

Interlaboratory Comparison on POPs in Food 2015



Sixteenth Round of an International Study

Nanna Bruun Bremnes
Cathrine Thomsen

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Summary

The sixteenth round of the Interlaboratory Comparison on POPs in Food was conducted in 2015 by the Norwegian Institute of Public Health (NIPH). The study included the determination of the 2,3,7,8-chlorinated dibenzo-*p*-dioxins (PCDDs) and dibenzofurans (PCDFs), as well as dioxin-like non-ortho and mono-ortho chlorinated biphenyls (PCBs) in three different food items. Additionally, the participating laboratories could determine the concentrations of six indicator PCBs, eight polybrominated diphenyl ethers (PBDEs) and hexabromocyclododecanes (HBCDs) in the same food samples.

The objectives of this interlaboratory comparison study were

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

In 2015 the study was performed on unfortified homogenates of German beef, salmon from the Baltic Sea and Norwegian cheese. If desired, the laboratories could also determine the concentrations of PCDDs/PCDFs, non-ortho PCBs, mono-ortho PCBs, indicator PCBs, PBDEs and α -HBCD in standard solutions from Cambridge Isotope Laboratories, provided by NIPH.

The test materials were sent to 87 laboratories in 46 different countries in January and early February 2015, and results were returned from 85 of these laboratories by the deadline in April.

A draft report was made available on our webpage www.fhi.no/ILC in July, and the deadline for commenting on the published results was set to the September 15th 2015.

This report presents the reported results for all seventeen 2,3,7,8-substituted PCDDs/PCDFs, the four non-ortho substituted PCBs #77, 81, 126 and 169 and the eight mono-ortho substituted PCBs #105, 114, 118,

123, 156, 157, 167, 189 in the three food items on a fresh weight and lipid weight basis.

The results of eight PBDEs #28, 47, 99, 100, 153, 154, 183 and 209, six indicator PCBs #28, 52, 101, 138, 153 and 180, and total HBCDs as well as the α -, β - and γ -isomers will also be presented.

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

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

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

Z-scores for the PCDD/PCDF TEQs were calculated for each laboratory using $\pm 20\%$ of the consensus TEQs (from 2012: WHO₂₀₀₅ TEQs as opposed to WHO₁₉₉₈ TEQs as in the reports published before 2012) 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. From 2015, Z-scores are calculated both on a fresh weight and a lipid weight basis.

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

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

For the determination of total TEQs in the beef and salmon samples, Z-scores within ± 1 were obtained on fresh weight basis by 84 and 85 % of the laboratories (Corresponding to a trueness of $\pm 20\%$). For the cheese-sample, which was low-contaminated, Z-scores within ± 1 were obtained by 40 % of the reporting participants (fresh weight). On fresh weight basis, the majority of all the laboratories (92 %) reported results for total TEQ with a trueness of $\pm 40\%$ for the beef- and salmon-sample (Z-score ± 2), and 58 % of the contributors achieved a Z-scores within ± 2 for the cheese-sample. The relative standard deviation (RSD) calculated for the total TEQ after removal of outliers was 9-10 % for the two samples that had the highest levels of contamination. For the more challenging cheese-samples the same RSD was 20 %. Considering this, it is concluded that the abilities and performance

of laboratories worldwide in determining dioxin-like compounds is generally good for the three food samples included in this study.

For the food samples, 43-59 laboratories reported results for the six indicator PCBs, 25-36 laboratories reported concentrations for all seven of the tetra- to hepta-PBDEs and 19-29 laboratories reported concentrations for PBDE-209. The concentrations of the sum of seven PBDEs on fresh weight basis were 22 (19 %), 2741 (13 %) and 28 (21 %) pg/g in beef, salmon and cheese, respectively, with average RSD given in parentheses. The consensus concentrations for PBDE-209 were 56 (n=23, RSD=50 %), 29 (n=29, RSD=45 %) and 28 (n=19, RSD=43 %) pg/g fresh weight in beef, salmon and cheese, respectively.

The total concentrations on fresh weight basis for six indicator PCBs were 2394 pg/g (19 %) in beef, 39149 pg/g (17 %) in salmon and 185 pg/g (21 %) in cheese, with average RSDs given in parentheses.

The consensus concentrations calculated for HBCDs are just indicative values because only few laboratories reported results (n=8-14).

Introduction

Maximum residue limits and official food control systems are established in many countries for the monitoring of the levels of dioxins and dioxin-like PCBs in food and feed, both to map and to reduce human and animal exposure to these highly toxic pollutants. To meet these requirements, there is a large demand for chemical analytical laboratories with the skills and abilities to determine these contaminants at very low concentrations and in complex matrixes. It is usually required by the authorities that laboratories performing such measurements are accredited according to ISO standards and prove their competence by successful participation in interlaboratory studies.

This is the 16th round of a world-wide interlaboratory comparison study on dioxin-like compounds in food, organized by the Department of Exposure and Risk Assessment, Division of Environmental Medicine, Norwegian Institute of Public Health (NIPH), Oslo, Norway.

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

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

The exercise took place from January 2015, when the samples were shipped to the laboratories for analysis, until the reporting deadline in April 2015, when the last reports with results were received. A draft report was made available to the participants on our webpage (<http://www.fhi.no/ILC>) in July.

All participants from previous rounds in this series of "Interlaboratory Comparisons on POPs in Food" were invited to participate. In addition, several other laboratories announced their interest and were invited to participate. There was no limit to the total number of participating laboratories. The 85 laboratories that submitted results, and thereby contributed to the study results, are presented in Table 1.

Table 1. Participants that reported results in the 16th round of Interlaboratory Comparison on POP's in food 2015

All-Russian State Center for Quality and Standardization of Veterinary Drugs and Feeds Department of safety of feed and food products(VGNKI) Moscow, Russia	ALS Czech Republic Pardubice, Czech Republic
AsureQuality Limited - Wellington Laboratory Wellington, New Zealand	AXYS Analytical Services Ltd. Sidney, Canada
Bálint Analitika LTD. Budapest, Hungary	Ballab Gida Laboratuvari Mersin, Turkiye
Bayerisches Landesamt für Umwelt Augsburg, Germany	BioDetection Systems Amsterdam, The Netherlands
Canadian Food Inspection Agency Calgary, Alberta, Canada	CARSO-LSEHL Lyon, France
Central Lab of Residue Analysis of Pesticides and Heavy Metals in Foods Giza, Egypt	Centre for Advanced Analytical Toxicology Services (CAATS) Penang, Malaysia

Chemisches und mikrobiologisches Institut UEG GmbH Wetzlar, Germany	Chemisches und Veterinäruntersuchungsamt (CVUA) Freiburg Freiburg, Germany
Chemisches und Veterinäruntersuchungsamt Münsterland Emscher Lippe (CVUA MEL) Münster, Germany	China National Center for Food Safety Risk Assessment Beijing, China
Chinese Academy of Sciences Center for Eco-Environmental Sciences Dioxin Lab Beijing, China	Council of Agriculture Agricultural Chemicals and Toxic Substances Research Institute Taichung, Taiwan (R.O.C.)
Danish Veterinary and Food Administration, Division of Residues Ringsted, Denmark	Dioxin laboratory of Comprehensive test center of Chinese Academy of Inspection and Quarantine Beijing, China
Environmental Laboratory - IQS Barcelona, Spain	Eurofins Laboratorium Zeeuws Vlaanderen Graauw, The Netherlands
Eurofins GfA Lab Service GmbH Hamburg, Germany	Food and Environment Research Agency (FERA) Sand Hutton, York, UK
Food GmbH Jena Analytik & Consulting Jena, Germany	Health Canada Health Products and Food Branch Food Research Division Ottawa, Canada
Hessisches Landeslabor Wiesbaden, Germany	Hong Kong SAR Government Additives, Contaminants and Composition Section Hong Kong, P.R. China
Hubei Provincial Centre for Disease Control and Prevention, Hubei Dioxin Lab Hubei Province, China	Istituto Zooprofilattico Sperimentale Abruzzo e Molise "G. Caporale" Teramo, Italy
Istituto Zooprofilattico Sperimentale Dell'Umbria e delle Marche Ancona, Italy	Istituto Zooprofilattico Sperimentale Lombardia Emilia Romagna Bologna, Italy
Japan Food Research Laboratories Japan	La Drôme Laboratoire Valence, France
LABERCA - ONIRIS Nantes, France	Laboratoire De Rouen Rouen, France
Laboratorio BDS Chile Ltda. Rancagua, Chile	Laboratory of SGS Bulgaria Ltd. Varna, Bulgaria
Laboratory of Vendee (LEAV) La Roche-sur-Yon, France	Landesamt für Umweltschutz Sachsen-Anhalt Halle, Germany
Landesamt für Umweltschutz Sachsen-Anhalt Halle, Germany	Landesuntersuchungsamt, Institut für Lebensmittelchemie Speyer, Germany
Marchwood Scientific Services Southampton, UK	mas münster analytical solutions gmbh Münster, Germany
Maxxam Analytics International Corporation Mississauga, Ontario, Canada	MicroPolluants Technologie (MPT) Saint Julien Les Metz, France
National Cheng Kung University Research Center for Environmental Trace Toxic Substances Tainan, Taiwan	National Institute for Health and Welfare Department of Environmental Health Kuopio, Finland
National Measurement Institute - Pymble Dioxin Analysis Sydney, Australia	NCSR "Demokritos", Greece Mass Spectrometry and Dioxin Analysis Lab Athens, Greece

