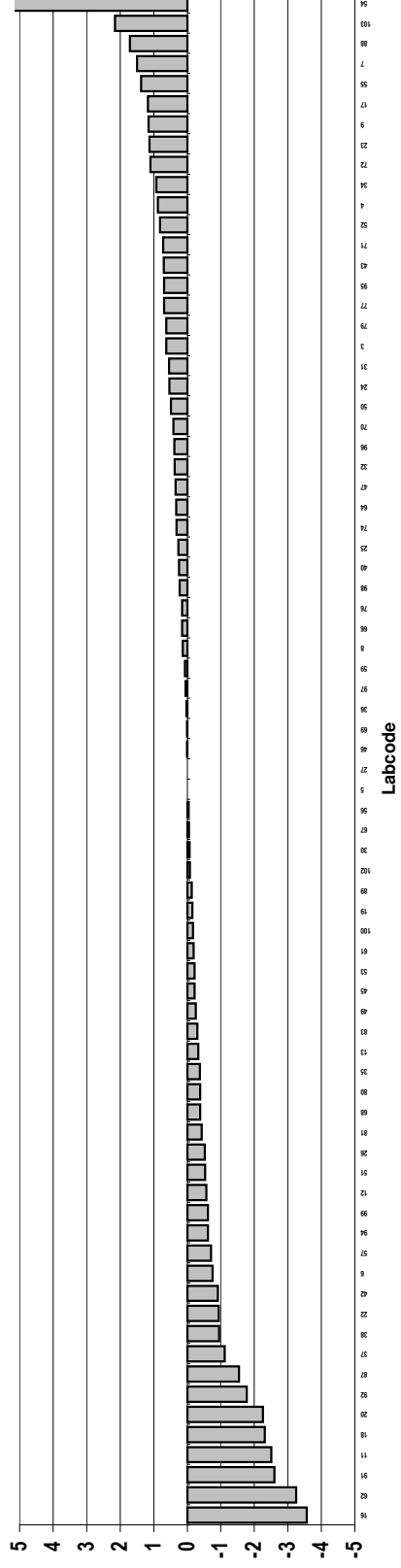
Consensus statistics

Consensus median, pg/g	542
Median all values pg/g	543
Consensus mean, pg/g	529
Standard deviation, pg/g	115
Relative standard deviation, %	22
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 105



Z-score: PCB 105



Herring

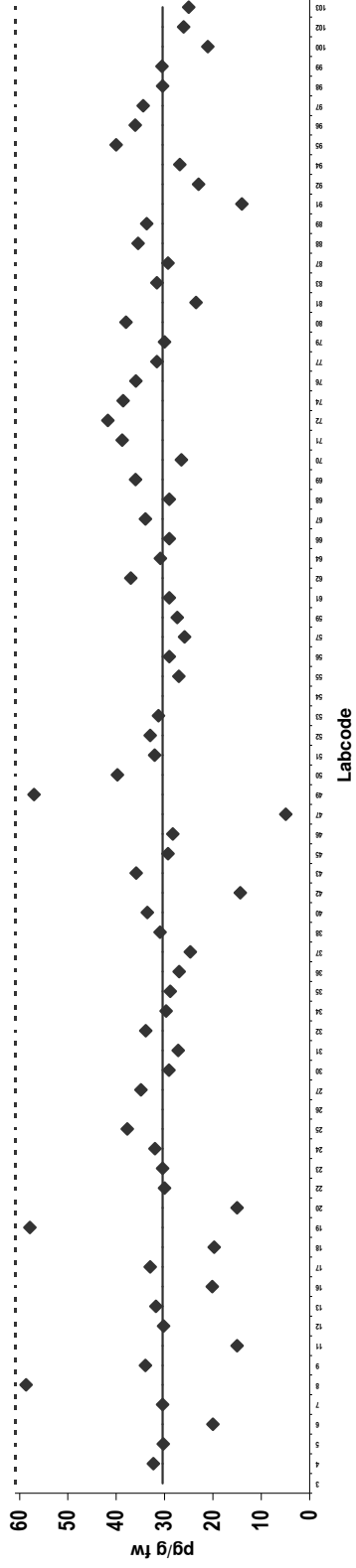
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	69		61	29	
4	32		62	37	
5	30		64	31	
6	20		66	29	
7	30		67	34	
8	59		68	29	
9	34		69	36	
11	15		70	27	
12	30		71	39	
13	32		72	42	
16	20		74	39	
17	33		76	36	
18	20		77	32	
19	58		79	30	
20	15		80	38	
22	30		81	23	
23	30		83	32	
24	32		87	29	
25	38		88	35	
26	77		89	34	
27	35		91	14	
30	29		92	23	
31	27		94	27	
32	34		95	40	
34	30		96	36	
35	29		97	34	
36	27		98	30	
37	25		99	31	
38	31		100	21	
40	34		102	26	
42	14		103	25	
43	36				
45	29				
46	28				
47	5.0				
49	57				
50	40				
51	32				
52	33				
53	31				
54	87				
55	27				
56	29				
57	26				
59	27				

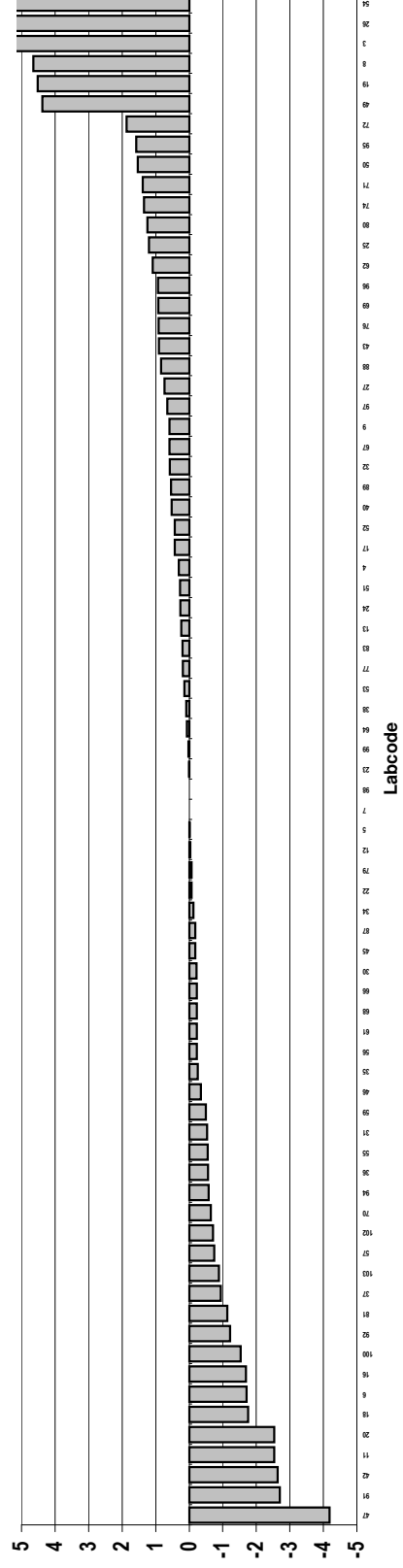
Consensus statistics

Consensus median, pg/g	30
Median all values pg/g	30
Consensus mean, pg/g	31
Standard deviation, pg/g	8.7
Relative standard deviation, %	28
No. of values reported	76
No. of values removed	3
No. of reported non-detects	1

PCB 114



Z-score: PCB 114



Herring

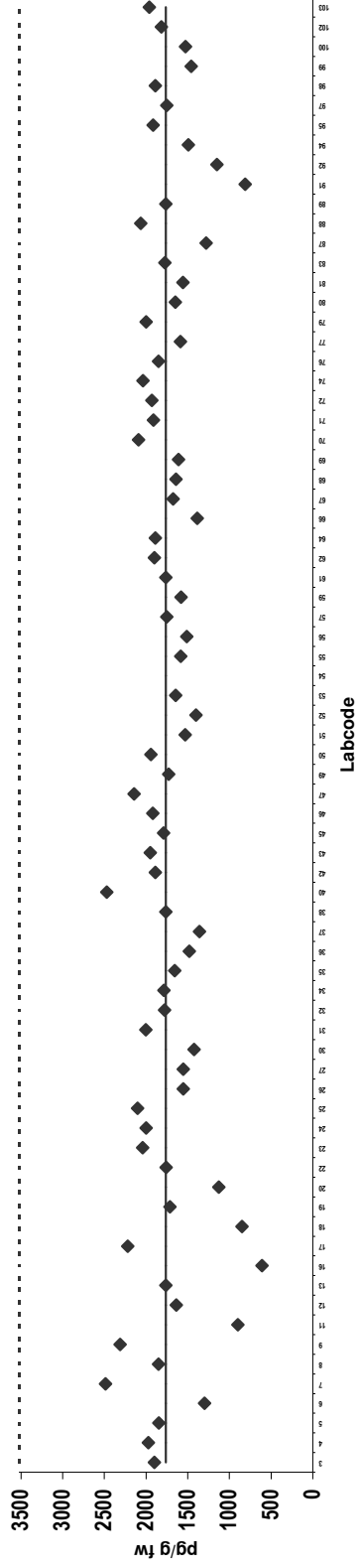
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	1901		61	1763	
4	1972		62	1900	
5	1845		64	1889	
6	1300		66	1384	
7	2485		67	1677	
8	1851		68	1640	
9	2309		69	1610	
11	900		70	2090	
12	1636		71	1910	
13	1763		72	1931	
16	611		74	2037	
17	2220		76	1852	
18	850		77	1587	
19	1712		79	2000	
20	1127		80	1650	
22	1760		81	1558	
23	2039		83	1773	
24	2000		87	1280	
25	2100		88	2065	
26	1554		89	1763	
27	1553		91	810	
30	1424		92	1150	
31	2003		94	1494	
32	1779		95	1916	
34	1785		97	1750	
35	1656		98	1890	
36	1480		99	1458	
37	1360		100	1526	
38	1762		102	1815	
40	2471		103	1962	
42	1888				
43	1950				
45	1790				
46	1920				
47	2145				
49	1730				
50	1942				
51	1529				
52	1400				
53	1645				
54	5300	Outlier			
55	1586				
56	1510				
57	1753				
59	1580				

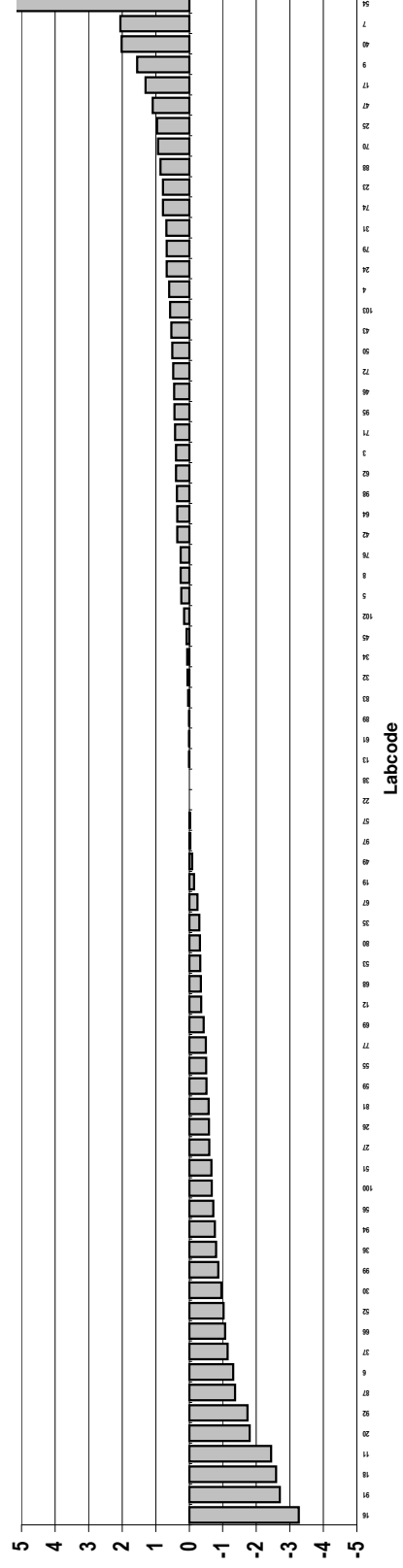
Consensus statistics

Consensus median, pg/g	1762
Median all values pg/g	1763
Consensus mean, pg/g	1712
Standard deviation, pg/g	348
Relative standard deviation, %	20
No. of values reported	75
No. of values removed	1
No. of reported non-detects	0

PCB 118



Z-score: PCB 118



Herring

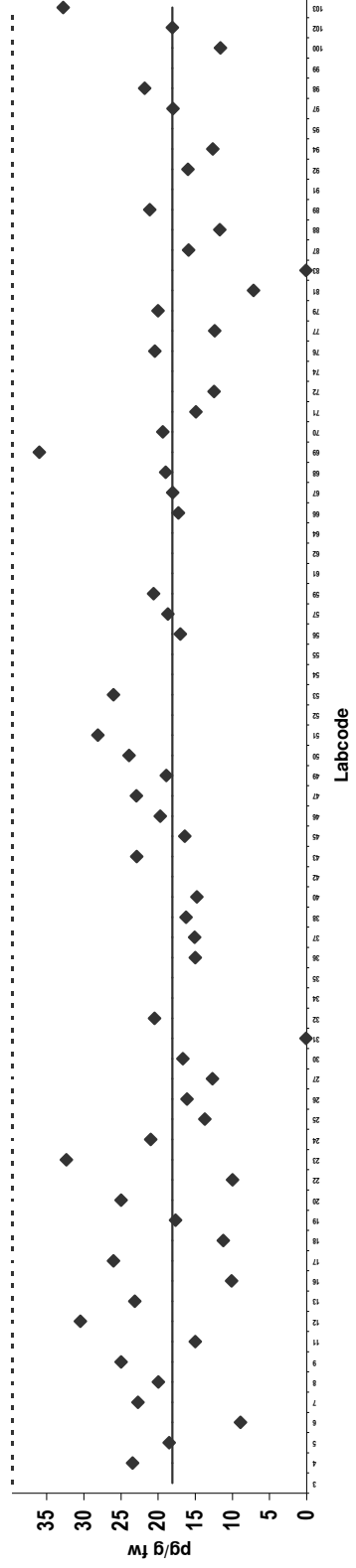
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	46		61	126	Outlier
4	23	Outlier	62	70	Outlier
5	19		64	56	Outlier
6	8.9		66	17	
7	23		67	18	
8	20		68	19	
9	25		69	36	
11	15		70	19	
12	30		71	15	
13	23		72	12	
16	10		74	78	Outlier
17	26		76	20	
18	11		77	12	
19	18		79	20	
20	25		81	7.2	
22	10		83	0.11	ND
23	32		87	16	
24	21		88	12	
25	14		89	21	
26	16		91	130	Outlier
27	13		92	16	
30	17		94	13	
31	0.10		95	105	Outlier
32	21		97	18	
34	83		98	22	
35	63		99	71	
36	15		100	12	Outlier
37	15		102	18	
38	16		103	33	
40	15				
42	118				
43	23				
45	16				
46	20				
47	23				
49	19				
50	24				
51	28				
52	73				
53	26				
54	741	Outlier			
55	271	Outlier			
56	17				
57	19				
59	21				