Neutron SPA - Analytical Laboratory Modena, Italy	Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit Lebensmittel-und Veterinärinstitut Oldenburg Oldenburg, Germany
NIFES - National Institute of Nutrition and Seafood Research Bergen, Norway	NILU (Norwegian Institute for Air Research) Kjeller, Norway
Nofalab BV Schiedam, The Netherlands	Oekometric GmbH Bayreuth , Germany
Oxigen Analiz Laboratuvar Hizmetleri Ticaret Ltd. Şti Istanbul, Turkey	Pacific Rim Laboratories Inc. Surrey, Canada
Pohang University of Science and Technology Scientific Environmental Analysis Laboratory Pohang, Korea	POP LabShenzhen Center for Disease Control & Prevention Shenzhen, Guangdong, China
QLIP N.V. Zutphen, Netherland	Research and Productivity Council (RPC) Fredericton, New Brunswick, Canada
RIKILT Wageningen, The Netherlands	Scientific Analysis Laboratories Manchester, UK
Servizos de Apoio á Investigación (Scientific Research Support Services) Coruña, Spain	SGS Belgium NV Antwerpen, Belgium
SGS Environmental Services Wilmington, USA	SGS Institut Fresenius GmbH Bayreuth, Germany
SGS Taiwan Enviromental Servise Dioxin Laboratory New Taipei City, Taiwan (R.O.C.)	Shanghai Academy of Public Measurement Bioassay and Safety Assessment Laboratory Shanghai, China
Shanghai Municipal Center for Disease Control and Prevention Shanghai, China	Sun Dream Environmental Technology CorporationFood Hygiene Laboratory Taichung City, Taiwan, China
State Laboratory County Kildare, Ireland	Tianjin Product Quality Supervision and Inspection Institute of Technology Tianjin, China
Toxicological Chemistry Unit, Department of the Environment and Primary Prevention Rome, Italy	Tshwane University of Technology Environmental-Analytical Chemistry laboratory Pretoria, South Africa
U.S. Food & Drug Administration, Arkansas Regional Laboratory Jefferson, Arkansas, United States of America	U.S. Food and Drug Administration Lenexa, Kansas, United States of America
Umeå Universitet, Kemiska institutionen Miljökemiska Laboratoriet Umeå, Sweden	University of Stirling Institute of Aquaculture Stirling, Scotland, UK
Veterinary Public Health Laboratory Chemistry Department Republic of Singapore	Wellington Laboratories Inc. Guelph, Ontario, Canada
WESSLING GmbH Altenberge, Germany	Western Region Laboratory, Health Canada Burnaby, Canada
Worthies Engineering Consultants Corp. Environmental Analysis Lab Taichung, Taiwan	

Design and practical implementation

Study design and reporting of results

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

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

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

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

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

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

The test materials consisted of homogenates of beef, salmon and cheese. The laboratories could choose to analyze one, two or all three food samples.

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

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

Collection, preparation, and distribution of samples

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

- Beef (~100 g)
- Salmon (~100 g)
- Cheese (~60 g)

The test materials consisted of natural products unfortified with standards.

The contaminated beef and salmon samples were generously provided by Dr. Elke Bruns-Weller, LAVES, Oldenburg, Germany and Søren Sørensen at the Danish Veterinary and Food Administration in Denmark, respectively. Mr Lars Haug kindly used his time and efforts to organize the procurement of the cheese sample on behalf on NIPH.

The contaminated beef from Germany was ground in a meat grinder at the NIPH, and then thoroughly mixed with commercially available Norwegian ground beef in a food grinder. The Baltic Salmon arrived as frozen halves of the whole fish. The skin was removed before grinding. The fish filets were then pooled and carefully homogenized in a food grinder.

All cheese used to produce the cheese samples were from the same production batch, and was coarsely ground at arrival. It was further ground in to a fine, powdery consistency from frozen state before finally being homogenized by means of stirring and shaking.

The homogeneity of the bulk samples was tested on ten sub samples of each matrix by an indirect approach involving the measurement of conductivity in the sample. The method is further described in Appendix D.

Sub-samples of at least 100 g of beef (Beef-2015), 100 g of salmon (Salmon-2015) and 60 g of cheese (Cheese-2015) were placed into screw-cap polystyrene bottles. The bottles were all carefully washed, rinsed with methanol and dried before use. All samples were stored at -20 °C until shipment to the participating laboratories.

Statistical analysis

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

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

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

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

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

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

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

Z-scores on both fresh weight and lipid weight basis for PCDD/PCDF TEQ as well as for the non-ortho PCB TEQ, the mono-ortho PCB TEQ, the total TEQ (WHO₂₀₀₅ TEFs), the sum of six indicator PCBs, the sum of eight PBDEs, total HBCD and for each congener were calculated for each laboratory according to the following equation:

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

Where x = reported value; X = consensus value (assigned value); s = target value for standard deviation. A s of 0.2 multiplied by the consensus value was used, i.e. Z-scores between +1 and -1 reflect a deviation of $\pm 20\%$ 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 July 2015.

The final report will be made available to the participants in pdf format at www.fhi.no/ILC. A certificate, stating the participant's laboratory code, will be sent to each participant who has contributed to the results by the end of 2015.

Co-ordination

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

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Results

Presentation in the report

85 laboratories in 46 different countries submitted their results within the deadline and the results will be presented in the following chapters. All participating laboratories 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.

Readers of the report can without being participants in the study or with access to laboratory codes, get a general overview of the analytical performance of laboratories worldwide on the determination on PCDD/PCDFs, dioxin-like PCBs, indicator PCBs, PBDEs and HBCD in regular food stuffs.

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

Individual results reported by the laboratories for each congener are given for beef, salmon and cheese in Appendix 2, 3 and 4. Results of the lipid determinations are presented in Appendix 5.

Summary of results

PCDDs/PCDFs

Analyte solution

Concentrations for PCDDs/PCDFs were reported by 69 laboratories. The average RSD for the 17 congeners was 8.0 % ranging from 6.8 % for 1,2,3,7,8-PeCDF to 9.2 % for 1,2,3,4,6,7,8,9-OCDF. The calculation of Z-scores for the TEQs (target 12.5 pg TEQ/ μ L based on TEF₂₀₀₅-values) of the PCDD/PCDF standard solution showed that 94 % of the laboratories were within the range of ± 20 % of the consensus value. This demonstrates

that the calibration solutions used by the laboratories generally are of high quality.

Beef

For the beef sample, PCDD/PCDF results from 63 laboratories were received. The consensus TEQ (PCDD/PCDF TEQ based on WHO2005-TEFs) was 0.074 pg TEQ/g fresh weight and 0.57 pg TEQ/g lipid weight.

The average RSD was 40 %, ranging from 25-63 % for 2,3,4,7,8-PeCDF and 1,2,3,7,8,9-HxCDF, respectively. Z-scores within ± 1 were obtained by 70 % of the laboratories and 83 % of the laboratories had Z-scores within ± 2 (fresh weight basis).

Salmon

PCDD/PCDF concentrations in the Baltic Salmon were reported by 69 laboratories. The consensus TEQ was 3.1 pg TEQ/g fresh weight, and 39 pg TEQ/g lipid weight (PCDD/PCDF TEQ based on WHO₂₀₀₅-TEFs). The average RSD was 34 % ranging from 21-64 % (2,3,7,8-TCDF and 1,2,3,4,7,8,9-HpCDF, respectively). Z-scores were within ± 1 for 90 % of the laboratories and within ± 2 for 93 % of the laboratories (fresh weight basis).

Cheese

PCDD/PCDF concentrations in the cheese-sample were determined by 52 laboratories. The consensus TEQ was 0.028 pg TEQ/g on fresh weight basis, and 0.11 pg TEQ/g on lipid weight basis (PCDD/PCDF TEQ based on WHO₂₀₀₅-TEFs). The average RSD was 53 % ranging from 39-72 % (1,2,3,6,7,8-HxCDD and 1,2,3,7,8,9-HxCDF, respectively). Z-scores for PCDD/PCDF TEQ within ± 1 were obtained by 38 % of the laboratories and 53 % had Z-scores within ± 2 (fresh weight basis).

Dioxin-like PCBs

Analyte solution

The 12 dioxin-like PCBs in the analyte solution were analyzed and reported by 67-68 laboratories. The RSDs for the different congeners were ranging from 7.3 for PCB-126 to 10 % for PCB-118, with an average of 9.2 %.

Beef

Dioxin-like PCB concentrations in the beef sample were reported from 62 laboratories. The concentrations of the 12 congeners varied between 0.13 pg/g fresh weight (PCB-81) and 630 pg/g fresh weight (CB-118) (On lipid weight basis, 1.0 p/g and 4904 p/g for PCB-81 and PCB-118, respectively). The average RSD for concentrations of individual dioxin-like PCB congeners was 25 % ranging from 20 % for PCB-118 to 39 % for PCB-81

The dioxin-like PCBs contribute 82 % to the total TEQ (WHO TEF₂₀₀₅) in the sample with PCB-126 as the main contributor (73 %).

Salmon

Of the participating laboratories, 69-70 measured and reported dioxin-like PCB concentrations in the salmon sample. The concentrations ranged from 2.3 pg/g fresh weight for PCB-81 (29 pg/g lipid weight) to 5626 pg/g fresh weight for PCB-118 (70636 pg/g lipid weight). The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 26 % ranging from 19 % for PCB-157 to 44 % for PCB-123.

The dioxin-like PCBs contribute to about 64 % of the total TEQ in the sample with PCB-126 as the main contributor (56 %).

Cheese

Dioxin-like PCBs in the cheese-sample were reported by 52 laboratories. Levels were ranging from 0.048

pg/g fresh weigh for PCB-169 (0.18 pg/g lipid weight) to 36 pg/g fresh weight for PCB-118 (136 pg/g lipid weight). The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 40 % ranging from 28 % for PCB-105 to 56 % for PCB-189. The contribution of the dioxin-like PCBs to the total TEQ was about 47 % with PCB-126 as the main contributor (41 % of total TEQ).

Total TEQ

The total TEQ for the beef sample was 0.42 pg TEQ/g fresh weight and 3.2 pg TEQ/g lipid weight (WHO TEF₂₀₀₅). The total TEQ of the salmon was 8.6 pg TEQ/g fresh weight and 108 pg TEQ/g lipid weight, and the cheese contained 0.054 pg TEQ/g fresh weight and 0.21 pg TEQ/g lipid weight.

The RSDs for total TEQs on fresh weight basis calculated from the RSD of individual congeners were 12 % for beef, 11 % for salmon and 20 % for cheese.

In Figure 1 the contribution on the TEQ-values of the three groups of compounds is depicted based on WHO TEF₂₀₀₅ and WHO TEF₁₉₉₈, respectively. In the selection of food-items included in this study the dioxin-like PCBs contributed from 47 % to 82 % to the total TEQ (using WHO TEF₂₀₀₅), demonstrating the variation in contribution, and the importance of the PCBs for the determination of the total TEQs related to the toxic potency of food samples.

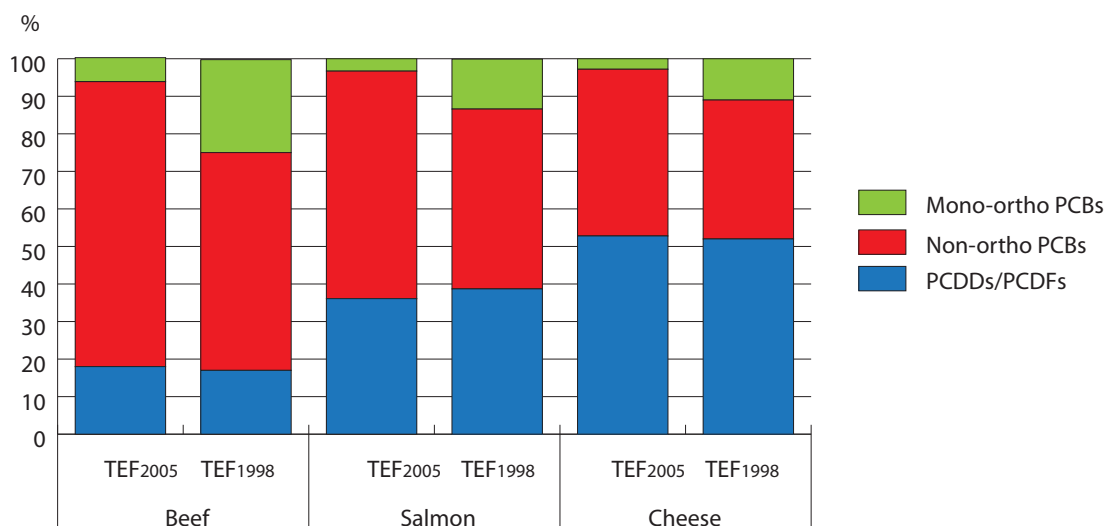


Figure 1. The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using both the WHO₂₀₀₅ TEFs and WHO₁₉₉₈ TEFs, in the three food samples.

Indicator PCBs

Analyte solution

60 laboratories reported indicator PCBs in the analyte solution. The average RSD was 11 % ranging from 10 to 14 %.

Beef

For the sample of beef, results for indicator PCBs were received from 54 laboratories. The consensus concentrations varied between 24 pg/g fresh weight/185 pg/g lipid weight (PCB-28) and 1023 pg/g fresh weight/7965 pg/g lipid weight (PCB-153). The RSDs were ranging from 32 to 45 % for PCB-153 and PCB-28, respectively, with an average of 37 % for all indicator PCBs. The consensus median for the sum of indicator PCBs was 2394 pg/g fresh weight.

Salmon

Within the deadline, 59 laboratories reported results for indicator PCBs in the salmon-sample. The consensus concentrations ranged from 703 pg/g fresh weight for PCB-28 (lipid weight: 8826 pg/g) to 15316 pg/g fresh weight for PCB-153 (lipid weight: 192291 pg/g) with a consensus median for the sum of indicator PCBs of 39149 pg/g fresh weight. The average RSD was 34 %, ranging from 31 to 41 % for PCB-180 and PCB-28, respectively.

Cheese

Results were obtained from 43 laboratories. The concentrations of indicator PCBs in the cheese-sample ranged from 13 pg/g fresh weight (PCB-28) to 56 pg/g (PCB-153) (lipid weight: 50 pg/g for PCB-28 and 215 pg/g for PCB-153) and the consensus median for the sum was 185 pg/g fresh weight. The average RSD was 48 %, ranging from 42 to 57 % for PCB-138 and PCB-28, respectively.

PBDEs

Analyte solution

The tri- to hepta-PBDE standard solution was analyzed by 33-34 laboratories and 26 laboratories reported values for PBDE-209. The RSDs were between 7.4-11 % for all congeners.

Beef

The PBDE concentrations in beef were reported by 29-30 laboratories, except for PBDE-209 for which 23 results were received. The consensus concentrations were in the range from 0.43 pg/g fresh weight for PBDE-28 to 11 pg/g fresh weight for PBDE-47 (lipid weight: 3.3 pg/g for PBDE-28, 88 pg/g for PBDE-47). The consensus concentration for PBDE-209 was 56

pg/g fresh weight. The sum of tri- to hepta-PBDEs was 22 pg/g fresh weight. The range of RSDs on fresh weight basis was 24-50 %, with an average of 34 % including PBDE-209.

Salmon

Within the deadline, 36 laboratories had reported results for tri- to hepta-PBDEs in salmon and 29 laboratories had reported results for PBDE-209. The consensus concentrations varied between 2.9 pg/g fresh weight (PBDE-183) and 1572 pg/g fresh weight (PBDE-47) (lipid weight: 36 pg/g for PBDE-183, 19742 pg/g for PBDE-47). The concentration for PBDE-209 was 22 pg/g fresh weight. The sum of tri- to hepta-PBDEs was 2741 pg/g fresh weight. The RSD calculated from the concentrations on fresh weight ranged from 11-45 %, with an average of 23 % for PBDEs including PBDE-209.

Cheese

25 laboratories reported results for tri- to hepta-PBDEs in cheese, and 19 reported results for PBDE-209. The concentrations varied between 0.30 pg/g fresh weight (PBDE-28) (lipid weight: 1.1 pg/g) and 13 pg/g (PBDE-47) (lipid weight: 51 pg/g). The concentration for PBDE-209 was 134 pg/g. The sum of tri- to hepta-PBDEs was 28 pg/g fresh weight. The RSDs for the individual congeners were ranging from 18 to 59 % with an average of 37 % including PBDE-209.

HBCD

Also in this round of the study, total HBCD and the isomers α -, β - and γ -HBCD could be determined and reported. A total of 12 laboratories reported α -HBCD in the standard solution and 4-14 laboratories reported one or more of the three isomers in the food samples. The consensus concentrations for the sum of individual HBCD isomers were 103 pg/g fresh weight for the beef sample, 3820 pg/g for the salmon and 11 pg/g fresh weight for the cheese sample. Since only a few laboratories reported HBCD, these results must be regarded as indicative values.

Lipid content

The mean and RSDs (in parentheses) for the lipid contents of the food samples were calculated to be 13 % (RSD=8.3 %) for the beef sample, 7.8 % (RSD=13 %) for the salmon and 25 % (RSD=14 %) for the cheese sample.

Acknowledgements

The laboratories are acknowledged for their participation in this interlaboratory comparison and in 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 thank Dr. Elke Bruns-Weller at Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit (LAVES), Germany, for generously donating the beef sample, and Søren Sørensen at the Danish Veterinary and Food Administration in Denmark

for making the Baltic salmon available. We are also grateful to Mr. Lars Haug for using his time to organize the procurement of the cheese sample and to Cambridge Isotope Laboratories, Inc. for providing the standard solutions for this interlaboratory study.

Interlaboratory Comparison on POPs in Food 2015

Sixteenth Round of an International Study

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Cathrine Thomsen

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Summary

The sixteenth round of the Interlaboratory Comparison on POPs in Food was conducted in 2015 by the Norwegian Institute of Public Health (NIPH). The study included the determination of the 2,3,7,8-chlorinated dibenzo-*p*-dioxins (PCDDs) and dibenzofurans (PCDFs), as well as dioxin-like non-ortho and mono-ortho chlorinated biphenyls (PCBs) in three different food items. Additionally, the participating laboratories could determine the concentrations of six indicator PCBs, eight polybrominated diphenyl ethers (PBDEs) and hexabromocyclododecanes (HBCDs) in the same food samples.

The objectives of this interlaboratory comparison study were

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

In 2015 the study was performed on unfortified homogenates of German beef, salmon from the Baltic Sea and Norwegian cheese. If desired, the laboratories could also determine the concentrations of PCDDs/PCDFs, non-ortho PCBs, mono-ortho PCBs, indicator PCBs, PBDEs and α -HBCD in standard solutions from Cambridge Isotope Laboratories, provided by NIPH.

The test materials were sent to 87 laboratories in 46 different countries in January and early February 2015, and results were returned from 85 of these laboratories by the deadline in April.

A draft report was made available on our webpage www.fhi.no/ILC in July, and the deadline for commenting on the published results was set to the September 15th 2015.

This report presents the reported results for all seventeen 2,3,7,8-substituted PCDDs/PCDFs, the four non-ortho substituted PCBs #77, 81, 126 and 169 and the eight mono-ortho substituted PCBs #105, 114, 118,

123, 156, 157, 167, 189 in the three food items on a fresh weight and lipid weight basis.

The results of eight PBDEs #28, 47, 99, 100, 153, 154, 183 and 209, six indicator PCBs #28, 52, 101, 138, 153 and 180, and total HBCDs as well as the α -, β - and γ -isomers will also be presented.

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

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

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

Z-scores for the PCDD/PCDF TEQs were calculated for each laboratory using $\pm 20\%$ of the consensus TEQs (from 2012: WHO₂₀₀₅ TEQs as opposed to WHO₁₉₉₈ TEQs as in the reports published before 2012) 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. From 2015, Z-scores are calculated both on a fresh weight and a lipid weight basis.

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

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

For the determination of total TEQs in the beef and salmon samples, Z-scores within ± 1 were obtained on fresh weight basis by 84 and 85 % of the laboratories (Corresponding to a trueness of ± 20 %). For the cheese-sample, which was low-contaminated, Z-scores within ± 1 were obtained by 40 % of the reporting participants (fresh weight). On fresh weight basis, the majority of all the laboratories (92 %) reported results for total TEQ with a trueness of ± 40 % for the beef- and salmon-sample (Z-score ± 2), and 58 % of the contributors achieved a Z-scores within ± 2 for the cheese-sample. The relative standard deviation (RSD) calculated for the total TEQ after removal of outliers was 9-10 % for the two samples that had the highest levels of contamination. For the more challenging cheese-samples the same RSD was 20 %. Considering this, it is concluded that the abilities and performance

of laboratories worldwide in determining dioxin-like compounds is generally good for the three food samples included in this study.