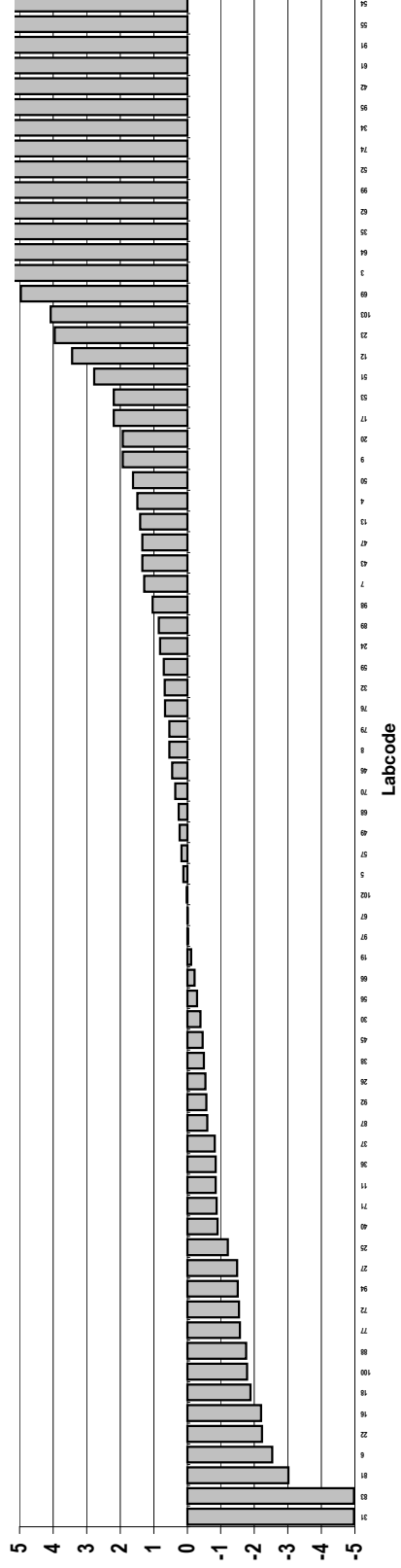
Consensus statistics

Consensus median, pg/g	18
Median all values pg/g	20
Consensus mean, pg/g	18
Standard deviation, pg/g	6.8
Relative standard deviation, %	38
No. of values reported	74
No. of values removed	14
No. of reported non-detects	2

PCB 123



Z-score: PCB 123



Herring

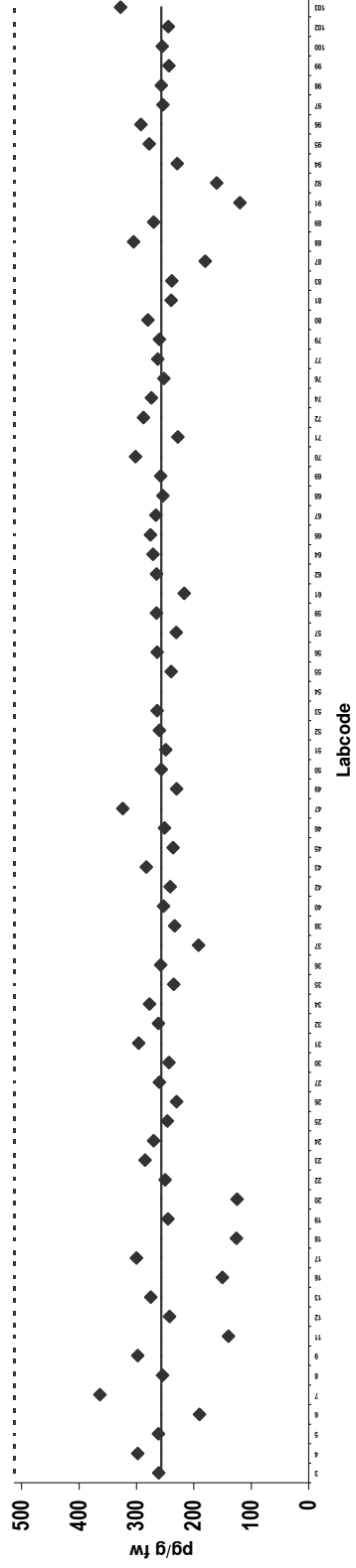
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	261		61	217	
4	298		62	265	
5	262		64	271	
6	190		66	275	
7	364		67	266	
8	255		68	254	
9	298		69	258	
11	140		70	302	
12	242		71	228	
13	275		72	288	
16	150		74	274	
17	300		76	252	
18	126		77	263	
19	245		79	260	
20	125		80	280	
22	250		81	240	
23	285		83	238	
24	270		87	180	
25	246		88	305	
26	230		89	270	
27	260		91	120	
30	244		92	160	
31	296		94	229	
32	262		95	278	
34	277		96	292	
35	235		97	254	
36	258		98	257	
37	192		99	244	
38	234		100	255	
40	253		102	244	
42	241		103	328	
43	283				
45	236				
46	251				
47	324				
49	230				
50	257				
51	249				
52	260				
53	264				
54	745	Outlier			
55	240				
56	264				
57	230				
59	265				

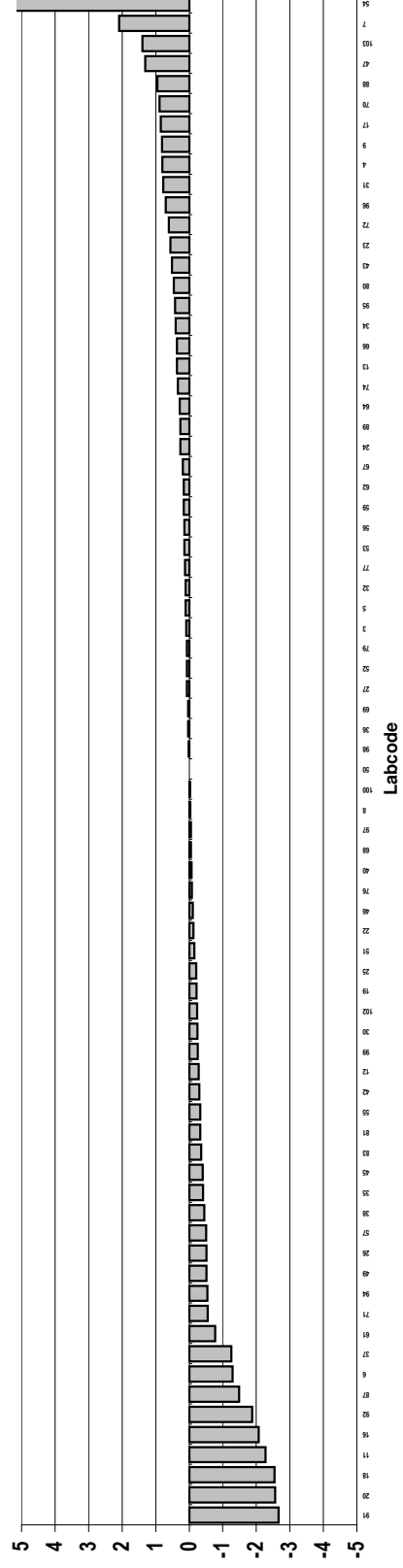
Consensus statistics

Consensus median, pg/g	257
Median all values pg/g	257
Consensus mean, pg/g	250
Standard deviation, pg/g	45
Relative standard deviation, %	18
No. of values reported	76
No. of values removed	1
No. of reported non-detects	0

PCB 156



Z-score: PCB 156



Herring

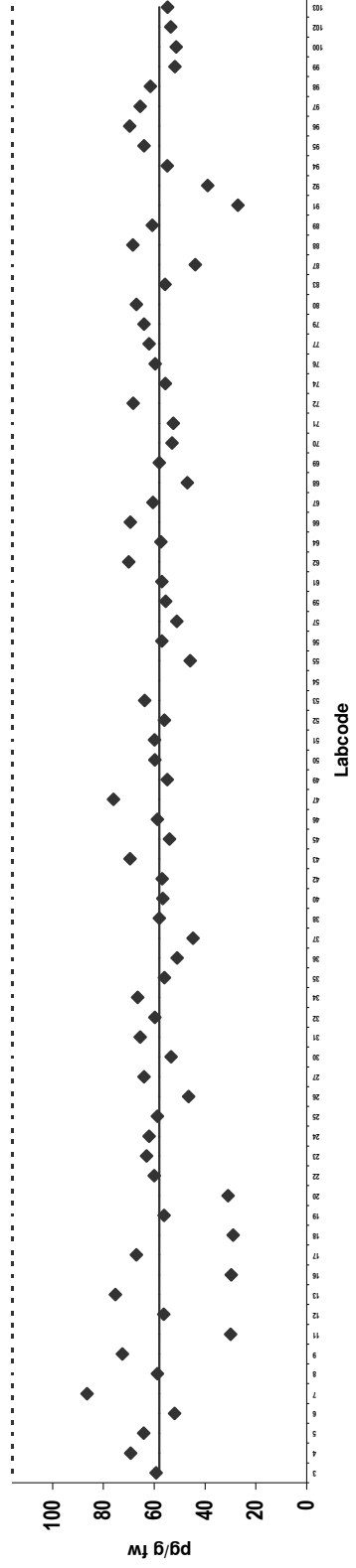
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	59		61	57	
4	69		62	70	
5	64		64	57	
6	52		66	69	
7	86		67	60	
8	59		68	47	
9	73		69	58	
11	30		70	53	
12	56		71	53	
13	75		72	68	
16	30		74	56	
17	67		76	60	
18	29		77	62	
19	56		79	64	
20	31		80	67	
22	60		83	56	
23	63		87	44	
24	62		88	68	
25	59		89	61	
26	47		91	27	
27	64		92	39	
30	53		94	55	
31	65		95	64	
32	60		96	70	
34	66		97	66	
35	56		98	62	
36	51		99	52	
37	45		100	51	
38	58		102	54	
40	57		103	55	
42	57				
43	70				
45	54				
46	59				
47	76				
49	55				
50	60				
51	60				
52	56				
53	64				
54	175				
55	46				
56	57				
57	51				
59	56				

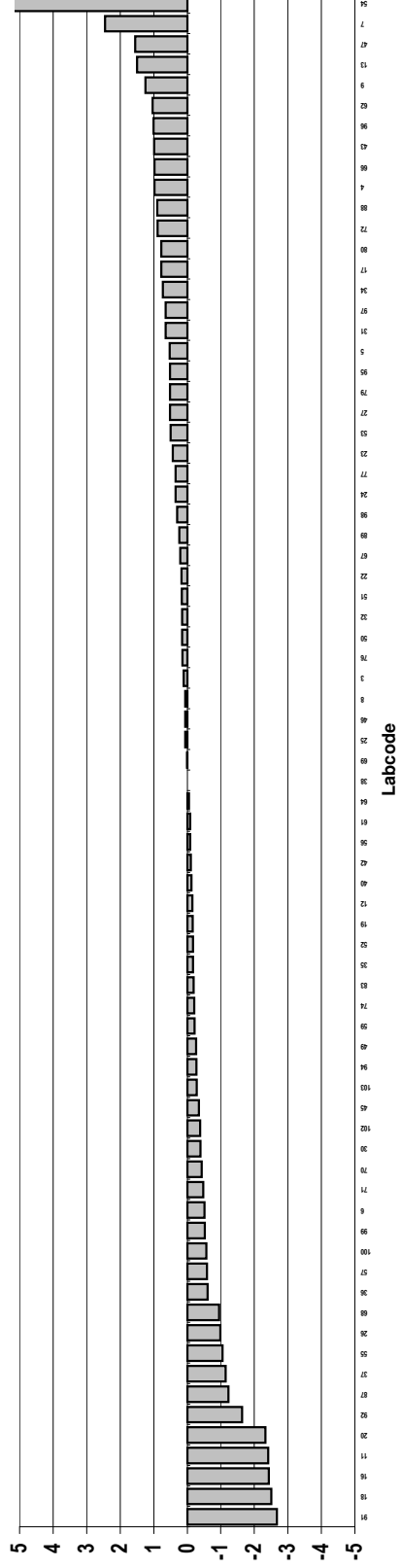
Consensus statistics

Consensus median, pg/g	58
Median all values pg/g	58
Consensus mean, pg/g	57
Standard deviation, pg/g	11
Relative standard deviation, %	19
No. of values reported	75
No. of values removed	1
No. of reported non-detects	0

PCB 157



Z-score: PCB 157



Herring

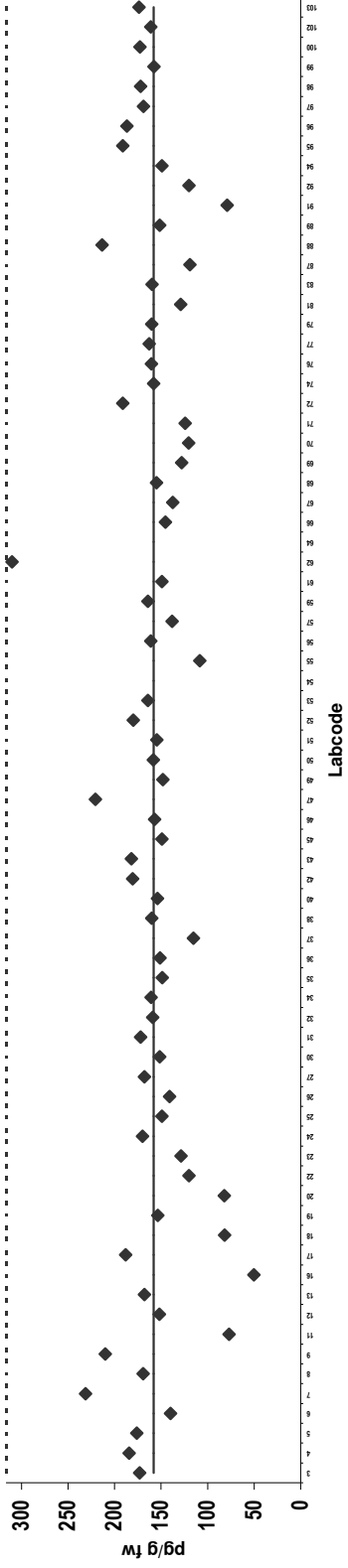
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	173		61	149	
4	184		62	310	
5	176		64	417	Outlier
6	140		66	145	
7	231		67	138	
8	169		68	155	
9	210		69	128	
11	77		70	120	
12	152		71	124	
13	168		72	191	
16	50		74	158	
17	188		76	160	
18	82		77	163	
19	153		79	160	
20	82		81	129	
22	120		83	160	
23	129		87	119	
24	170		88	213	
25	149		89	151	
26	141		91	79	
27	168		92	120	
30	152		94	149	
31	172		95	191	
32	159		96	187	
34	161		97	169	
35	149		98	172	
36	151		99	158	
37	115		100	173	
38	160		102	161	
40	154		103	174	
42	181				
43	182				
45	149				
46	157				
47	220				
49	148				
50	158				
51	154				
52	180				
53	164				
54	523	Outlier			
55	109				
56	161				
57	138				
59	164				

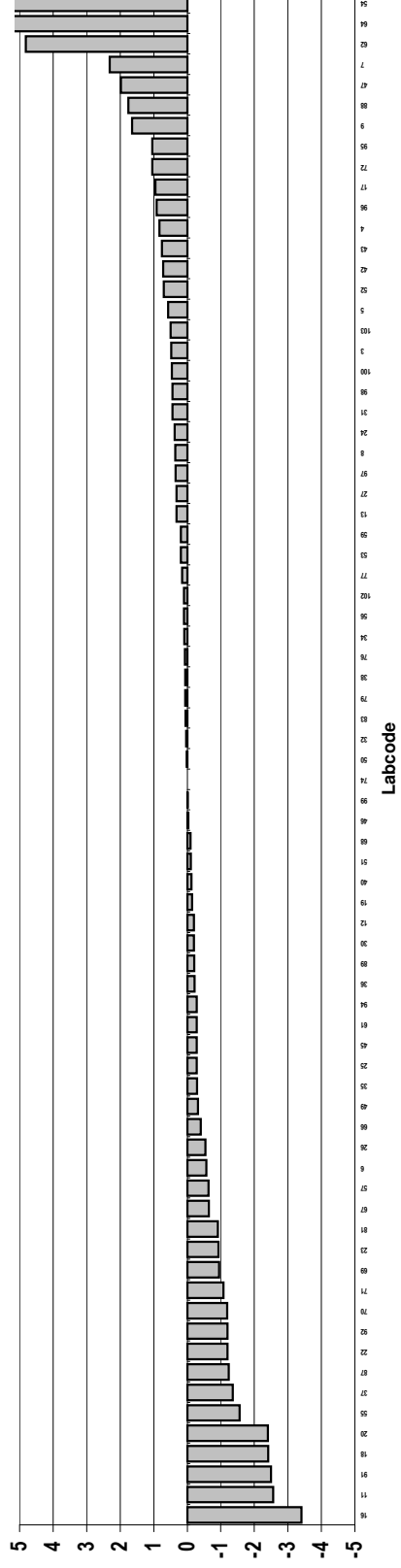
Consensus statistics

Consensus median, pg/g	158
Median all values pg/g	158
Consensus mean, pg/g	156
Standard deviation, pg/g	37
Relative standard deviation, %	24
No. of values reported	75
No. of values removed	2
No. of reported non-detects	0

PCB 167



Z-score: PCB 167



Herring

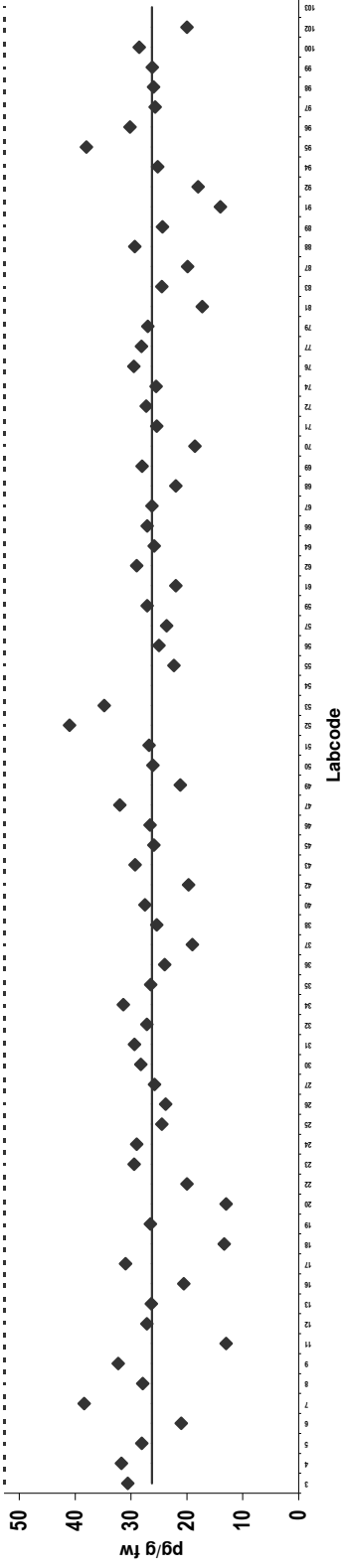
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	31		61	22	
4	32		62	29	
5	28		64	26	
6	21		66	27	
7	38		67	26	
8	28		68	22	
9	32		69	28	
11	13		70	19	
12	27		71	25	
13	26		72	27	
16	21		74	26	
17	31		76	29	
18	13		77	28	
19	27		79	27	
20	13		81	17	
22	20		83	25	
23	29		87	20	
24	29		88	29	
25	25		89	24	
26	24		91	14	
27	26		92	18	
30	28		94	25	
31	29		95	38	
32	27		96	30	
34	31		97	26	
35	26		98	26	
36	24		99	26	
37	19		100	29	
38	25		102	20	
40	28		103	65	Outlier
42	20				
43	29				
45	26				
46	27				
47	32				
49	21				
50	26				
51	27				
52	41				
53	35				
54	91				
55	22	Outlier			
56	25				
57	24				
59	27				

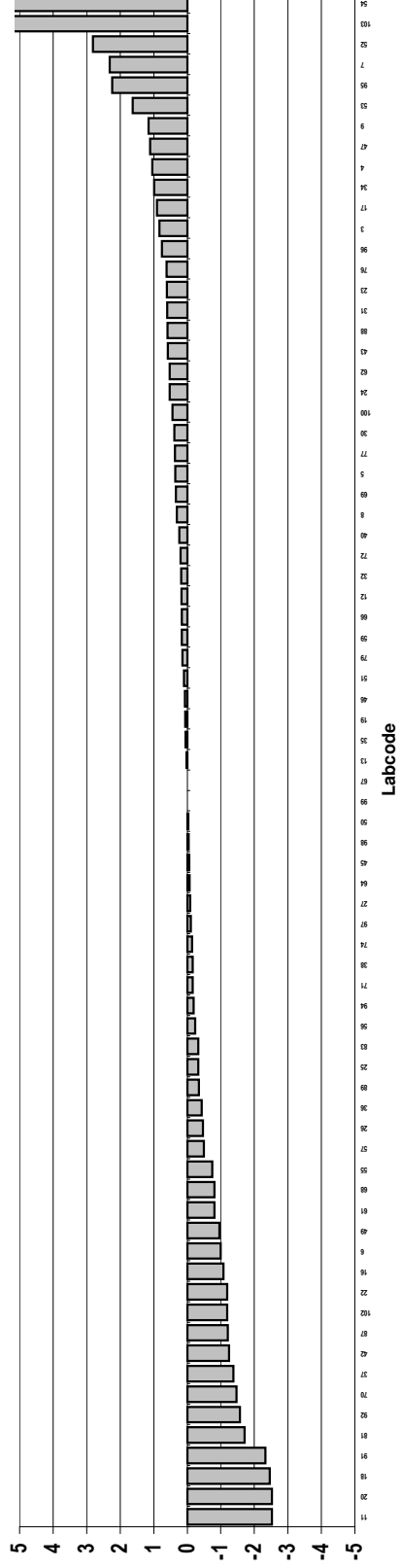
Consensus statistics

Consensus median, pg/g	26
Median all values pg/g	26
Consensus mean, pg/g	26
Standard deviation, pg/g	5.4
Relative standard deviation, %	21
No. of values reported	75
No. of values removed	2
No. of reported non-detects	0

PCB 189



Z-score: PCB 189



Herring

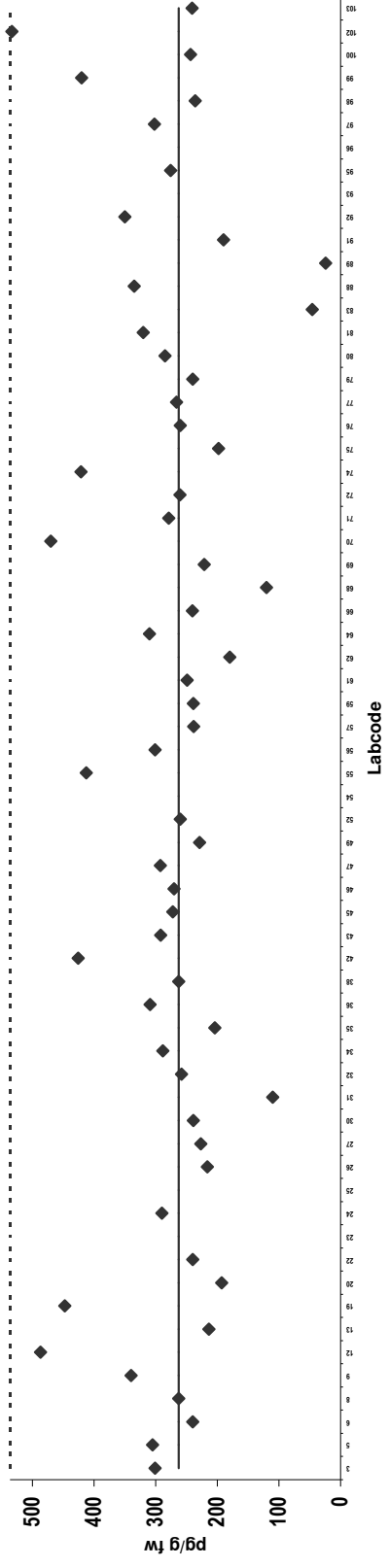
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	301		76	260	
5	305		77	266	
6	240		79	240	
8	263		80	285	
9	340		81	320	
12	487		83	46	ND
13	214		88	335	
19	448		89	24	
20	193		91	190	
22	240		92	350	
23	593	Outlier	93	1981	Outlier
24	290		95	276	
25	1170	Outlier	96	2000	Outlier,ND
26	216		97	302	
27	227		98	236	
30	239		99	420	
31	110		100	243	
32	258		102	533	
34	288		103	241	
35	204				
36	309				
38	263				
42	426				
43	292				
45	272				
46	270				
47	292				
49	229				
52	260				
54	565				
55	413				
56	301				
57	238				
59	239				
61	249				
62	180				
64	310				
66	240				
68	120				
69	221				
70	470				
71	279				
72	261				
74	421				
75	198				

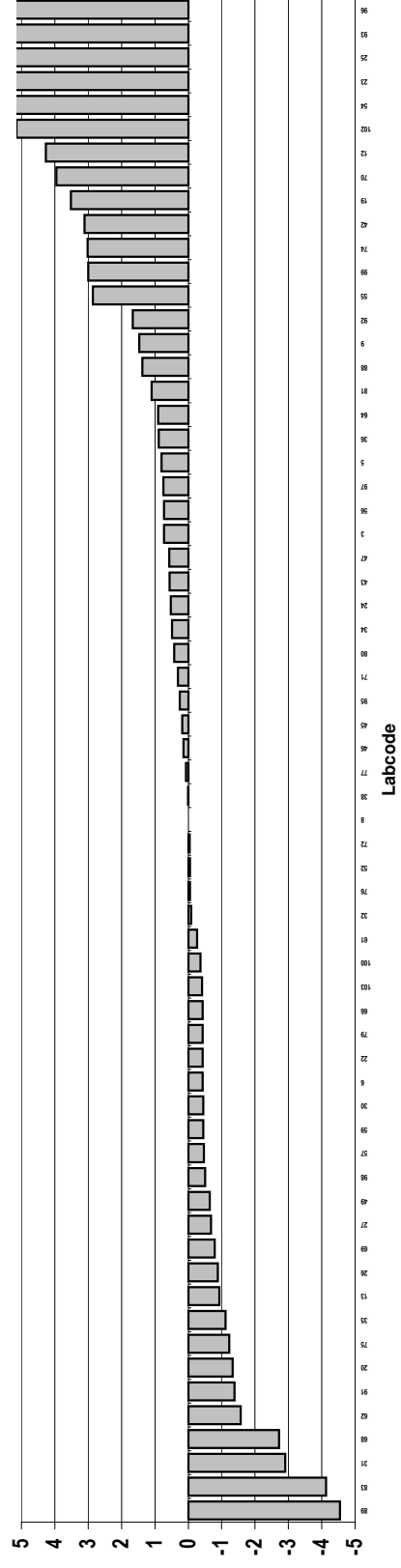
Consensus statistics

Consensus median, pg/g	263
Median all values pg/g	268
Consensus mean, pg/g	274
Standard deviation, pg/g	94
Relative standard deviation, %	34
No. of values reported	64
No. of values removed	5
No. of reported non-detects	2

CB 28



Z-score: CB 28



Herring

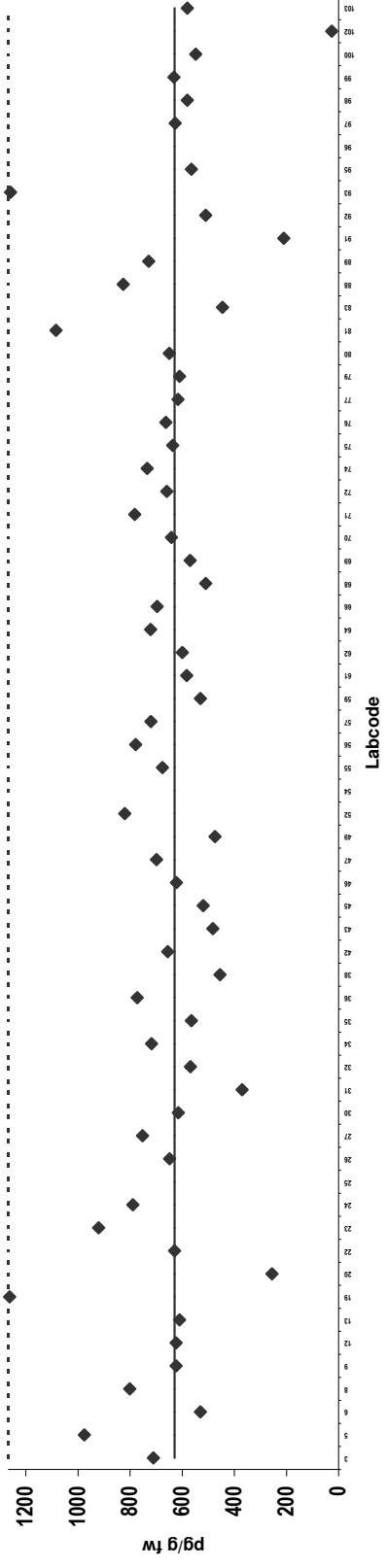
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	711		76	663	
5	976		77	617	
6	530		79	610	
8	801		80	650	
9	624		81	1085	
12	624		83	445	
13	611		88	827	
19	1263		89	729	
20	256		91	210	
22	630		92	510	
23	921		93	1259	
24	790		95	565	
25	1810		96	2000	Outlier,ND
26	649		97	627	
27	752		98	580	
30	615	Outlier	99	631	
31	370		100	549	
32	569		102	26	
34	718		103	580	
35	565				
36	773				
38	455				
42	656				
43	483				
45	520				
46	622				
47	699				
49	474				
52	820				
54	2450	Outlier			
55	676				
56	779				
57	721				
59	530				
61	583				
62	600				
64	721				
66	696				
68	510				
69	570				
70	642				
71	782				
72	660				
74	734				
75	637				

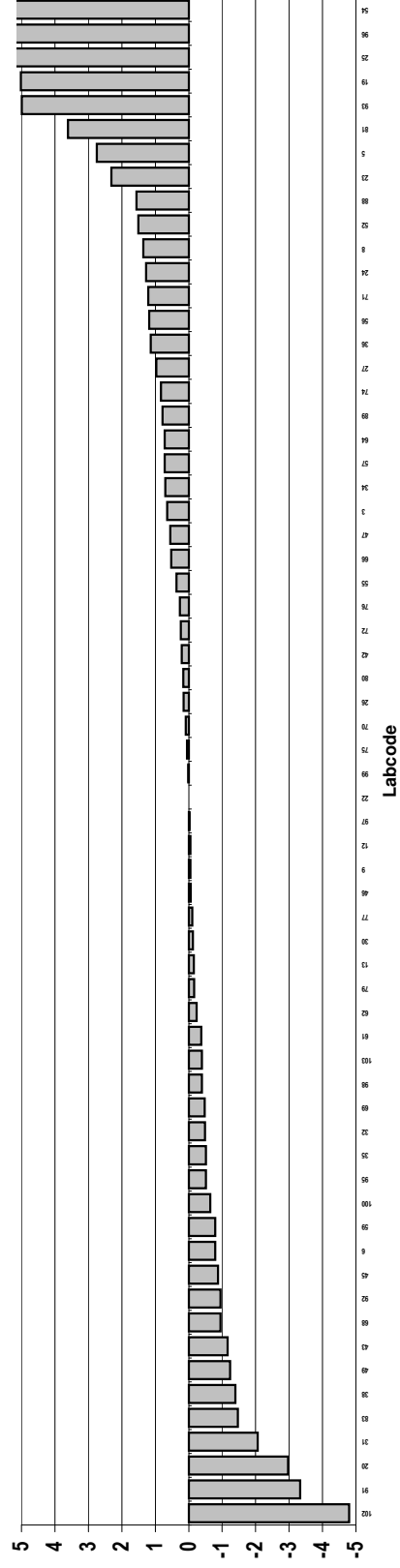
Consensus statistics

Consensus median, pg/g	630
Median all values pg/g	634
Consensus mean, pg/g	647
Standard deviation, pg/g	201
Relative standard deviation, %	31
No. of values reported	64
No. of values removed	3
No. of reported non-detects	1