For the food samples, 43-59 laboratories reported results for the six indicator PCBs, 25-36 laboratories reported concentrations for all seven of the tetra- to hepta-PBDEs and 19-29 laboratories reported concentrations for PBDE-209. The concentrations of the sum of seven PBDEs on fresh weight basis were 22 (19 %), 2741 (13 %) and 28 (21 %) pg/g in beef, salmon and cheese, respectively, with average RSD given in parentheses. The consensus concentrations for PBDE-209 were 56 (n=23, RSD=50 %), 29 (n=29, RSD=45 %) and 28 (n=19, RSD=43 %) pg/g fresh weight in beef, salmon and cheese, respectively.

The total concentrations on fresh weight basis for six indicator PCBs were 2394 pg/g (19 %) in beef, 39149 pg/g (17 %) in salmon and 185 pg/g (21 %) in cheese, with average RSDs given in parentheses.

The consensus concentrations calculated for HBCDs are just indicative values because only few laboratories reported results (n=8-14).

Introduction

Maximum residue limits and official food control systems are established in many countries for the monitoring of the levels of dioxins and dioxin-like PCBs in food and feed, both to map and to reduce human and animal exposure to these highly toxic pollutants. To meet these requirements, there is a large demand for chemical analytical laboratories with the skills and abilities to determine these contaminants at very low concentrations and in complex matrixes. It is usually required by the authorities that laboratories performing such measurements are accredited according to ISO standards and prove their competence by successful participation in interlaboratory studies.

This is the 16th round of a world-wide interlaboratory comparison study on dioxin-like compounds in food, organized by the Department of Exposure and Risk Assessment, Division of Environmental Medicine, Norwegian Institute of Public Health (NIPH), Oslo, Norway.

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

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

The exercise took place from January 2015, when the samples were shipped to the laboratories for analysis, until the reporting deadline in April 2015, when the last reports with results were received. A draft report was made available to the participants on our webpage (<http://www.fhi.no/ILC>) in July.

All participants from previous rounds in this series of "Interlaboratory Comparisons on POPs in Food" were invited to participate. In addition, several other laboratories announced their interest and were invited to participate. There was no limit to the total number of participating laboratories. The 85 laboratories that submitted results, and thereby contributed to the study results, are presented in Table 1.

Table 1. Participants that reported results in the 16th round of Interlaboratory Comparison on POP's in food 2015

All-Russian State Center for Quality and Standardization of Veterinary Drugs and Feeds Department of safety of feed and food products(VGNKI) Moscow, Russia	ALS Czech Republic Pardubice, Czech Republic
AsureQuality Limited - Wellington Laboratory Wellington, New Zealand	AXYS Analytical Services Ltd. Sidney, Canada
Bálint Analitika LTD. Budapest, Hungary	Ballab Gida Laboratuvari Mersin, Turkiye
Bayerisches Landesamt für Umwelt Augsburg, Germany	BioDetection Systems Amsterdam, The Netherlands
Canadian Food Inspection Agency Calgary, Alberta, Canada	CARSO-LSEHL Lyon, France
Central Lab of Residue Analysis of Pesticides and Heavy Metals in Foods Giza, Egypt	Centre for Advanced Analytical Toxicology Services (CAATS) Penang, Malaysia

Chemisches und mikrobiologisches Institut UEG GmbH Wetzlar, Germany	Chemisches und Veterinäruntersuchungsamt (CVUA) Freiburg Freiburg, Germany
Chemisches und Veterinäruntersuchungsamt Münsterland Emscher Lippe (CVUA MEL) Münster, Germany	China National Center for Food Safety Risk Assessment Beijing, China
Chinese Academy of Sciences Center for Eco-Environmental Sciences Dioxin Lab Beijing, China	Council of Agriculture Agricultural Chemicals and Toxic Substances Research Institute Taichung, Taiwan (R.O.C.)
Danish Veterinary and Food Administration, Division of Residues Ringsted, Denmark	Dioxin laboratory of Comprehensive test center of Chinese Academy of Inspection and Quarantine Beijing, China
Environmental Laboratory - IQS Barcelona, Spain	Eurofins Laboratorium Zeeuws Vlaanderen Graauw, The Netherlands
Eurofins GfA Lab Service GmbH Hamburg, Germany	Food and Environment Research Agency (FERA) Sand Hutton, York, UK
Food GmbH Jena Analytik & Consulting Jena, Germany	Health Canada Health Products and Food Branch Food Research Division Ottawa, Canada
Hessisches Landeslabor Wiesbaden, Germany	Hong Kong SAR Government Additives, Contaminants and Composition Section Hong Kong, P.R. China
Hubei Provincial Centre for Disease Control and Prevention, Hubei Dioxin Lab Hubei Province, China	Istituto Zooprofilattico Sperimentale Abruzzo e Molise "G. Caporale" Teramo, Italy
Istituto Zooprofilattico Sperimentale Dell'Umbria e delle Marche Ancona, Italy	Istituto Zooprofilattico Sperimentale Lombardia Emilia Romagna Bologna, Italy
Japan Food Research Laboratories Japan	La Drôme Laboratoire Valence, France
LABERCA - ONIRIS Nantes, France	Laboratoire De Rouen Rouen, France
Laboratorio BDS Chile Ltda. Rancagua, Chile	Laboratory of SGS Bulgaria Ltd. Varna, Bulgaria
Laboratory of Vendee (LEAV) La Roche-sur-Yon, France	Landesamt für Umweltschutz Sachsen-Anhalt Halle, Germany
Landesamt für Umweltschutz Sachsen-Anhalt Halle, Germany	Landesuntersuchungsamt, Institut für Lebensmittelchemie Speyer, Germany
Marchwood Scientific Services Southampton, UK	mas münster analytical solutions gmbh Münster, Germany
Maxxam Analytics International Corporation Mississauga, Ontario, Canada	MicroPolluants Technologie (MPT) Saint Julien Les Metz, France
National Cheng Kung University Research Center for Environmental Trace Toxic Substances Tainan, Taiwan	National Institute for Health and Welfare Department of Environmental Health Kuopio, Finland
National Measurement Institute - Pymble Dioxin Analysis Sydney, Australia	NCSR "Demokritos", Greece Mass Spectrometry and Dioxin Analysis Lab Athens, Greece

Neutron SPA - Analytical Laboratory Modena, Italy	Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit Lebensmittel-und Veterinärinstitut Oldenburg Oldenburg, Germany
NIFES - National Institute of Nutrition and Seafood Research Bergen, Norway	NILU (Norwegian Institute for Air Research) Kjeller, Norway
Nofalab BV Schiedam, The Netherlands	Oekometric GmbH Bayreuth , Germany
Oxigen Analiz Laboratuvar Hizmetleri Ticaret Ltd. Şti Istanbul, Turkey	Pacific Rim Laboratories Inc. Surrey, Canada
Pohang University of Science and Technology Scientific Environmental Analysis Laboratory Pohang, Korea	POP LabShenzhen Center for Disease Control & Prevention Shenzhen, Guangdong, China
QLIP N.V. Zutphen, Netherland	Research and Productivity Council (RPC) Fredericton, New Brunswick, Canada
RIKILT Wageningen, The Netherlands	Scientific Analysis Laboratories Manchester, UK
Servizos de Apoio á Investigación (Scientific Research Support Services) Coruña, Spain	SGS Belgium NV Antwerpen, Belgium
SGS Environmental Services Wilmington, USA	SGS Institut Fresenius GmbH Bayreuth, Germany
SGS Taiwan Enviromental Servise Dioxin Laboratory New Taipei City, Taiwan (R.O.C.)	Shanghai Academy of Public Measurement Bioassay and Safety Assessment Laboratory Shanghai, China
Shanghai Municipal Center for Disease Control and Prevention Shanghai, China	Sun Dream Environmental Technology CorporationFood Hygiene Laboratory Taichung City, Taiwan, China
State Laboratory County Kildare, Ireland	Tianjin Product Quality Supervision and Inspection Institute of Technology Tianjin, China
Toxicological Chemistry Unit, Department of the Environment and Primary Prevention Rome, Italy	Tshwane University of Technology Environmental-Analytical Chemistry laboratory Pretoria, South Africa
U.S. Food & Drug Administration, Arkansas Regional Laboratory Jefferson, Arkansas, United States of America	U.S. Food and Drug Administration Lenexa, Kansas, United States of America
Umeå Universitet, Kemiska institutionen Miljökemiska Laboratoriet Umeå, Sweden	University of Stirling Institute of Aquaculture Stirling, Scotland, UK
Veterinary Public Health Laboratory Chemistry Department Republic of Singapore	Wellington Laboratories Inc. Guelph, Ontario, Canada
WESSLING GmbH Altenberge, Germany	Western Region Laboratory, Health Canada Burnaby, Canada
Worthies Engineering Consultants Corp. Environmental Analysis Lab Taichung, Taiwan	

Design and practical implementation

Study design and reporting of results

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

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

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

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

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

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

The test materials consisted of homogenates of beef, salmon and cheese. The laboratories could choose to analyze one, two or all three food samples.

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

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

Collection, preparation, and distribution of samples

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

- Beef (~100 g)
- Salmon (~100 g)
- Cheese (~60 g)

The test materials consisted of natural products unfortified with standards.

The contaminated beef and salmon samples were generously provided by Dr. Elke Bruns-Weller, LAVES, Oldenburg, Germany and Søren Sørensen at the Danish Veterinary and Food Administration in Denmark, respectively. Mr Lars Haug kindly used his time and efforts to organize the procurement of the cheese sample on behalf on NIPH.

The contaminated beef from Germany was ground in a meat grinder at the NIPH, and then thoroughly mixed with commercially available Norwegian ground beef in a food grinder. The Baltic Salmon arrived as frozen halves of the whole fish. The skin was removed before grinding. The fish filets were then pooled and carefully homogenized in a food grinder.

All cheese used to produce the cheese samples were from the same production batch, and was coarsely ground at arrival. It was further ground in to a fine, powdery consistency from frozen state before finally being homogenized by means of stirring and shaking.

The homogeneity of the bulk samples was tested on ten sub samples of each matrix by an indirect approach involving the measurement of conductivity in the sample. The method is further described in Appendix D.