CB 52



Z-score: CB 52



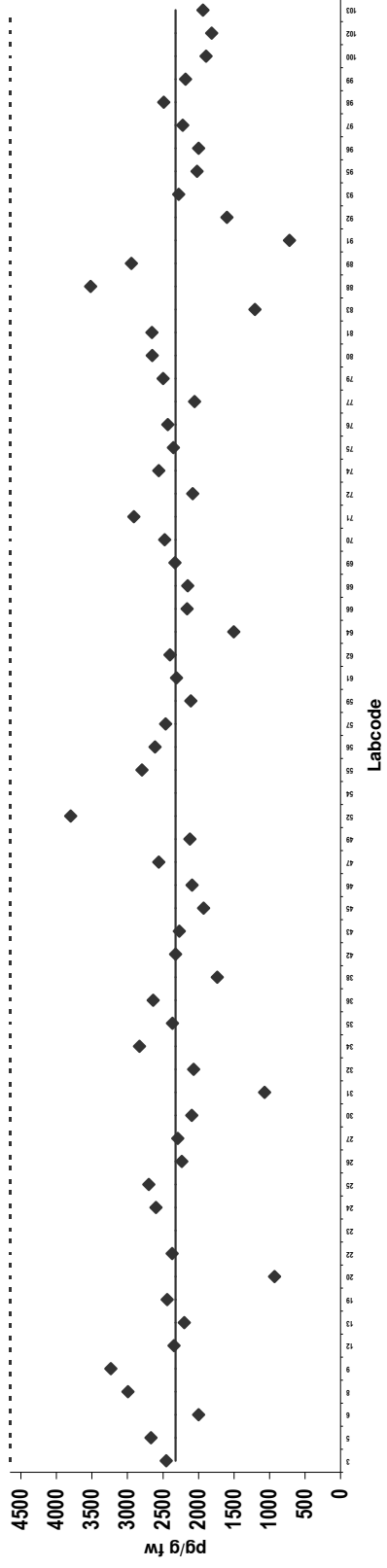
Herring
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	2434		76	2432	
5	2670		77	2054	
6	2000		79	2500	
8	2995		80	2650	
9	3234		81	2654	
12	2344		83	1206	
13	2201		88	3518	
19	2440		89	2943	
20	929		91	720	
22	2370		92	1600	
23	4735	Outlier	93	2277	
24	2600		95	2021	ND
25	2700		96	2000	
26	2237		97	2220	
27	2290		98	2490	
30	2095		99	2183	
31	1070		100	1891	
32	2068		102	1815	
34	2833		103	1935	
35	2367				
36	2640				
38	1737				
42	2324				
43	2270				
45	1930				
46	2090				
47	2558				
49	2120				
52	3800				
54	8570				
55	2797				
56	2610				
57	2461				
59	2110				
61	2309				
62	2400				
64	1501				
66	2160				
68	2150				
69	2330				
70	2475				
71	2910				
72	2080				
74	2560				
75	2352				

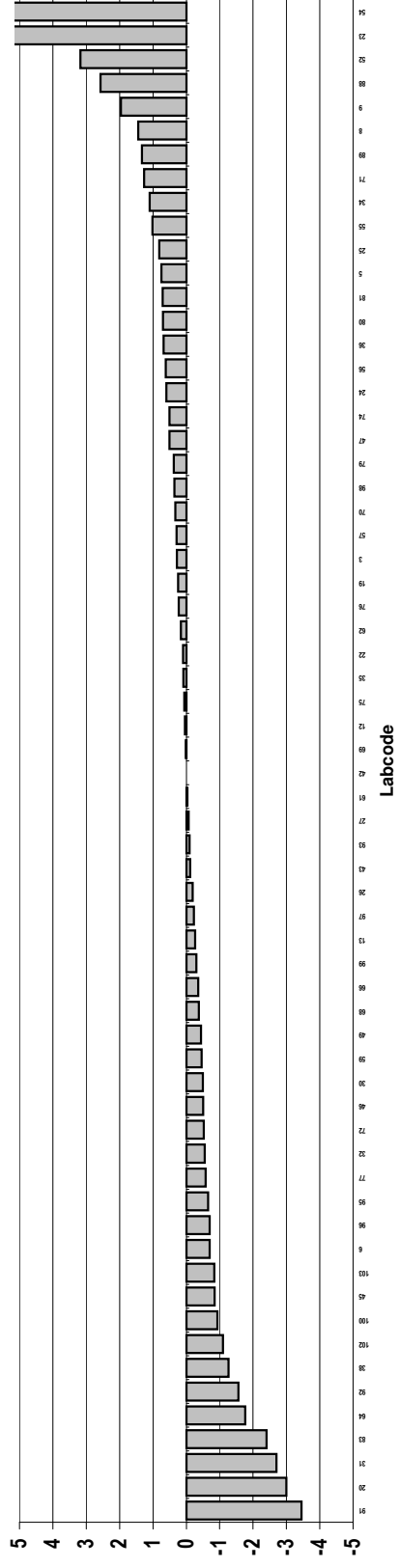
Consensus statistics

Consensus median, pg/g	2324
Median all values pg/g	2327
Consensus mean, pg/g	2285
Standard deviation, pg/g	535
Relative standard deviation, %	23
No. of values reported	64
No. of values removed	2
No. of reported non-detects	1

CB 101



Z-score: CB 101



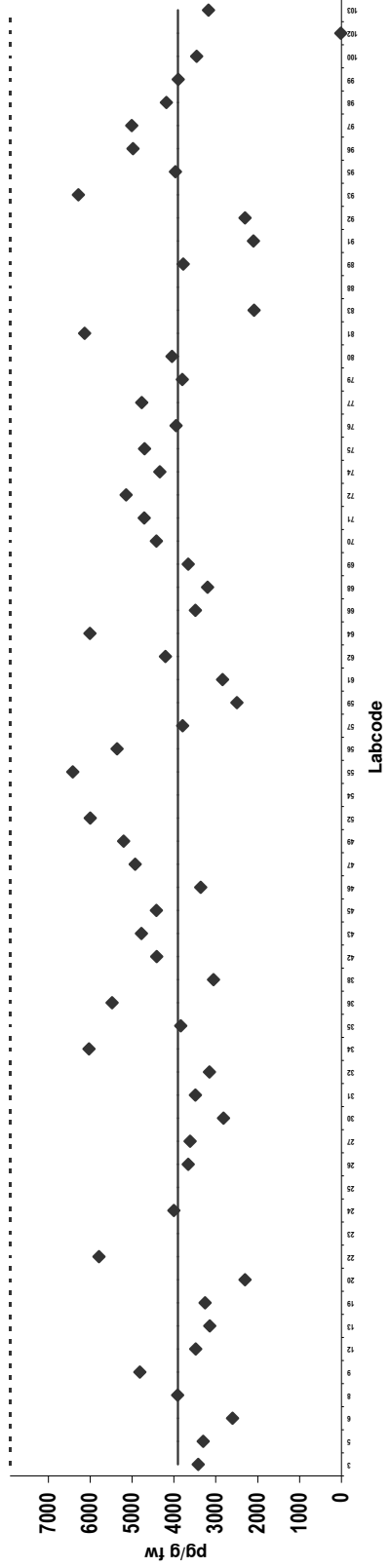
Herring Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	3422		76	3949	
5	3302		77	4768	
6	2600		79	3800	
8	3915		80	4050	
9	4815		81	6133	
12	3482		83	2090	
13	3146		88	8393	
19	3255		89	3779	
20	2304		91	2100	
22	5790		92	2300	
23	13356	Outlier	93	6283	
24	4000		95	3966	
25	9370		96	4980	
26	3660	Outlier	97	5010	
27	3616		98	4180	
30	2818		99	3899	
31	3490		100	3458	
32	3154		102	18	
34	6030		103	3173	
35	3839				
36	5480				
38	3058				
42	4413				
43	4780				
45	4420				
46	3360				
47	4929				
49	5200				
52	6000				
54	10400				
55	6419				
56	5360				
57	3794				
59	2500				
61	2842				
62	4200				
64	6007				
66	3490				
68	3200				
69	3660				
70	4419				
71	4710				
72	5139				
74	4338				
75	4704				

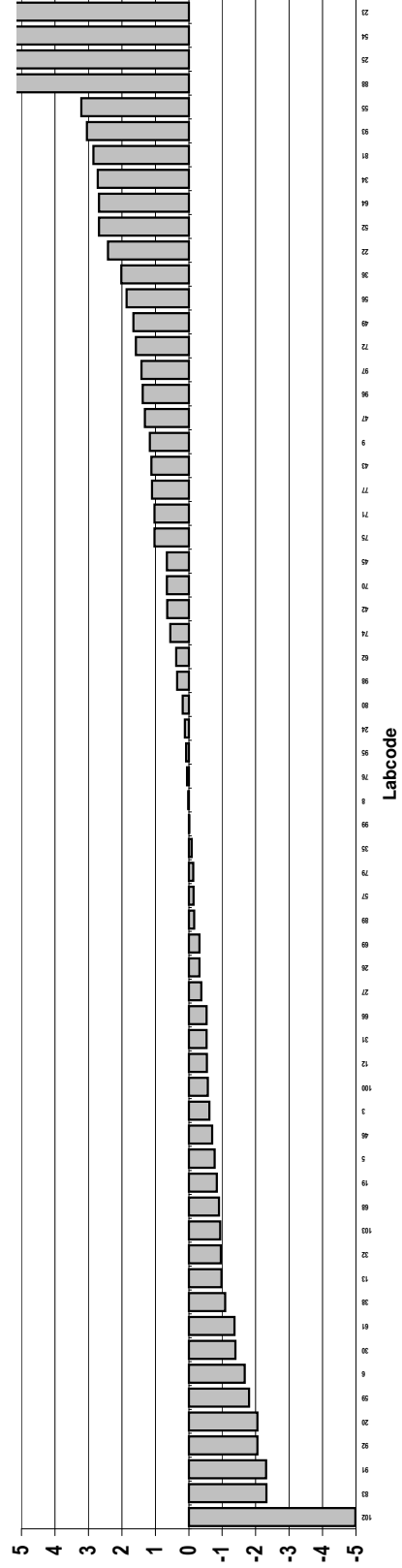
Consensus statistics

Consensus median, pg/g	3907
Median all values pg/g	3957
Consensus mean, pg/g	4017
Standard deviation, pg/g	1215
Relative standard deviation, %	30
No. of values reported	64
No. of values removed	4
No. of reported non-detects	0

CB 138



Z-score: CB 138



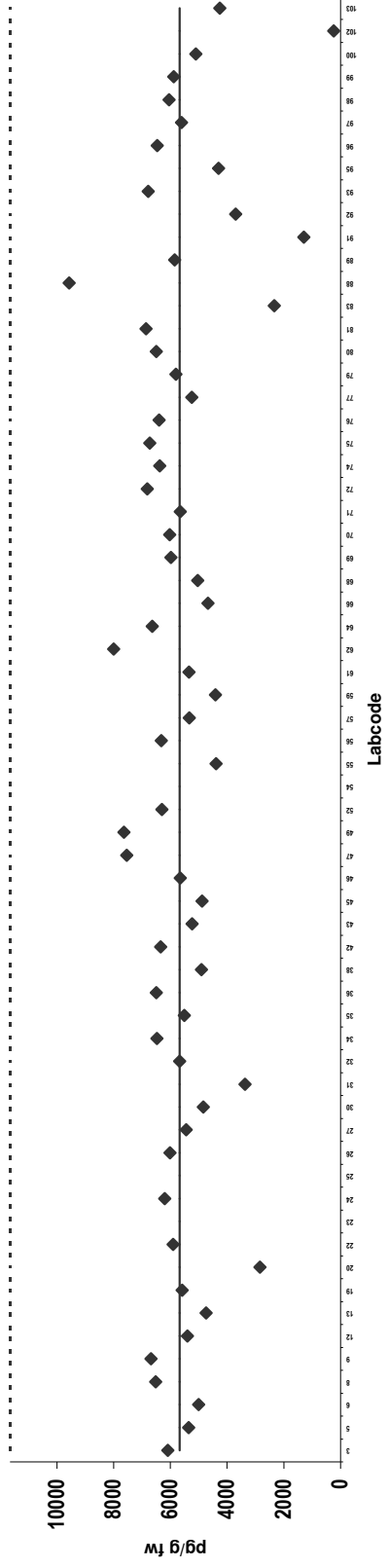
Herring Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	6093		76	6395	
5	5357		77	5244	
6	5000		79	5800	
8	6512		80	6500	
9	6678		81	6852	
12	5396		83	2333	
13	4741		88	9569	
19	5581		89	5852	
20	2847		91	1300	
22	5900		92	3700	
23	12561	Outlier	93	6786	
24	6200		95	4303	
25	15700	Outlier	96	6460	
26	6018		97	5610	
27	5441		98	6050	
30	4841		99	5878	
31	3370		100	5101	
32	5675		102	244	
34	6472		103	4260	
35	5512				
36	6490				
38	4903				
42	6337				
43	5230				
45	4880				
46	5650				
47	7532				
49	7640				
52	6300				
54	12500				
55	4386				
56	6320				
57	5332				
59	4410				
61	5347				
62	8000				
64	6639				
66	4673				
68	5040				
69	5980				
70	6019				
71	5650				
72	6816				
74	6373				
75	6725				

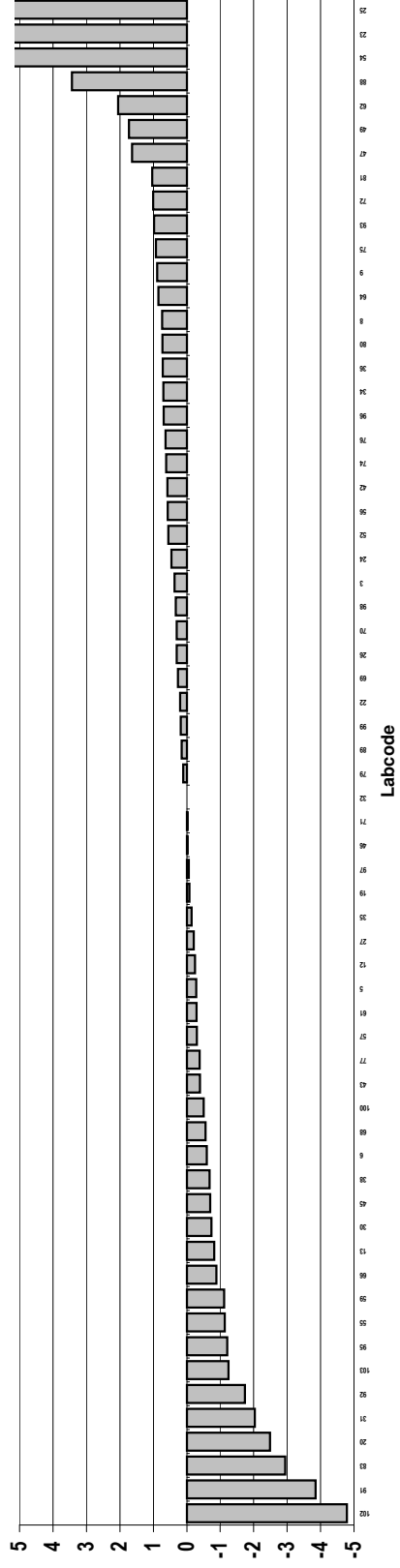
Consensus statistics

Consensus median, pg/g	5675
Median all values pg/g	5826
Consensus mean, pg/g	5550
Standard deviation, pg/g	1475
Relative standard deviation, %	27
No. of values reported	64
No. of values removed	3
No. of reported non-detects	0

CB 153



Z-score: CB 153



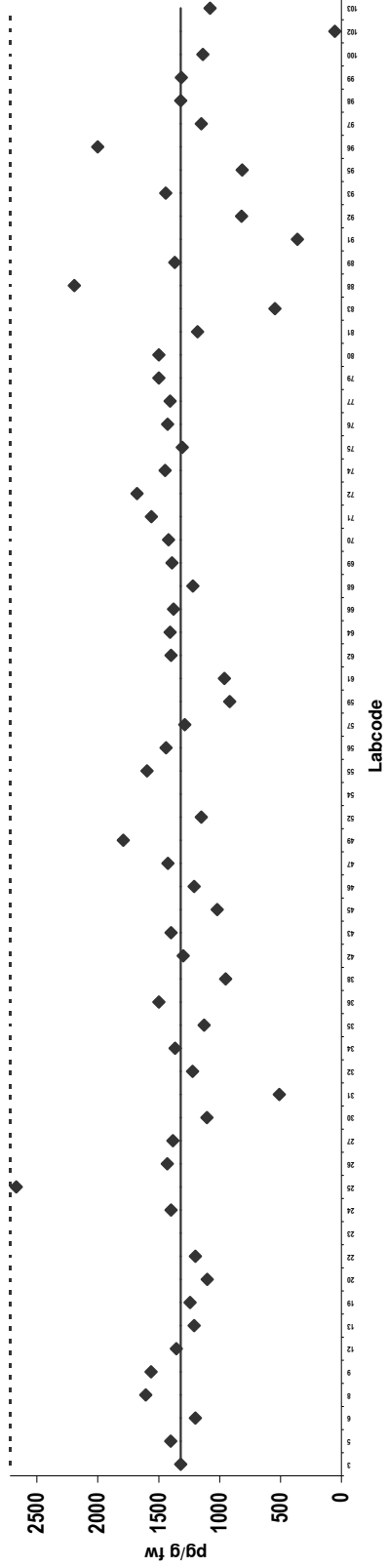
Herring
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	1320		76	1428	
5	1402		77	1406	
6	1200		79	1500	
8	1607		80	1500	
9	1562		81	1181	
12	1356		83	545	
13	1209		88	2192	
19	1243		89	1367	
20	1101		91	360	
22	1200		92	820	
23	3094	Outlier	93	1442	
24	1400		95	814	
25	2670		96	2000	ND
26	1429		97	1150	
27	1384		98	1320	
30	1103		99	1314	
31	510		100	1138	
32	1222		102	54	
34	1365		103	1079	
35	1128				
36	1500				
38	950				
42	1300				
43	1400				
45	1020				
46	1210				
47	1425				
49	1790				
52	1150				
54	2890	Outlier			
55	1597				
56	1440				
57	1287				
59	918				
61	960				
62	1400				
64	1408				
66	1378				
68	1220				
69	1390				
70	1419				
71	1560				
72	1677				
74	1448				
75	1307				

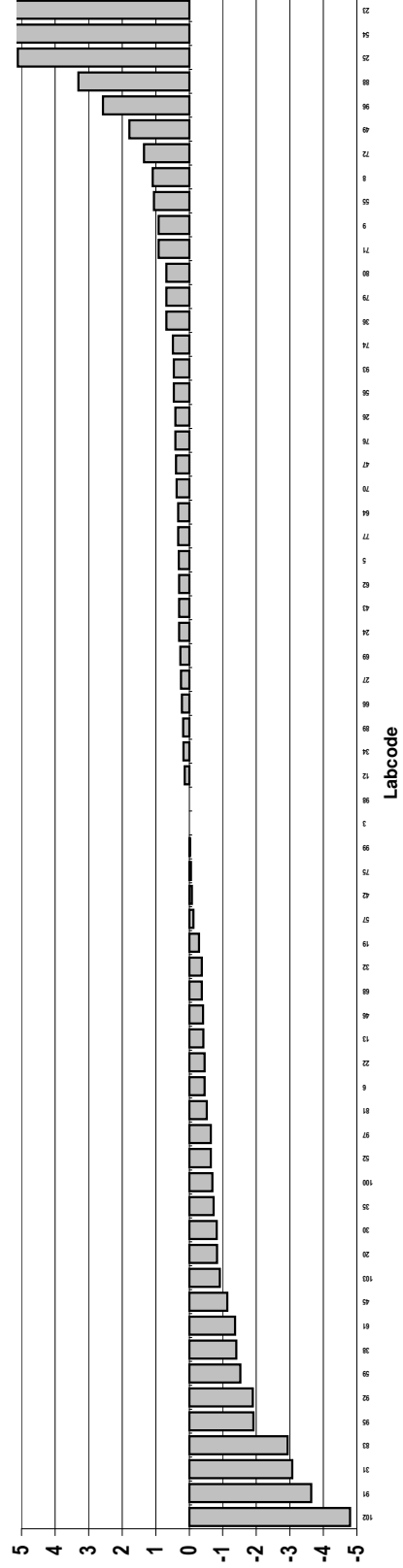
Consensus statistics

Consensus median, pg/g	1320
Median all values pg/g	1360
Consensus mean, pg/g	1293
Standard deviation, pg/g	385
Relative standard deviation, %	30
No. of values reported	64
No. of values removed	2
No. of reported non-detects	1

CB 180



Z-score: CB 180



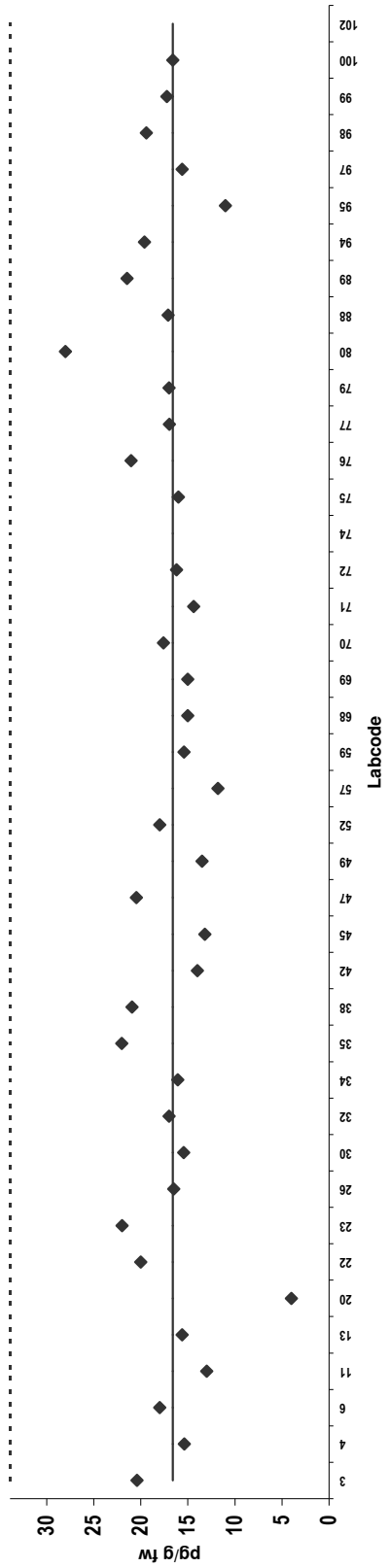
Herring
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	20				
4	15				
6	18				
11	13				
13	16				
20	4.0				
22	20				
23	22				
26	17				
30	15				
32	17				
34	16				
35	22				
38	21				
42	14				
45	13				
47	20				
49	14				
52	18				
57	12				
59	15				
68	15				
69	15				
70	18				
71	14				
72	16				
74	38	Outlier			
75	16				
76	21				
77	17				
79	17				
80	28				
88	17				
89	21				
94	20				
95	11				
97	16				
98	19				
99	17				
100	17				
102	161	Outlier			

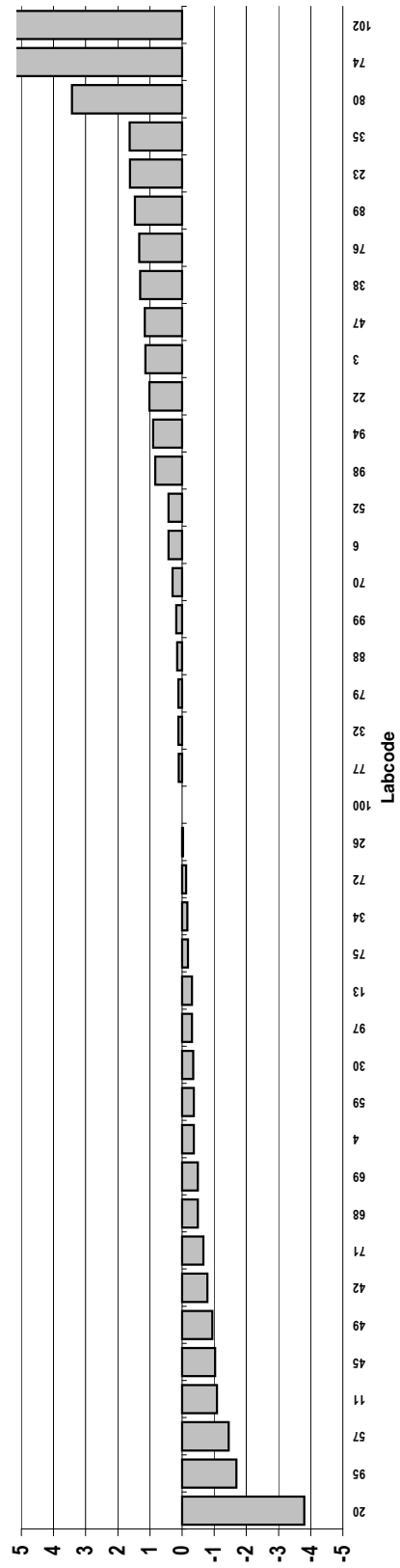
Consensus statistics

Consensus median, pg/g	17
Median all values pg/g	17
Consensus mean, pg/g	17
Standard deviation, pg/g	3.9
Relative standard deviation, %	23
No. of values reported	41
No. of values removed	2
No. of reported non-detects	0

BDE 28



Z-score: BDE 28



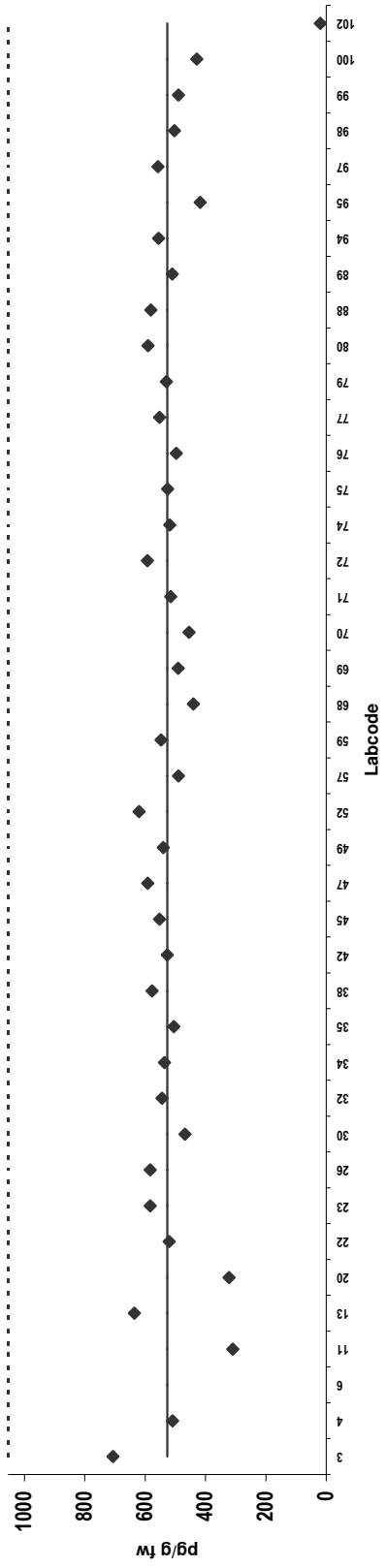
Herring Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	706				
4	509				
6	1100				
11	310	Outlier			
13	635				
20	322				
22	520				
23	583				
26	583				
30	468				
32	544				
34	535				
35	505				
38	577				
42	527				
45	552				
47	592				
49	540				
52	620				
57	489				
59	547				
68	440				
69	490				
70	455				
71	515				
72	592				
74	518				
75	525				
76	497				
77	552				
79	530				
80	590				
88	581				
89	510				
94	555				
95	417				
97	557				
98	503				
99	490				
100	428				
102	20				

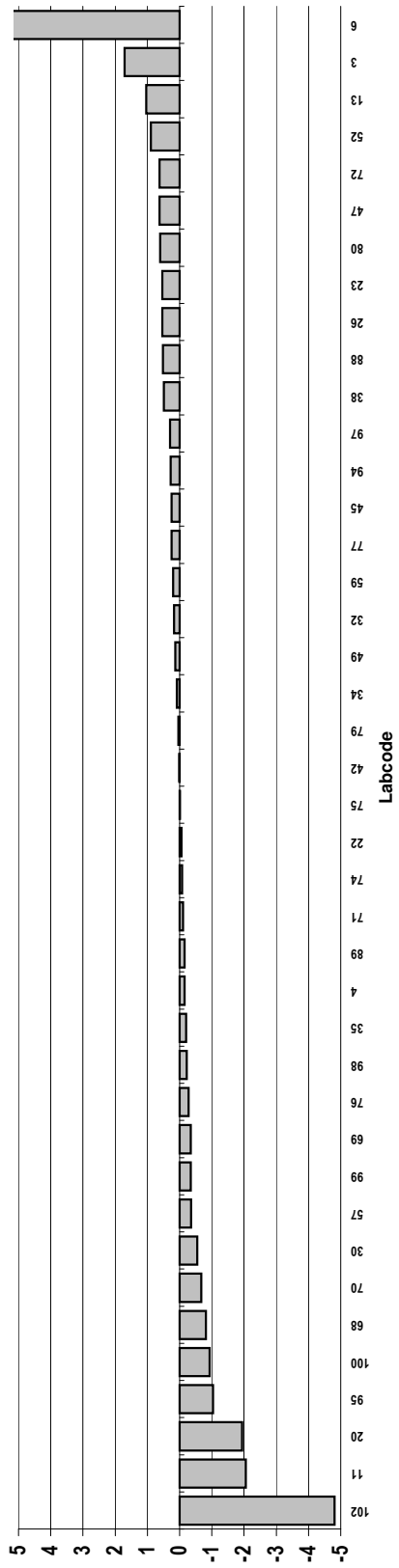
Consensus statistics

Consensus median, pg/g	526
Median all values pg/g	527
Consensus mean, pg/g	511
Standard deviation, pg/g	109
Relative standard deviation, %	21
No. of values reported	41
No. of values removed	1
No. of reported non-detects	0

BDE 47



Z-score: BDE 47



Herring

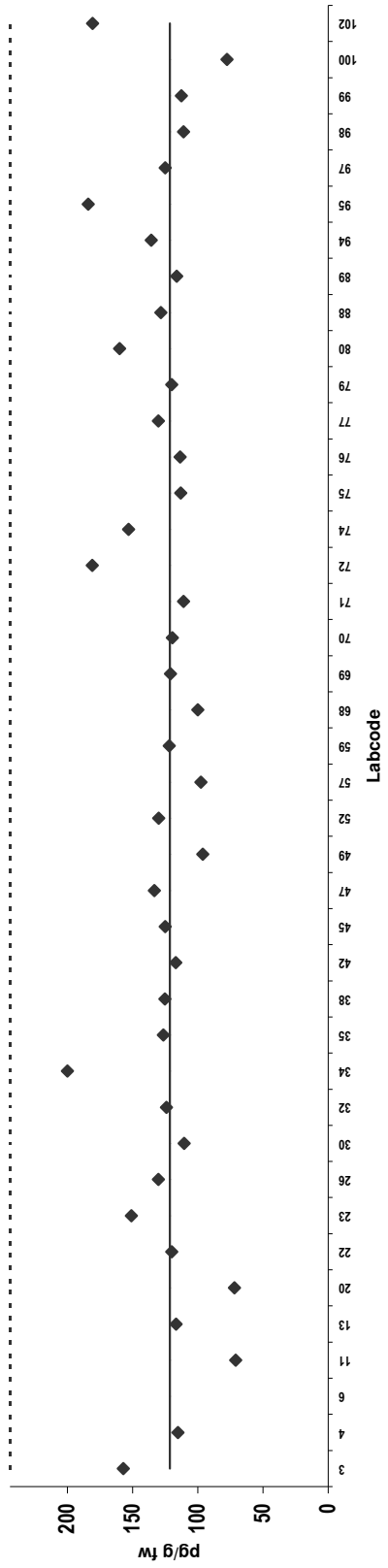
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	157				
4	115				
6	270				
11	71	Outlier			
13	117				
20	72				
22	120				
23	151				
26	130				
30	110				
32	124				
34	200				
35	127				
38	125				
42	117				
45	125				
47	133				
49	96				
52	130				
57	98				
59	122				
68	100				
69	121				
70	119				
71	111				
72	181				
74	153				
75	113				
76	114				
77	130				
79	120				
80	160				
88	128				
89	116				
94	136				
95	184				
97	125				
98	111				
99	113				
100	78				
102	181				