Sub-samples of at least 100 g of beef (Beef-2015), 100 g of salmon (Salmon-2015) and 60 g of cheese (Cheese-2015) were placed into screw-cap polystyrene bottles. The bottles were all carefully washed, rinsed with methanol and dried before use. All samples were stored at -20 °C until shipment to the participating laboratories.

Statistical analysis

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

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

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

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

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

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

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

Z-scores on both fresh weight and lipid weight basis for PCDD/PCDF TEQ as well as for the non-ortho PCB TEQ, the mono-ortho PCB TEQ, the total TEQ (WHO₂₀₀₅ TEFs), the sum of six indicator PCBs, the sum of eight PBDEs, total HBCD and for each congener were calculated for each laboratory according to the following equation:

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

Where x = reported value; X = consensus value (assigned value); s = target value for standard deviation. A s of 0.2 multiplied by the consensus value was used, i.e. Z-scores between +1 and -1 reflect a deviation of $\pm 20\%$ 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 July 2015.

The final report will be made available to the participants in pdf format at www.fhi.no/ILC. A certificate, stating the participant's laboratory code, will be sent to each participant who has contributed to the results by the end of 2015.

Co-ordination

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

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Results

Presentation in the report

85 laboratories in 46 different countries submitted their results within the deadline and the results will be presented in the following chapters. All participating laboratories 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.

Readers of the report can without being participants in the study or with access to laboratory codes, get a general overview of the analytical performance of laboratories worldwide on the determination on PCDD/PCDFs, dioxin-like PCBs, indicator PCBs, PBDEs and HBCD in regular food stuffs.

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

Individual results reported by the laboratories for each congener are given for beef, salmon and cheese in Appendix 2, 3 and 4. Results of the lipid determinations are presented in Appendix 5.

Summary of results

PCDDs/PCDFs

Analyte solution

Concentrations for PCDDs/PCDFs were reported by 69 laboratories. The average RSD for the 17 congeners was 8.0 % ranging from 6.8 % for 1,2,3,7,8-PeCDF to 9.2 % for 1,2,3,4,6,7,8,9-OCDF. The calculation of Z-scores for the TEQs (target 12.5 pg TEQ/ μ L based on TEF₂₀₀₅-values) of the PCDD/PCDF standard solution showed that 94 % of the laboratories were within the range of ± 20 % of the consensus value. This demonstrates

that the calibration solutions used by the laboratories generally are of high quality.

Beef

For the beef sample, PCDD/PCDF results from 63 laboratories were received. The consensus TEQ (PCDD/PCDF TEQ based on WHO2005-TEFs) was 0.074 pg TEQ/g fresh weight and 0.57 pg TEQ/g lipid weight.

The average RSD was 40 %, ranging from 25-63 % for 2,3,4,7,8-PeCDF and 1,2,3,7,8,9-HxCDF, respectively. Z-scores within ± 1 were obtained by 70 % of the laboratories and 83 % of the laboratories had Z-scores within ± 2 (fresh weight basis).

Salmon

PCDD/PCDF concentrations in the Baltic Salmon were reported by 69 laboratories. The consensus TEQ was 3.1 pg TEQ/g fresh weight, and 39 pg TEQ/g lipid weight (PCDD/PCDF TEQ based on WHO₂₀₀₅-TEFs). The average RSD was 34 % ranging from 21-64 % (2,3,7,8-TCDF and 1,2,3,4,7,8,9-HpCDF, respectively). Z-scores were within ± 1 for 90 % of the laboratories and within ± 2 for 93 % of the laboratories (fresh weight basis).

Cheese

PCDD/PCDF concentrations in the cheese-sample were determined by 52 laboratories. The consensus TEQ was 0.028 pg TEQ/g on fresh weight basis, and 0.11 pg TEQ/g on lipid weight basis (PCDD/PCDF TEQ based on WHO₂₀₀₅-TEFs). The average RSD was 53 % ranging from 39-72 % (1,2,3,6,7,8-HxCDD and 1,2,3,7,8,9-HxCDF, respectively). Z-scores for PCDD/PCDF TEQ within ± 1 were obtained by 38 % of the laboratories and 53 % had Z-scores within ± 2 (fresh weight basis).

Dioxin-like PCBs

Analyte solution

The 12 dioxin-like PCBs in the analyte solution were analyzed and reported by 67-68 laboratories. The RSDs for the different congeners were ranging from 7.3 for PCB-126 to 10 % for PCB-118, with an average of 9.2 %.

Beef

Dioxin-like PCB concentrations in the beef sample were reported from 62 laboratories. The concentrations of the 12 congeners varied between 0.13 pg/g fresh weight (PCB-81) and 630 pg/g fresh weight (CB-118) (On lipid weight basis, 1.0 p/g and 4904 p/g for PCB-81 and PCB-118, respectively). The average RSD for concentrations of individual dioxin-like PCB congeners was 25 % ranging from 20 % for PCB-118 to 39 % for PCB-81

The dioxin-like PCBs contribute 82 % to the total TEQ (WHO TEF₂₀₀₅) in the sample with PCB-126 as the main contributor (73 %).

Salmon

Of the participating laboratories, 69-70 measured and reported dioxin-like PCB concentrations in the salmon sample. The concentrations ranged from 2.3 pg/g fresh weight for PCB-81 (29 pg/g lipid weight) to 5626 pg/g fresh weight for PCB-118 (70636 pg/g lipid weight). The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 26 % ranging from 19 % for PCB-157 to 44 % for PCB-123.

The dioxin-like PCBs contribute to about 64 % of the total TEQ in the sample with PCB-126 as the main contributor (56 %).

Cheese

Dioxin-like PCBs in the cheese-sample were reported by 52 laboratories. Levels were ranging from 0.048

pg/g fresh weigh for PCB-169 (0.18 pg/g lipid weight) to 36 pg/g fresh weight for PCB-118 (136 pg/g lipid weight). The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 40 % ranging from 28 % for PCB-105 to 56 % for PCB-189. The contribution of the dioxin-like PCBs to the total TEQ was about 47 % with PCB-126 as the main contributor (41 % of total TEQ).

Total TEQ

The total TEQ for the beef sample was 0.42 pg TEQ/g fresh weight and 3.2 pg TEQ/g lipid weight (WHO TEF₂₀₀₅). The total TEQ of the salmon was 8.6 pg TEQ/g fresh weight and 108 pg TEQ/g lipid weight, and the cheese contained 0.054 pg TEQ/g fresh weight and 0.21 pg TEQ/g lipid weight.

The RSDs for total TEQs on fresh weight basis calculated from the RSD of individual congeners were 12 % for beef, 11 % for salmon and 20 % for cheese.

In Figure 1 the contribution on the TEQ-values of the three groups of compounds is depicted based on WHO TEF₂₀₀₅ and WHO TEF₁₉₉₈, respectively. In the selection of food-items included in this study the dioxin-like PCBs contributed from 47 % to 82 % to the total TEQ (using WHO TEF₂₀₀₅), demonstrating the variation in contribution, and the importance of the PCBs for the determination of the total TEQs related to the toxic potency of food samples.

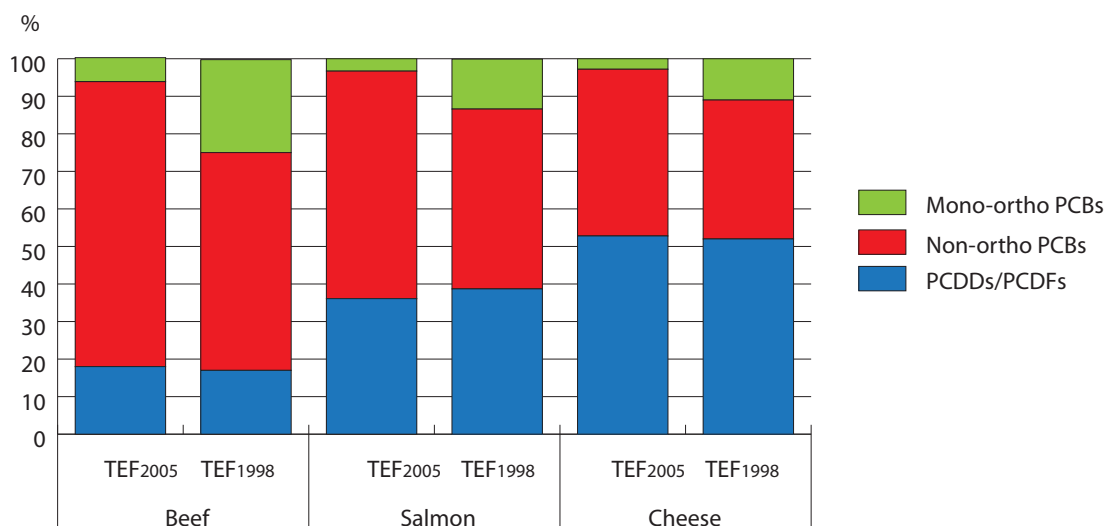


Figure 1. The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using both the WHO₂₀₀₅ TEFs and WHO₁₉₉₈ TEFs, in the three food samples.

Indicator PCBs

Analyte solution

60 laboratories reported indicator PCBs in the analyte solution. The average RSD was 11 % ranging from 10 to 14 %.

Beef

For the sample of beef, results for indicator PCBs were received from 54 laboratories. The consensus concentrations varied between 24 pg/g fresh weight/185 pg/g lipid weight (PCB-28) and 1023 pg/g fresh weight/7965 pg/g lipid weight (PCB-153). The RSDs were ranging from 32 to 45 % for PCB-153 and PCB-28, respectively, with an average of 37 % for all indicator PCBs. The consensus median for the sum of indicator PCBs was 2394 pg/g fresh weight.

Salmon

Within the deadline, 59 laboratories reported results for indicator PCBs in the salmon-sample. The consensus concentrations ranged from 703 pg/g fresh weight for PCB-28 (lipid weight: 8826 pg/g) to 15316 pg/g fresh weight for PCB-153 (lipid weight: 192291 pg/g) with a consensus median for the sum of indicator PCBs of 39149 pg/g fresh weight. The average RSD was 34 %, ranging from 31 to 41 % for PCB-180 and PCB-28, respectively.