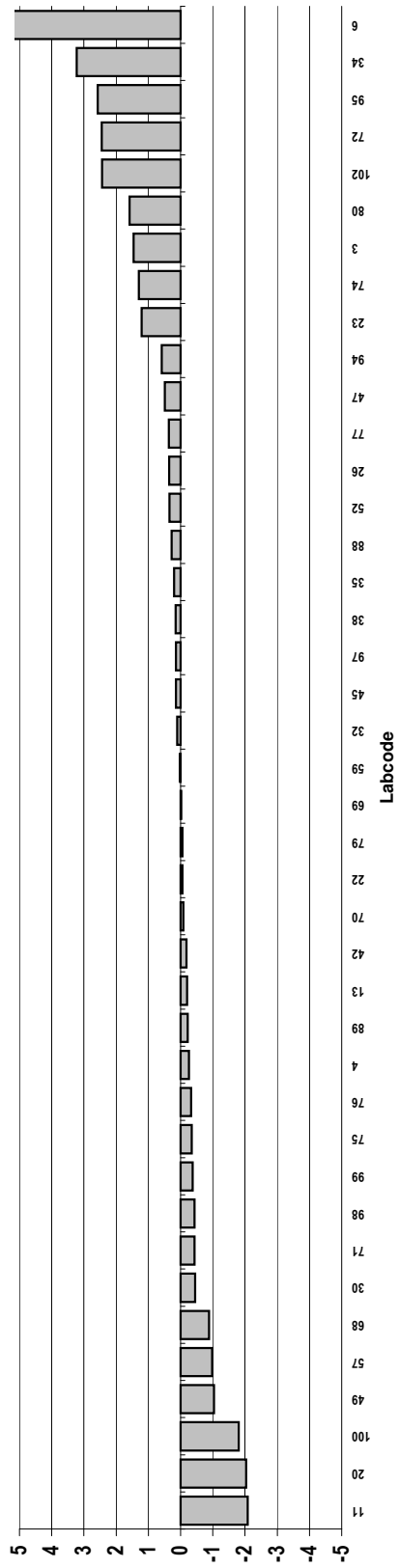
Consensus statistics

Consensus median, pg/g	122
Median all values pg/g	122
Consensus mean, pg/g	126
Standard deviation, pg/g	28
Relative standard deviation, %	22
No. of values reported	41
No. of values removed	1
No. of reported non-detects	0

BDE 99



Z-score: BDE 99



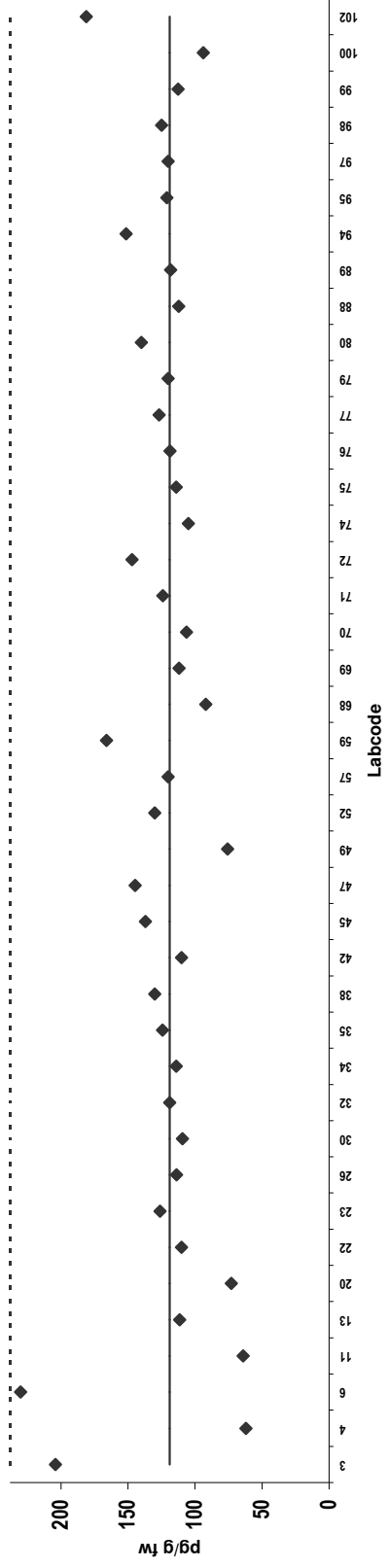
Herring
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	204				
4	62				
6	230				
11	64				
13	111				
20	73				
22	110				
23	126				
26	114				
30	109				
32	119				
34	114				
35	124				
38	130				
42	110				
45	137				
47	145				
49	76				
52	130				
57	120				
59	166				
68	92				
69	112				
70	106				
71	124				
72	147				
74	105				
75	114				
76	119				
77	127				
79	120				
80	140				
88	112				
89	118				
94	151				
95	121				
97	120				
98	125				
99	113				
100	94				
102	181				

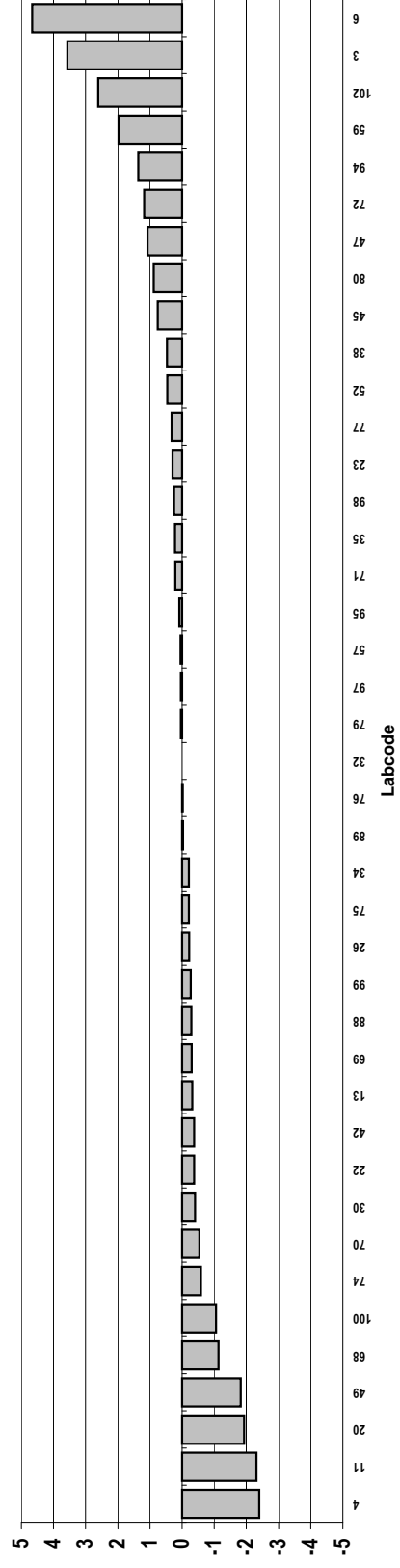
Consensus statistics

Consensus median, pg/g	119
Median all values pg/g	119
Consensus mean, pg/g	122
Standard deviation, pg/g	32
Relative standard deviation, %	26
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0

BDE 100



Z-score: BDE 100



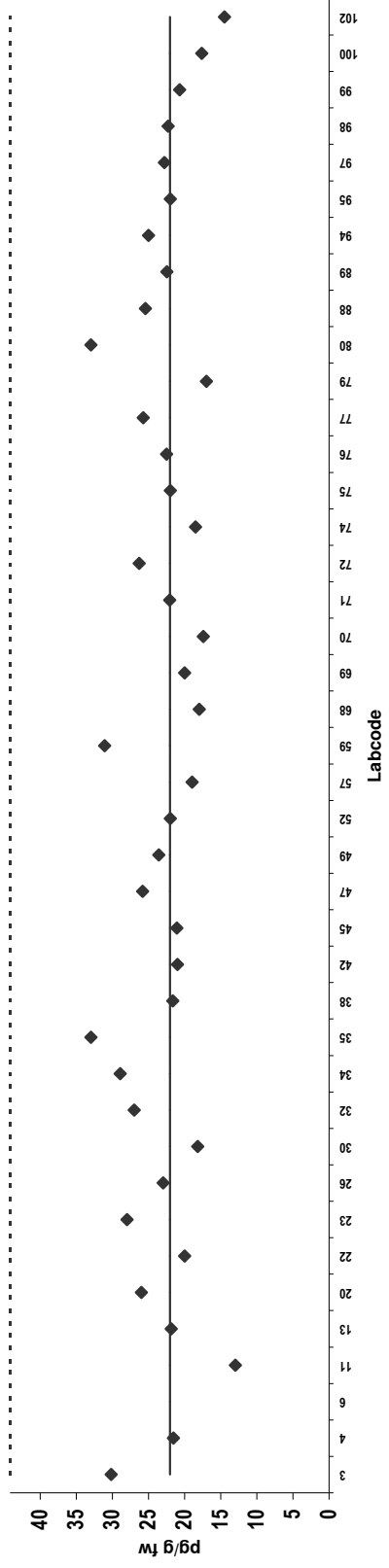
Herring
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	30				
4	22				
6	48				
11	13				
13	22				
20	26				
22	20				
23	28				
26	23				
30	18				
32	27				
34	29				
35	33				
38	22				
42	21				
45	21				
47	26				
49	24				
52	22				
57	19				
59	31				
68	18				
69	20				
70	17				
71	22				
72	26				
74	19				
75	22				
76	23				
77	26				
79	17				
80	33				
88	25				
89	22				
94	25				
95	22				
97	23				
98	22				
99	21				
100	18				
102	15				
		Outlier			

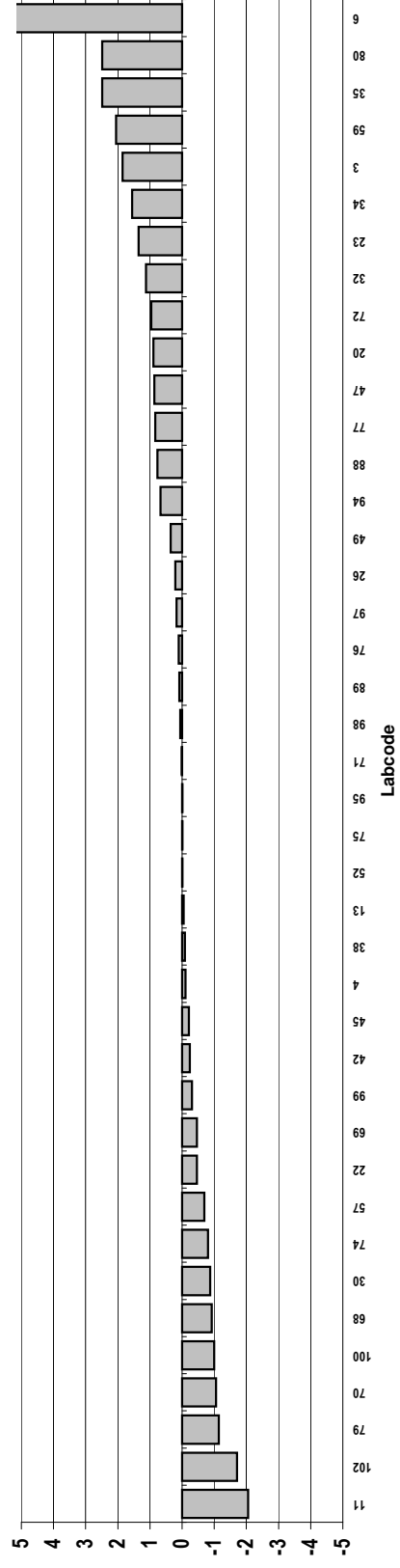
Consensus statistics

Consensus median, pg/g	22
Median all values pg/g	22
Consensus mean, pg/g	23
Standard deviation, pg/g	4.6
Relative standard deviation, %	20
No. of values reported	41
No. of values removed	1
No. of reported non-detects	0

BDE 153



Z-score: BDE 153



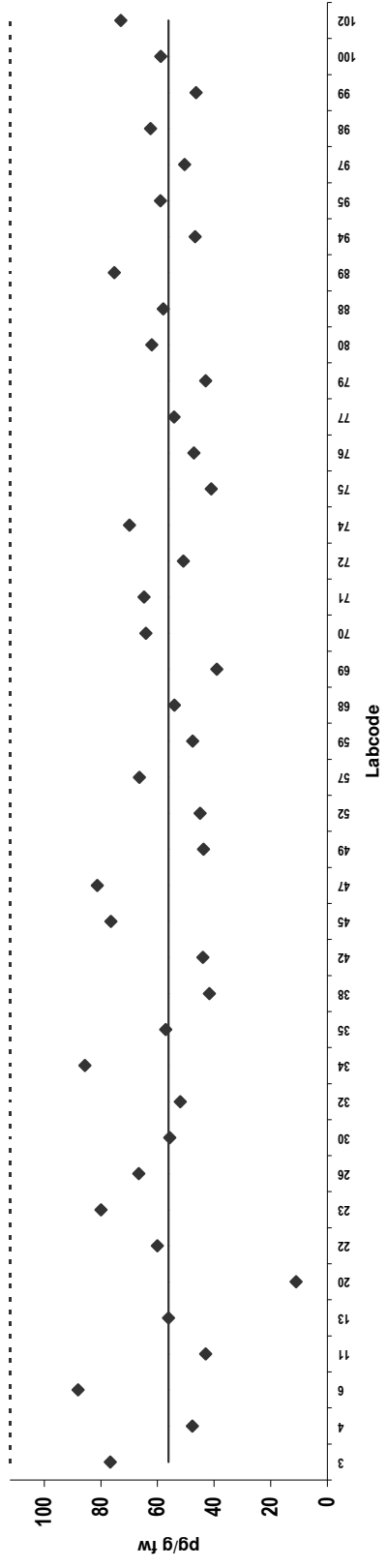
Herring
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	77				
4	48				
6	88				
11	43				
13	56				
20	11				
22	60				
23	80				
26	67				
30	56				
32	52				
34	86				
35	57				
38	42				
42	44				
45	76				
47	81				
49	44				
52	45				
57	66				
59	48				
68	54				
69	39				
70	64				
71	65				
72	51				
74	70				
75	41				
76	47				
77	54				
79	43				
80	62				
88	58				
89	75				
94	47				
95	59				
97	50				
98	63				
99	46				
100	59				
102	73				

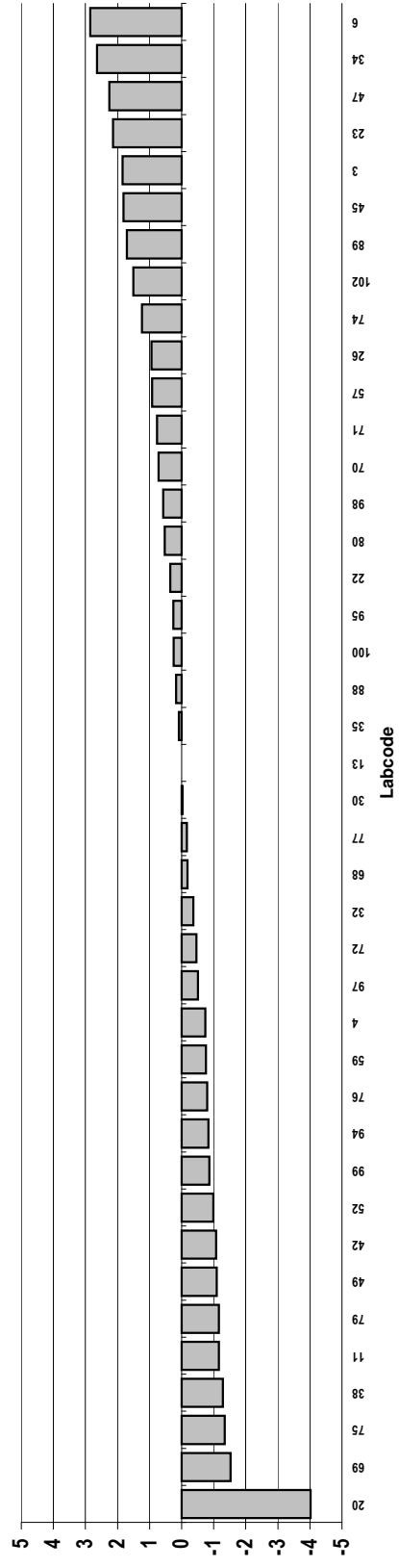
Consensus statistics

Consensus median, pg/g	56
Median all values pg/g	56
Consensus mean, pg/g	57
Standard deviation, pg/g	15
Relative standard deviation, %	27
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0

BDE 154



Z-score: BDE 154



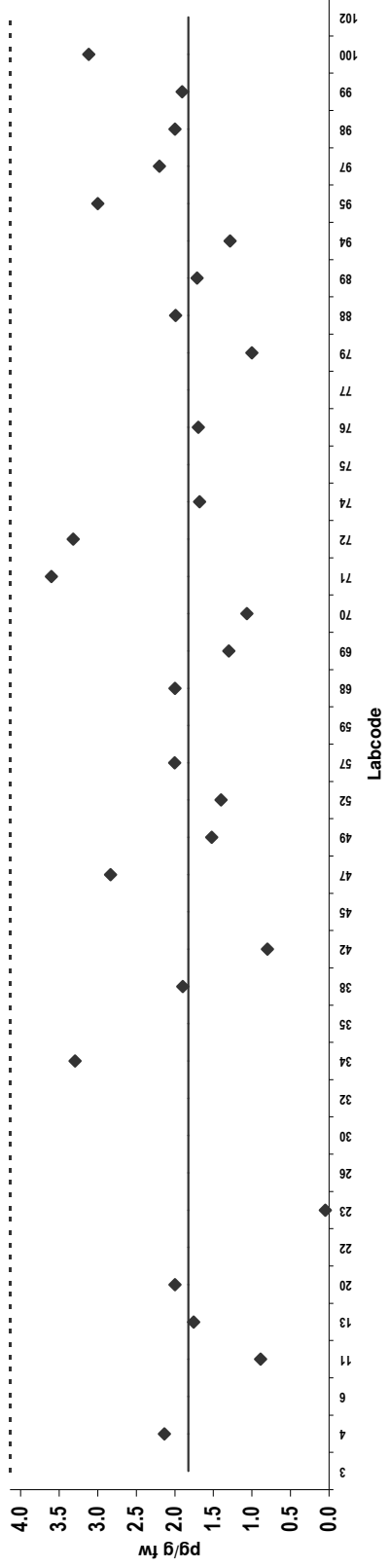
Herring
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	6.8	Outlier			
4	2.1				
6	4.9	Outlier			
11	0.89				
13	1.8				
20	2.0	ND			
22	10	Outlier,ND			
23	0.050	ND			
26	4.4	Outlier,ND			
30	7.4	Outlier			
32	6.0	Outlier			
34	3.3				
35	41	Outlier			
38	1.9				
42	0.80	ND			
45	33	Outlier			
47	2.8	ND			
49	1.5				
52	1.4				
57	2.0				
59	10	Outlier,ND			
68	2.0				
69	1.3				
70	1.1	ND			
71	3.6				
72	3.3	ND			
74	1.7				
75	6.0	Outlier			
76	1.7				
77	9.0	Outlier			
79	1.0				
88	2.0				
89	1.7				
94	1.3				
95	3.0				
97	2.2	ND			
98	2.0	ND			
99	1.9				
100	3.1				
102	5.0	Outlier,ND			

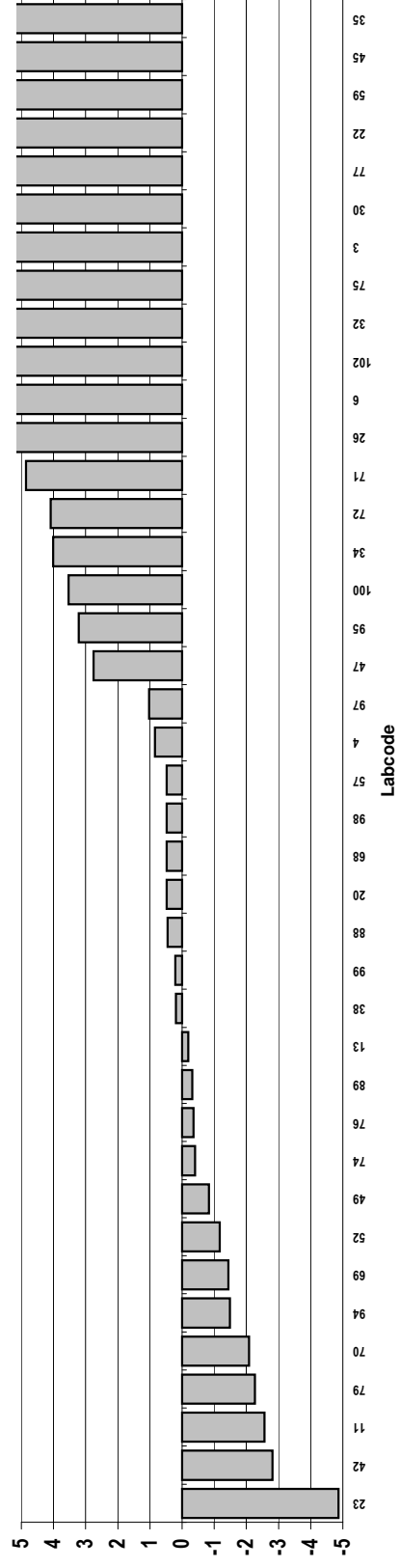
Consensus statistics

Consensus median, pg/g	1.8
Median all values pg/g	2.1
Consensus mean, pg/g	1.9
Standard deviation, pg/g	0.84
Relative standard deviation, %	44
No. of values reported	40
No. of values removed	12
No. of reported non-detects	12

BDE 183



Z-score: BDE 183



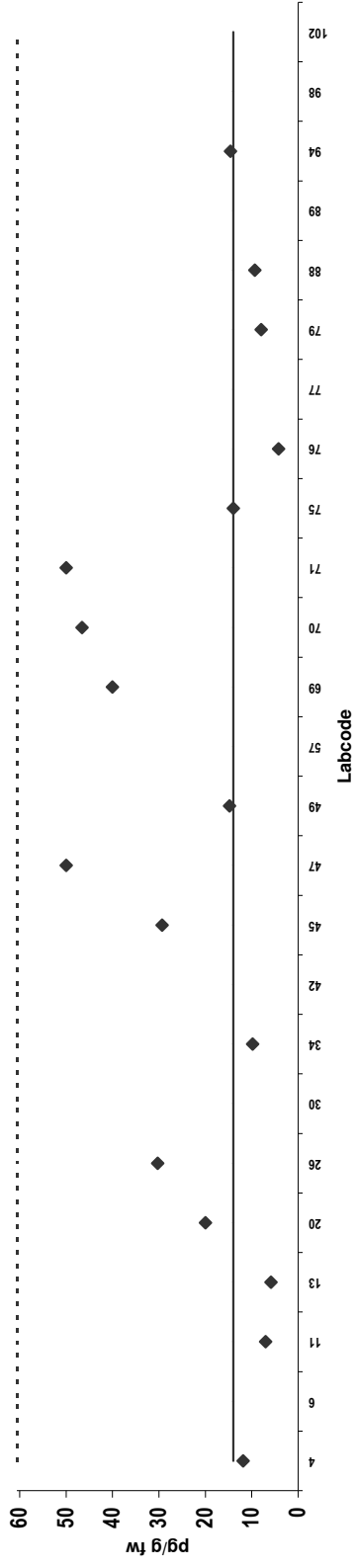
Herring
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	12				
6	2100	Outlier			
11	7.0	ND			
13	5.9				
20	20	ND			
26	30	ND			
30	1606	Outlier			
34	9.8				
42	79	Outlier			
45	29				
47	50	ND			
49	15				
57	161	Outlier			
69	40				
70	47				
71	50	ND			
75	14				
76	4.2	ND			
77	183	Outlier			
79	8.0				
88	9.4				
89	113	Outlier			
94	15				
98	318	Outlier			
102	80	Outlier,ND			

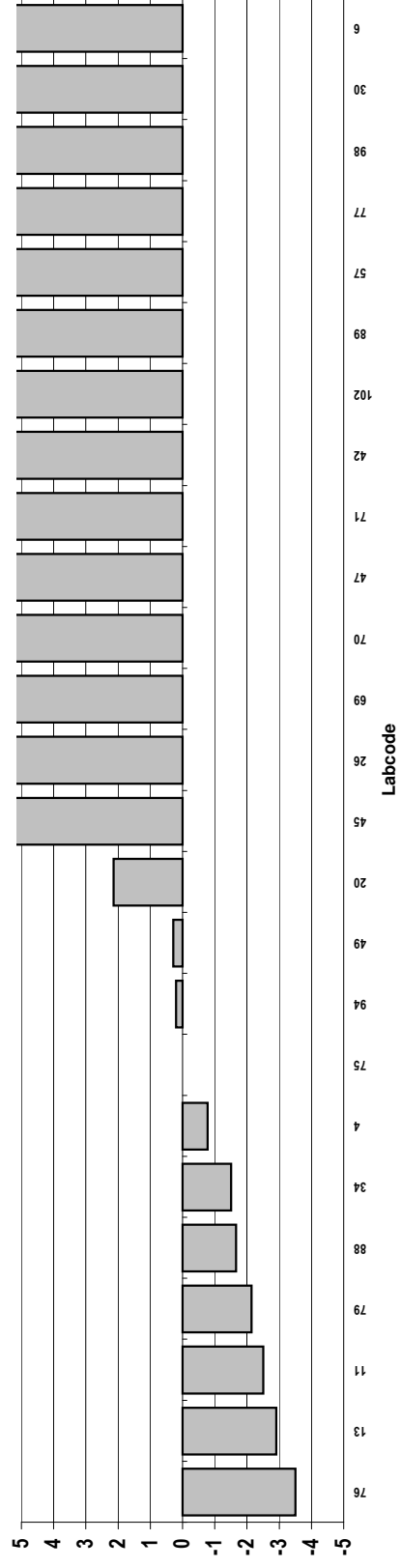
Consensus statistics

Consensus median, pg/g	14
Median all values pg/g	30
Consensus mean, pg/g	22
Standard deviation, pg/g	16
Relative standard deviation, %	75
No. of values reported	25
No. of values removed	8
No. of reported non-detects	7

BDE 209



Z-score: BDE 209



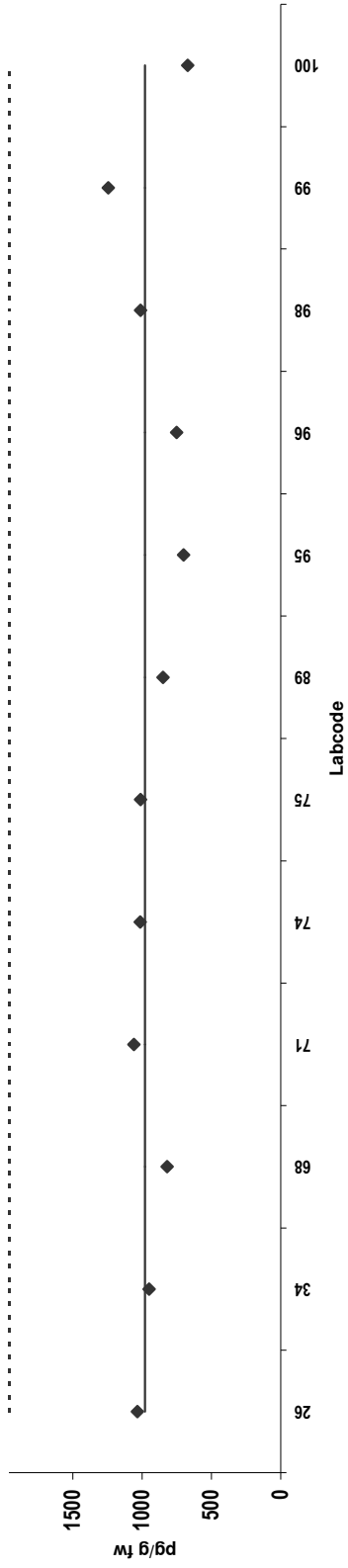
Herring
Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	1034				
34	950				
68	820				
71	1060				
74	1013				
75	1011				
89	848				
95	700				
96	752				
98	1010				
99	1244				
100	672				

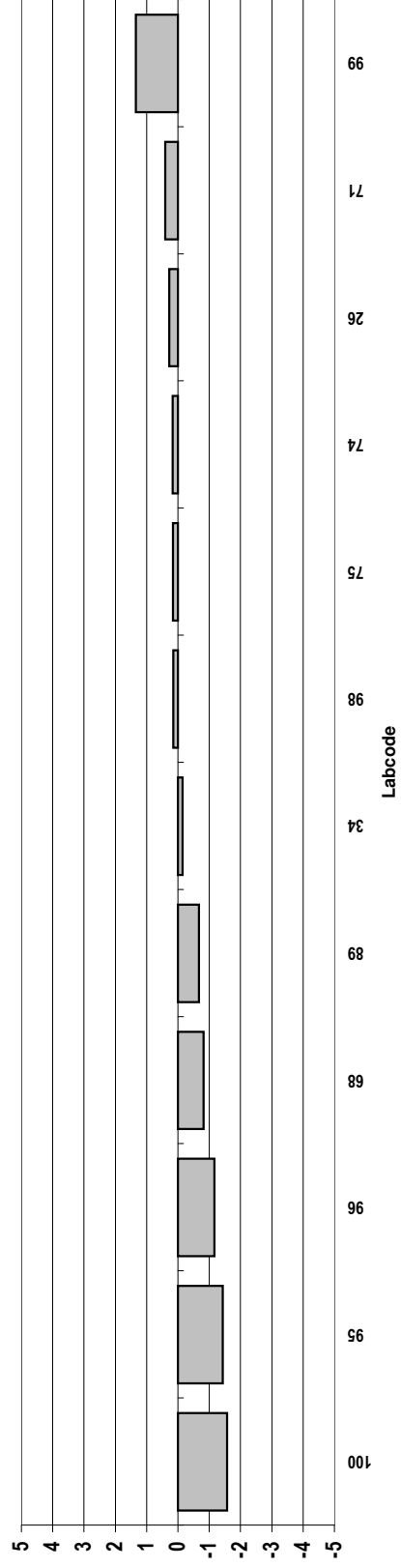
Consensus statistics

Consensus median, pg/g	980
Median all values pg/g	980
Consensus mean, pg/g	926
Standard deviation, pg/g	170
Relative standard deviation, %	18
No. of values reported	12
No. of values removed	0
No. of reported non-detects	0