Cheese

Results were obtained from 43 laboratories. The concentrations of indicator PCBs in the cheese-sample ranged from 13 pg/g fresh weight (PCB-28) to 56 pg/g (PCB-153) (lipid weight: 50 pg/g for PCB-28 and 215 pg/g for PCB-153) and the consensus median for the sum was 185 pg/g fresh weight. The average RSD was 48 %, ranging from 42 to 57 % for PCB-138 and PCB-28, respectively.

PBDEs

Analyte solution

The tri- to hepta-PBDE standard solution was analyzed by 33-34 laboratories and 26 laboratories reported values for PBDE-209. The RSDs were between 7.4-11 % for all congeners.

Beef

The PBDE concentrations in beef were reported by 29-30 laboratories, except for PBDE-209 for which 23 results were received. The consensus concentrations were in the range from 0.43 pg/g fresh weight for PBDE-28 to 11 pg/g fresh weight for PBDE-47 (lipid weight: 3.3 pg/g for PBDE-28, 88 pg/g for PBDE-47). The consensus concentration for PBDE-209 was 56

pg/g fresh weight. The sum of tri- to hepta-PBDEs was 22 pg/g fresh weight. The range of RSDs on fresh weight basis was 24-50 %, with an average of 34 % including PBDE-209.

Salmon

Within the deadline, 36 laboratories had reported results for tri- to hepta-PBDEs in salmon and 29 laboratories had reported results for PBDE-209. The consensus concentrations varied between 2.9 pg/g fresh weight (PBDE-183) and 1572 pg/g fresh weight (PBDE-47) (lipid weight: 36 pg/g for PBDE-183, 19742 pg/g for PBDE-47). The concentration for PBDE-209 was 22 pg/g fresh weight. The sum of tri- to hepta-PBDEs was 2741 pg/g fresh weight. The RSD calculated from the concentrations on fresh weight ranged from 11-45 %, with an average of 23 % for PBDEs including PBDE-209.

Cheese

25 laboratories reported results for tri- to hepta-PBDEs in cheese, and 19 reported results for PBDE-209. The concentrations varied between 0.30 pg/g fresh weight (PBDE-28) (lipid weight: 1.1 pg/g) and 13 pg/g (PBDE-47) (lipid weight: 51 pg/g). The concentration for PBDE-209 was 134 pg/g. The sum of tri- to hepta-PBDEs was 28 pg/g fresh weight. The RSDs for the individual congeners were ranging from 18 to 59 % with an average of 37 % including PBDE-209.

HBCD

Also in this round of the study, total HBCD and the isomers α -, β - and γ -HBCD could be determined and reported. A total of 12 laboratories reported α -HBCD in the standard solution and 4-14 laboratories reported one or more of the three isomers in the food samples. The consensus concentrations for the sum of individual HBCD isomers were 103 pg/g fresh weight for the beef sample, 3820 pg/g for the salmon and 11 pg/g fresh weight for the cheese sample. Since only a few laboratories reported HBCD, these results must be regarded as indicative values.

Lipid content

The mean and RSDs (in parentheses) for the lipid contents of the food samples were calculated to be 13 % (RSD=8.3 %) for the beef sample, 7.8 % (RSD=13 %) for the salmon and 25 % (RSD=14 %) for the cheese sample.

Acknowledgements

The laboratories are acknowledged for their participation in this interlaboratory comparison and in 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.

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Appendix A:

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and addresses

Appendix A: Affiliations and addresses of participants

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Appendix B:

Study announcement and
instructions for participants

Announcement for Interlaboratory Comparison on POPs in Food 2015

Introduction

We hereby announce the 16th round of the Interlaboratory Comparison on the Determination of POPs in Food. The study is open for academic, regulatory as well as commercial laboratories world-wide. The organizer of this study is the Division of Environmental Medicine, Department of Exposure and Risk Assessment at the Norwegian Institute of Public Health, Oslo, Norway. The study is scheduled to take place from January to April 2015. A draft report will be available by mid July 2015, and the final report will be available to the participants by November 2015. All participants who have contributed to the results will receive a certificate of participation in the study.

Objectives

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

Participants

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

Analytical requirements

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

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

Test material

The test materials consist of three unfortified natural food product homogenates, Beef (labelled “Beef-2015”) ~100 g, Salmon (labelled “Salmon-2015”) ~100 g and Cheese

(labelled “Cheese-2015”) ~60 g, and will be distributed by an international courier service to the participating laboratories.

Please note:

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

Instructions for analysis and reporting

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

In short, the participating laboratories should:

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

Time schedule

Announcement	December 2014
Return of registration form	January 05, 2015
Shipment of test material	Third week, 2015
Confirmation of receipt of test material by participant	Within 7 days
Reporting of test results ^{a)}	April 24, 2015
Publication of draft report on web-site	July 2015
Final report available to all participants	November 2015

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

Participation fee

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

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Interlaboratory Comparison on Dioxins in Food 2015

Instructions for participants

January 2015

1. Introduction

This is the 16th Round of the Interlaboratory Comparison Study on the Determination of POPs in Food organised by the Department of Exposure and Risk Assessment, Norwegian Institute of Public Health, Oslo, Norway. The objective of this exercise is to assess the interlaboratory comparability of the results from analyses of all dioxins and dioxin-like PCBs included in the WHO-TEF schemes in regular foods. Participants may also determine and report concentrations of six marker PCBs, eight polybrominated diphenylethers (PBDEs) and hexabromocyclododecane (HBCD). The exercise serves as a quality assurance instrument for the participating laboratories. A further objective is to assess the world-wide readiness and capacity for the determination of dioxin-like compounds, marker PCBs, PBDEs and HBCD in food. Instructions for the analysis and submission of results are given below.

Please read these instructions carefully before starting the experimental work.

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

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

in samples of Beef (Beef-2015), Salmon (Salmon-2015) and Cheese (Cheese-2015). The mentioned analytes should also be determined in the respective six standard solutions. For HBCD, concentrations of α -HBCD, β -HBCD and γ -HBCD as well as the total of these isomers will be assessed. Both results from GC-MS and LC-MS or LC-MS/MS are welcome.

2. Participants

A list of participants is attached. 84 laboratories have announced their participation in the study.

3. Design of the study

3.1 Test materials

Samples

One standard solution of each:

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

One sample of each

- ca. 100 g beef
- ca. 100 g salmon
- ca. 60 g cheese

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	Beef-2015
Salmon	Salmon-2015
Cheese	Cheese-2015

The above sample coding is marked on the sample bottles.

3.3 Analytical procedure

Methods to be used

Laboratories shall use

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

- their own lipid determination procedure

Standard solutions

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

General

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

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

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

4. Reporting

4.1 Results to be reported

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

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

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

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

4.2 Checklist

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

4.3 Submitting results

Three Microsoft Excel files are provided to each participant comprising:

Participants confirmation

- confirmation of receiving test materials

Report form dioxins and dioxinlike PCBs

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

Report form marker PCBs, PBDEs and HBCD

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

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

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

The electronic report shall be sent to dioxin@fhi.no within the deadline.

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

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

Deadline

The reports must be in our hands no later than April 24, 2015 to enable us to prepare the draft report to be published by the end of July 2015. There will normally be no extension of this deadline. A confirmation for the receipt of your results will be sent to you by e-mail within a week.

5. Statistical evaluations

Prior to the final report, a draft version will be prepared based on the data reported by April 24th. The co-ordinators will calculate mean, median and between-laboratory standard deviations for each congener. Outliers will be removed, and consensus values will be calculated. In case of extreme deviation from normal distribution, appropriate procedures will be used to get a best available estimate of the true value. For the dioxin-like compounds, TEQ values will be calculated for each laboratory and a consensus TEQ value based on the consensus of the congeners. Z-scores will be calculated for laboratories' results for PCDD/PCDF TEQs and PCB TEQs.

6. Final report

The final report will be prepared by the co-ordinators by November 2015 and will then be made available for all interested parties in an electronic version on <http://www.fhi.no>. All participants will be presented by their laboratory code. Prior to this, a draft will be published on the Internet by the end of July.

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

7. Fee

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

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

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

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

8. Time schedule

Announcement	December 2014
Return of registration form	January 05, 2015
Shipment of test material	Third week, 2015
Confirmation of receipt of test material by participant	Within 7 days
Reporting of test results ^{a)}	April 24, 2015
Publication of draft report on web-site	July 2015
Final report available to all participants	November 2015

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

9. Co-ordinators of the study

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Interlaboratory Comparison on Dioxins in Food 2015

Checklist

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

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

Appendix C:

WHO TEFs for human risk assessment

WHO TEFs for human risk assessment based on the conclusions of the World Health

Organisation Meeting in Stockholm, Sweden, 15-18 June 1997 and International Programme on Chemical Safety expert meeting in Geneva, June 2005

(M. van den Berg et al., Environ Health Perspect 1998;106:775-792; M. van den Berg et al., Toxicological sciences 93(2), 223-241 (2006))

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

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

Appendix D:

Homogeneity testing

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

Introduction

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

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

Summary results

Consensus of congener concentrations

Consensus of TEQ values

Consensus statistics

Laboratories' reported TEQs

Laboratories' Z-scores

Z-score plots

Consensus congener concentrations

	Beef		Salmon		Cheese	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
2,3,7,8 TCDD	0.0089	0.069	0.39	4.9	0.0063	0.024
1,2,3,7,8 PeCDD	0.021	0.16	0.68	8.5	0.0093	0.036
1,2,3,4,7,8 HxCDD	0.013	0.10	0.037	0.46	0.0071	0.027
1,2,3,6,7,8 HxCDD	0.039	0.31	0.27	3.4	0.012	0.046
1,2,3,7,8,9 HxCDD	0.011	0.082	0.020	0.26	0.0078	0.030
1,2,3,4,6,7,8 HpCDD	0.075	0.59	0.036	0.46	0.030	0.12
1,2,3,4,6,7,8,9 OCDD	0.10	0.77	0.12	1.5	0.078	0.30
2,3,7,8 TCDF	0.0077	0.060	5.7	72	0.010	0.038
1,2,3,7,8 PeCDF	0.0050	0.039	0.86	11	0.0052	0.020
2,3,4,7,8 PeCDF	0.086	0.67	4.5	56	0.018	0.071
1,2,3,4,7,8 HxCDF	0.037	0.29	0.12	1.5	0.0090	0.034
1,2,3,6,7,8 HxCDF	0.028	0.22	0.17	2.1	0.009	0.034
2,3,4,6,7,8 HxCDF	0.028	0.22	0.15	1.9	0.0077	0.030
1,2,3,7,8,9 HxCDF	0.0047	0.036	0.0056	0.070	0.0044	0.017
1,2,3,4,6,7,8 HpCDF	0.020	0.16	0.016	0.19	0.012	0.046
1,2,3,4,7,8,9 HpCDF	0.0049	0.038	0.0050	0.063	0.0049	0.019
1,2,3,4,6,7,8,9 OCDF	0.015	0.12	0.021	0.26	0.019	0.071
PCB 77	1.8	14	106	1333	0.82	3.1
PCB 126	3.0	24	48	607	0.22	0.86
PCB 169	0.44	3.4	12	147	0.048	0.18
PCB 81	0.13	1.0	2.3	29	0.056	0.21
PCB 105	87	680	1972	24758	8.6	33
PCB 114	12	96	120	1507	1.0	3.8
PCB 118	630	4904	5626	70636	36	136
PCB 123	6.7	52	64	804	0.55	2.1
PCB 156	85	665	876	10997	3.1	12
PCB 157	17	134	207	2595	0.62	2.4
PCB 167	40	314	469	5888	1.5	5.9
PCB 189	8.1	63	93	1168	0.24	0.92

fw. - fresh weight

lw. - lipid weight

Consensus congener concentrations

	Beef		Salmon		Cheese	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
PCB 28	24	185	703	8826	13	50
PCB 52	35	274	1593	19996	18	68
PCB 101	100	779	6220	78092	45	172
PCB 138	787	6121	10606	133160	38	145
PCB 153	1023	7965	15316	192291	56	215
PCB 180	425	3307	4711	59146	15	58
PBDE 28	0.43	3.3	62	781	0.30	1.1
PBDE 47	11	88	1572	19742	13	51
PBDE 99	5.4	42	333	4181	8.9	34
PBDE 100	1.3	10	416	5217	1.7	6.5
PBDE 153	2.1	17	93	1165	1.4	5.5
PBDE 154	0.90	7.0	262	3293	0.80	3.0
PBDE 183	0.83	6.5	2.9	36	1.0	3.9
PBDE 209	56	435	22	281	134	515
α-HBCD	60	467	3388	42535	6.0	23
β-HBCD	10	78	40	502	0.82	3.1
γ-HBCD	33	254	120	1507	5.1	20
Tot HBCD	103	802	3820	47960	11	43
Sum PCB	2394	18631	39149	491511	185	709
Sum PBDE without 209	22	173	2741	34415	28	106
Sum PBDE	78	608	2764	34696	162	621

fw. - fresh weight

lw. - lipid weight

Consensus of TEQs

TEF₂₀₀₅

	Beef		Salmon		Cheese	
	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	0.0089	0.069	0.39	4.9	0.0063	0.024
1,2,3,7,8-PeCDD	0.021	0.16	0.68	8.5	0.009	0.036
1,2,3,4,7,8-HxCDD	0.0013	0.010	0.0037	0.046	0.00071	0.0027
1,2,3,6,7,8-HxCDD	0.0039	0.031	0.027	0.34	0.0012	0.0046
1,2,3,7,8,9-HxCDD	0.0011	0.0082	0.0020	0.026	0.00078	0.0030
1,2,3,4,6,7,8-HpCDD	0.00075	0.0059	0.00036	0.0046	0.00030	0.0012
1,2,3,4,6,7,8,9-OCDD	0.000030	0.00023	0.000036	0.00045	0.000023	0.000089
2,3,7,8-TCDF	0.00077	0.0060	0.57	7.2	0.0010	0.0038
1,2,3,7,8-PeCDF	0.00015	0.0012	0.026	0.32	0.00016	0.00060
2,3,4,7,8-PeCDF	0.026	0.20	1.4	17	0.0055	0.021
1,2,3,4,7,8-HxCDF	0.0037	0.029	0.012	0.15	0.00090	0.0034
1,2,3,6,7,8-HxCDF	0.0028	0.022	0.017	0.21	0.0009	0.0034
2,3,4,6,7,8-HxCDF	0.0028	0.022	0.015	0.19	0.00077	0.0030
1,2,3,7,8,9-HxCDF	0.00047	0.0036	0.00056	0.0070	0.00044	0.0017
1,2,3,4,6,7,8-HpCDF	0.00020	0.0016	0.00016	0.0019	0.00012	0.00046
1,2,3,4,7,8,9-HpCDF	0.000049	0.00038	0.000050	0.00063	0.000049	0.00019
1,2,3,4,6,7,8,9-OCDF	0.0000044	0.000035	0.0000062	0.000078	0.0000056	0.000021
PCB 77	0.00018	0.0014	0.011	0.13	0.000082	0.00031
PCB 126	0.30	2.4	4.8	61	0.022	0.086
PCB 169	0.013	0.10	0.35	4.4	0.0014	0.0055
PCB 81	0.000039	0.00031	0.00069	0.0087	0.000017	0.000064
PCB 105	0.0026	0.020	0.059	0.74	0.00026	0.0010
PCB 114	0.00037	0.0029	0.0036	0.045	0.000030	0.00011
PCB 118	0.019	0.15	0.17	2.1	0.0011	0.0041
PCB 123	0.00020	0.0016	0.0019	0.024	0.000017	0.000063
PCB 156	0.0026	0.020	0.026	0.33	0.000092	0.00035
PCB 157	0.00052	0.0040	0.0062	0.078	0.000019	0.000071
PCB 167	0.0012	0.0094	0.014	0.18	0.000046	0.00018
PCB 189	0.00024	0.0019	0.0028	0.035	0.0000072	0.000027
PCDDs/PCDFs	0.074	0.57	3.1	39	0.028	0.11
Non-ortho PCBs	0.32	2.5	5.2	65	0.024	0.092
Mono-ortho PCBs	0.027	0.21	0.28	3.6	0.0015	0.0059
Total TEQ	0.42	3.2	8.6	108	0.054	0.21

fw. - fresh weight

lw. - lipid weight

Consensus of TEQs

TEF₁₉₉₈

	Beef		Salmon		Cheese	
	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	0.0089	0.069	0.39	4.9	0.0063	0.024
1,2,3,7,8-PeCDD	0.021	0.16	0.68	8.5	0.0093	0.036
1,2,3,4,7,8-HxCDD	0.0013	0.010	0.0037	0.046	0.00071	0.0027
1,2,3,6,7,8-HxCDD	0.0039	0.031	0.027	0.34	0.0012	0.0046
1,2,3,7,8,9-HxCDD	0.0011	0.0082	0.0020	0.026	0.00078	0.0030
1,2,3,4,6,7,8-HpCDD	0.00075	0.0059	0.00036	0.0046	0.00030	0.0012
1,2,3,4,6,7,8,9-OCDD	0.000010	0.000077	0.0000120	0.00015	0.0000078	0.000030
2,3,7,8-TCDF	0.00077	0.0060	0.57	7.2	0.0010	0.0038
1,2,3,7,8-PeCDF	0.00025	0.0019	0.043	0.54	0.00026	0.0010
2,3,4,7,8-PeCDF	0.043	0.34	2.3	28	0.0092	0.035
1,2,3,4,7,8-HxCDF	0.0037	0.029	0.012	0.15	0.00090	0.0034
1,2,3,6,7,8-HxCDF	0.0028	0.022	0.017	0.21	0.00088	0.0034
2,3,4,6,7,8-HxCDF	0.0028	0.022	0.015	0.19	0.00077	0.0030
1,2,3,7,8,9-HxCDF	0.00047	0.0036	0.00056	0.0070	0.00044	0.0017
1,2,3,4,6,7,8-HpCDF	0.00020	0.0016	0.00016	0.0019	0.00012	0.00046
1,2,3,4,7,8,9-HpCDF	0.000049	0.00038	0.000050	0.00063	0.000049	0.00019
1,2,3,4,6,7,8,9-OCDF	0.0000015	0.000012	0.0000021	0.000026	0.0000019	0.0000071
PCB 77	0.00018	0.0014	0.011	0.13	0.000082	0.00031
PCB 126	0.30	2.4	4.8	61	0.022	0.086
PCB 169	0.0044	0.034	0.12	1.5	0.00048	0.0018
PCB 81	0.000013	0.00010	0.00023	0.0029	0.0000056	0.000021
PCB 105	0.0087	0.068	0.20	2.5	0.00086	0.0033
PCB 114	0.0061	0.048	0.060	0.75	0.00050	0.0019
PCB 118	0.063	0.49	0.56	7.1	0.0036	0.014
PCB 123	0.00067	0.0052	0.0064	0.080	0.000055	0.00021
PCB 156	0.043	0.33	0.44	5.5	0.0015	0.0058
PCB 157	0.0086	0.067	0.10	1.3	0.00031	0.0012
PCB 167	0.00040	0.0031	0.0047	0.059	0.000015	0.000059
PCB 189	0.00081	0.0063	0.0093	0.12	0.000024	0.000092
PCDDs/PCDFs	0.091	0.71	4.0	50	0.032	0.12
Non-ortho PCBs	0.31	2.4	5.0	62	0.023	0.088
Mono-ortho PCBs	0.13	1.0	1.4	17	0.0068	0.026
Total TEQ	0.53	4.1	10	130	0.062	0.24