α -HBCD



Z-score: α -HBCD

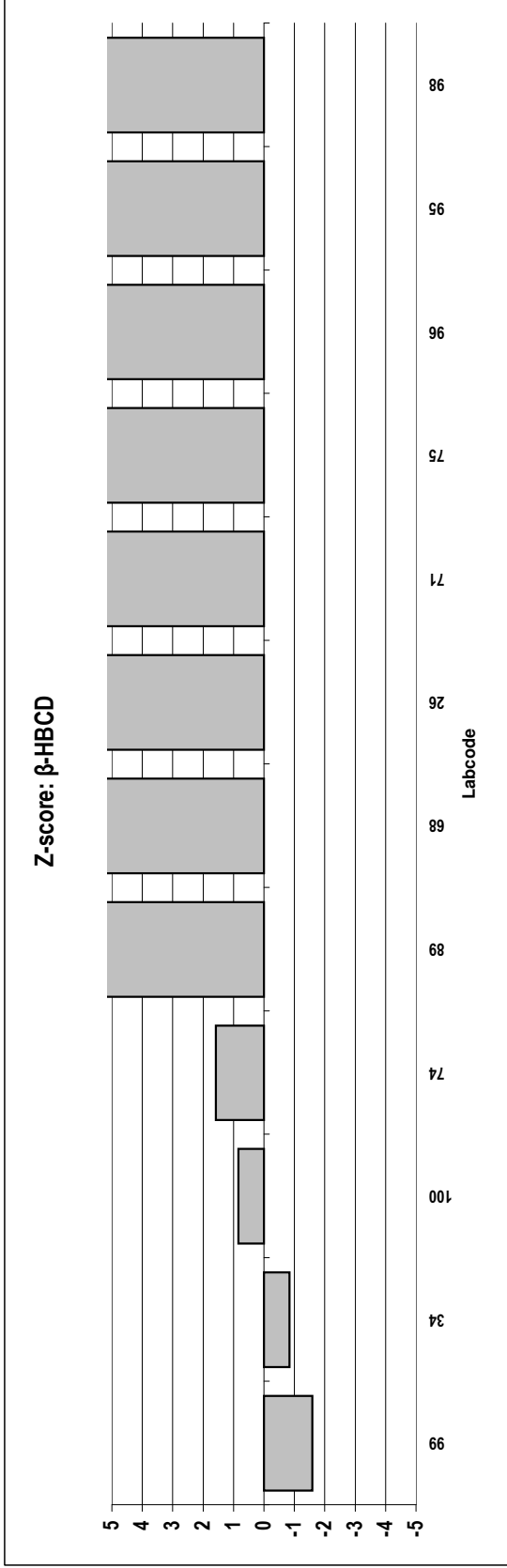
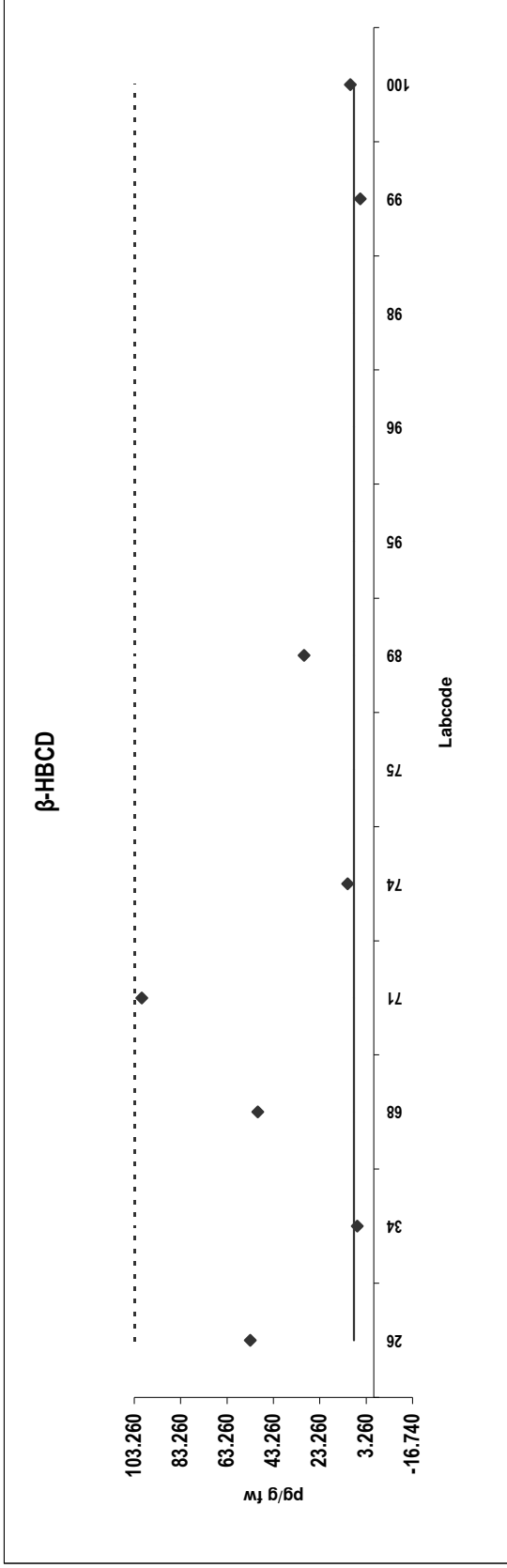


Herring Congener: β -HBBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	53	ND			
34	7.1				
68	50	ND			
71	100	ND			
74	11				
75	105	Outlier			
89	30	ND			
95	400	Outlier			
96	150	Outlier,ND			
98	400	Outlier,ND			
99	5.9				
100	10				

Consensus statistics

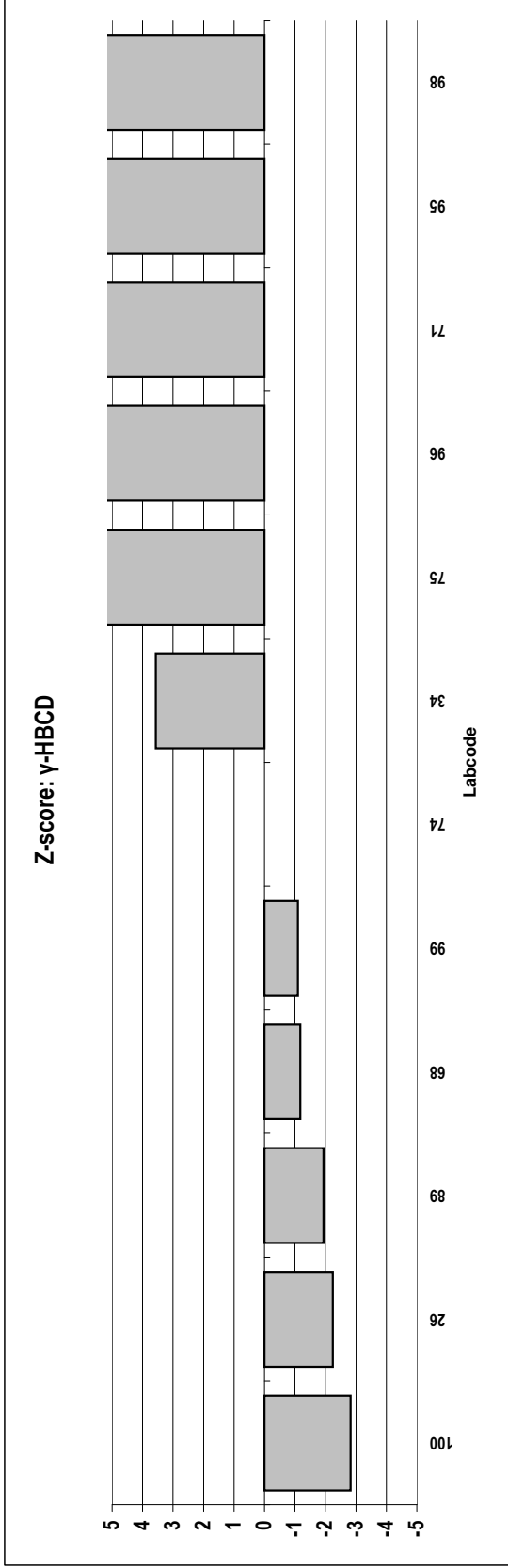
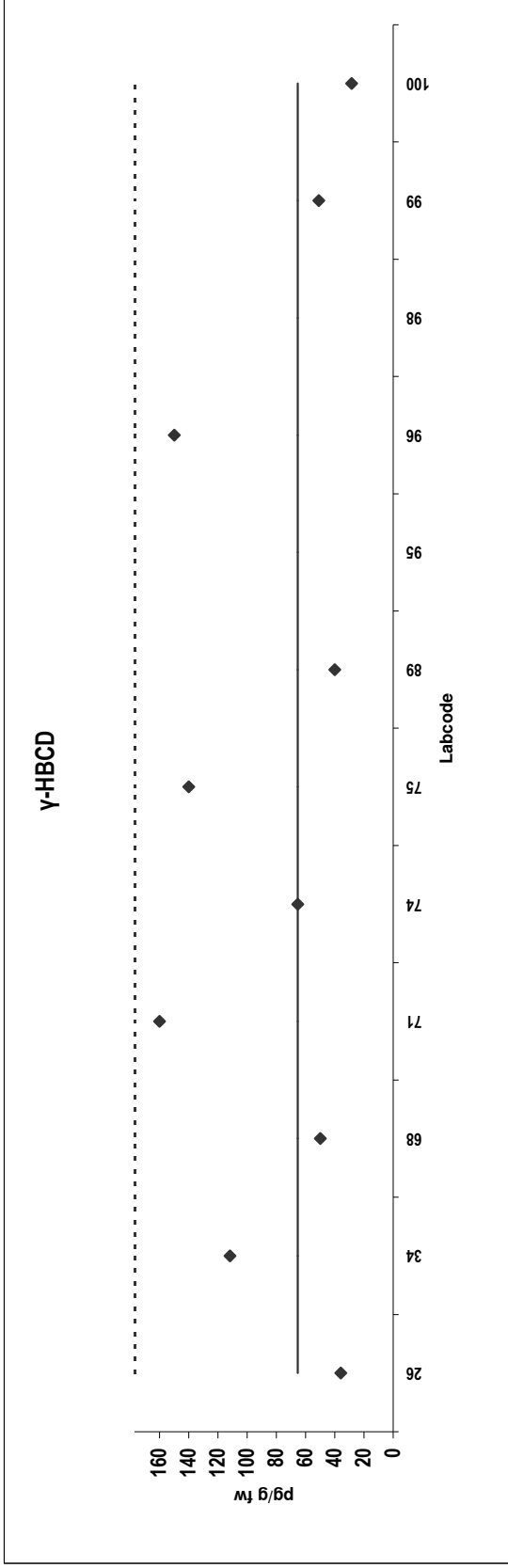
Consensus median, pg/g	8.6
Median all values pg/g	52
Consensus mean, pg/g	33
Standard deviation, pg/g	33
Relative standard deviation, %	99
No. of values reported	12
No. of values removed	4
No. of reported non-detects	6



Herring Congener: γ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	36				
34	112				
68	50				
71	160	ND			
74	65				
75	140				
89	40	ND			
95	400	Outlier			
96	150	ND			
98	400	Outlier,ND			
99	51				
100	28				

Consensus statistics	
Consensus median, pg/g	65
Median all values pg/g	89
Consensus mean, pg/g	83
Standard deviation, pg/g	52
Relative standard deviation, %	62
No. of values reported	12
No. of values removed	2
No. of reported non-detects	4

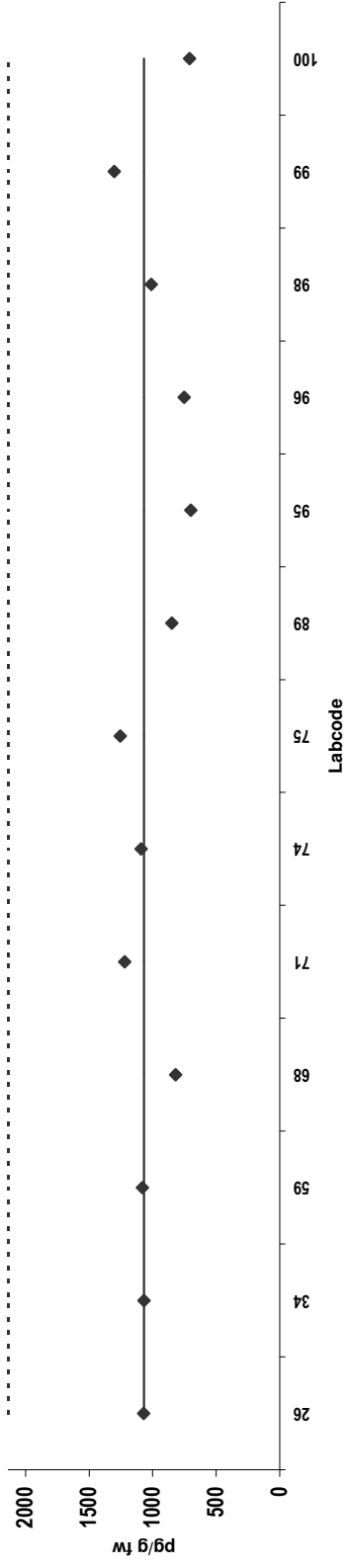


Herring
Congener: total HBCD

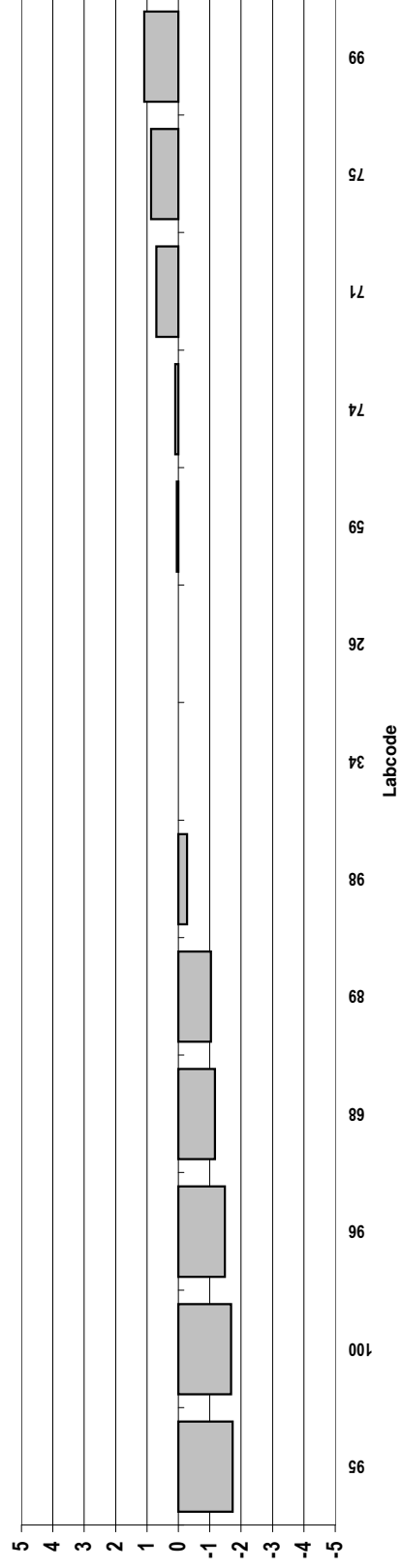
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
26	1070				
34	1069				
59	1080				
68	820				
71	1220				
74	1090				
75	1256				
89	848				
95	700				
96	752				
98	1010				
99	1301				
100	710				

Consensus statistics	
Consensus median, pg/g	1069
Median all values pg/g	1069
Consensus mean, pg/g	994
Standard deviation, pg/g	208
Relative standard deviation, %	21
No. of values reported	13
No. of values removed	0
No. of reported non-detects	0

total HBCD



Z-score: total HBCD



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