fw. - fresh weight

lw. - lipid weight

Consensus statistics

Analyte solution

	Target value pg/µl	Consensus median, pg/µl	Median all values pg/µl	Consensus mean, pg/µl	Standard deviation, pg/µl	Relative standard deviation, %	No. of values reported	No. of values removed
2,3,7,8 TCDD	2.0	2.0	2.0	2.0	0.19	9.2	69	3
1,2,3,7,8 PeCDD	5.0	4.8	4.9	4.8	0.37	7.7	69	2
1,2,3,4,7,8 HxCDD	5.0	4.8	4.9	4.8	0.42	8.7	69	4
1,2,3,6,7,8 HxCDD	5.0	4.9	4.9	4.8	0.41	8.6	69	4
1,2,3,7,8,9 HxCDD	5.0	5.1	5.1	5.1	0.38	7.5	69	3
1,2,3,4,6,7,8 HpCDD	5.0	4.9	4.9	4.9	0.36	7.3	69	3
1,2,3,4,6,7,8,9 OCDD	10	9.8	9.8	9.8	0.8	8.4	69	2
2,3,7,8 TCDF	2.0	1.9	1.9	2.0	0.16	7.9	69	3
1,2,3,7,8 PeCDF	5.0	5.0	5.0	5.0	0.34	6.8	69	3
2,3,4,7,8 PeCDF	5.0	4.8	4.8	4.8	0.39	8.2	69	3
1,2,3,4,7,8 HxCDF	5.0	4.9	4.9	4.9	0.36	7.4	69	3
1,2,3,6,7,8 HxCDF	5.0	4.9	4.9	4.9	0.34	7.0	69	3
2,3,4,6,7,8 HxCDF	5.0	4.9	4.9	5.0	0.34	6.9	69	3
1,2,3,7,8,9 HxCDF	5.0	4.9	5.0	4.9	0.38	7.9	69	3
1,2,3,4,6,7,8 HpCDF	5.0	4.9	5.0	4.9	0.39	8.0	69	3
1,2,3,4,7,8,9 HpCDF	5.0	5.0	5.0	5.0	0.43	8.6	69	3
1,2,3,4,6,7,8,9 OCDF	10	10	10	9.7	0.90	9.2	68	3
PCB 77	10	9.8	9.8	9.7	0.98	10	68	3
PCB 126	10	10	10	10	0.75	7.3	68	3
PCB 169	10	10	10	10	0.75	7.5	68	3
PCB 81	10	10	10	10	0.97	9.6	68	3
PCB 105	100	99	99	100	9.6	9.6	67	2
PCB 114	100	100	100	99	9.6	9.7	67	3
PCB 118	100	100	100	100	10	10	67	3
PCB 123	100	101	101	100	9.3	9.3	67	2
PCB 156	100	100	100	100	9.7	9.7	67	2
PCB 157	100	99	99	99	8.9	9.0	67	2
PCB 167	100	100	100	99	9.1	9.1	67	3
PCB 189	100	100	100	100	9.0	9.1	67	2

Consensus statistics

Analyte solution

	Target value pg/ul	Median, pg/ul all values	Median, pg/ul outliers removed	Mean, pg/ul all values	Mean, pg/ul outliers removed
PCB 28	100	98	98	97	97
PCB 52	100	98	98	98	98
PCB 101	100	98	98	98	98
PCB 138	100	98	98	98	98
PCB 153	100	98	98	98	98
PCB 180	100	98	98	99	99
PBDE 28	25	25	25	758	25
PBDE 47	25	25	25	745	25
PBDE 99	25	25	25	703	25
PBDE 100	25	24	24	724	24
PBDE 153	25	25	25	725	25
PBDE 154	25	25	25	715	24
PBDE 183	25	25	24	660	24
PBDE 209	100	100	99	106	97
α -HBCD *	500	500	500	489	489

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Number of reported values	Number of reported outliers
PCB 28	14	14	60	0
PCB 52	10	10	60	0
PCB 101	11	11	60	0
PCB 138	11	11	60	0
PCB 153	10	10	60	0
PCB 180	11	11	60	0
PBDE 28	564	8.5	34	1
PBDE 47	564	7.4	34	1
PBDE 99	563	8.6	34	1
PBDE 100	564	8.7	34	1
PBDE 153	563	9.3	34	1
PBDE 154	563	9.6	34	1
PBDE 183	553	11	33	1
PBDE 209	26	11	26	3
α -HBCD *	10	10	12	0

NDs: Non-detects

* : Indicative value due to few reported values

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-detects
2,3,7,8 TCDD	0.0089	0.0093	0.0088	0.0039	44	63	5	19
1,2,3,7,8 PeCDD	0.021	0.021	0.021	0.0070	33	63	2	9
1,2,3,4,7,8 HxCDD	0.013	0.014	0.014	0.0049	36	63	5	12
1,2,3,6,7,8 HxCDD	0.039	0.040	0.040	0.011	26	63	3	4
1,2,3,7,8,9 HxCDD	0.011	0.011	0.011	0.0043	39	63	9	12
1,2,3,4,6,7,8 HpCDD	0.075	0.077	0.077	0.023	29	63	2	2
1,2,3,4,6,7,8,9 OCDD	0.10	0.11	0.10	0.041	39	63	11	5
2,3,7,8 TCDF	0.0077	0.011	0.0093	0.0051	55	63	15	14
1,2,3,7,8 PeCDF	0.0050	0.0060	0.0057	0.0028	50	63	16	29
2,3,4,7,8 PeCDF	0.086	0.086	0.086	0.022	25	63	1	1
1,2,3,4,7,8 HxCDF	0.037	0.038	0.039	0.012	32	63	3	3
1,2,3,6,7,8 HxCDF	0.028	0.028	0.027	0.0076	28	63	3	4
2,3,4,6,7,8 HxCDF	0.028	0.029	0.027	0.0087	32	63	3	5
1,2,3,7,8,9 HxCDF	0.0047	0.0060	0.0051	0.0032	63	63	12	44
1,2,3,4,6,7,8 HpCDF	0.020	0.023	0.023	0.0081	36	63	12	5
1,2,3,4,7,8,9 HpCDF	0.0049	0.0060	0.0053	0.0030	57	63	17	34
1,2,3,4,6,7,8,9 OCDF	0.015	0.019	0.016	0.0094	58	63	13	21
PCB 77	1.8	1.9	1.9	0.47	25	62	6	0
PCB 126	3.0	3.0	3.0	0.62	20	62	0	0
PCB 169	0.44	0.44	0.45	0.12	27	62	1	1
PCB 81	0.13	0.13	0.13	0.050	39	62	5	6
PCB 105	87	88	90	18	20	62	1	0
PCB 114	12	12	12	2.4	20	62	1	0
PCB 118	630	630	635	125	20	62	0	0
PCB 123	6.7	6.8	6.5	2.4	38	62	2	4
PCB 156	85	86	86	17	20	62	1	0
PCB 157	17	17	17	3.7	21	62	0	0
PCB 167	40	40	39	9.1	23	62	2	0
PCB 189	8.1	8.1	8.2	1.8	22	62	0	1

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
PCB 28	27	23	24	104	24	25
PCB 52	36	35	35	267	33	34
PCB 101	101	98	100	184	96	98
PCB 138	793	787	787	793	767	767
PCB 153	1025	1023	1023	999	971	971
PCB 180	426	425	425	407	397	397
PBDE 28	0.52	0.43	0.43	1.9	0.45	0.45
PBDE 47	12	11	11	38	12	12
PBDE 99	5.6	5.4	5.4	14	5.8	5.8
PBDE 100	1.5	1.3	1.3	7.1	1.4	1.4
PBDE 153	2.2	2.2	2.1	3.9	2.3	2.2
PBDE 154	0.96	0.92	0.90	5.7	0.91	0.88
PBDE 183	0.95	0.84	0.83	1.5	0.88	0.81
PBDE 209	65	54	56	165	57	58
α -HBCD *	63	60	60	80	63	63
β -HBCD *	15	12.0	10	21	12.8	10
γ -HBCD *	35	30	33	222	35	36
Tot HBCD *	116	103	103	339	104	104

	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
PCB 28	462	50	45	54	12	2
PCB 52	569	42	38	54	10	1
PCB 101	259	37	34	54	6	1
PCB 138	43	37	37	54	1	0
PCB 153	37	32	32	54	1	0
PCB 180	38	35	35	54	1	0
PBDE 28	263	47	47	30	8	3
PBDE 47	288	35	35	30	5	0
PBDE 99	192	24	24	30	6	0
PBDE 100	360	25	25	30	7	1
PBDE 153	187	33	31	30	2	2
PBDE 154	410	31	30	30	5	4
PBDE 183	97	37	32	29	6	7
PBDE 209	268	54	50	23	4	3
α -HBCD *	51	16	16	12	2	0
β -HBCD *	95	70	54	12	3	5
γ -HBCD *	275	39	37	12	2	1
Tot HBCD *	186	27	27	14	3	0

NDs: Non-detects

* : Indicative value due to few reported values

Consensus statistics

Salmon, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
2,3,7,8 TCDD	0.39	0.39	0.38	0.092	24	69	2	2
1,2,3,7,8 PeCDD	0.68	0.68	0.66	0.15	23	69	0	1
1,2,3,4,7,8 HxCDD	0.037	0.038	0.036	0.011	31	69	7	9
1,2,3,6,7,8 HxCDD	0.27	0.27	0.27	0.065	24	69	2	2
1,2,3,7,8,9 HxCDD	0.020	0.023	0.021	0.0067	33	69	12	10
1,2,3,4,6,7,8 HpCDD	0.036	0.039	0.036	0.013	35	69	13	8
1,2,3,4,6,7,8,9 OCDD	0.12	0.12	0.12	0.047	39	69	9	8
2,3,7,8 TCDF	5.7	5.7	5.5	1.2	21	69	1	0
1,2,3,7,8 PeCDF	0.86	0.86	0.85	0.23	27	69	3	1
2,3,4,7,8 PeCDF	4.5	4.5	4.4	1.0	22	69	1	0
1,2,3,4,7,8 HxCDF	0.12	0.12	0.12	0.034	29	69	3	2
1,2,3,6,7,8 HxCDF	0.17	0.17	0.17	0.047	28	69	4	0
2,3,4,6,7,8 HxCDF	0.15	0.15	0.14	0.038	27	69	4	3
1,2,3,7,8,9 HxCDF	0.0056	0.009	0.0062	0.0035	56	69	22	37
1,2,3,4,6,7,8 HpCDF	0.016	0.020	0.018	0.0083	47	69	15	16
1,2,3,4,7,8,9 HpCDF	0.0050	0.0077	0.0061	0.0039	64	69	19	40
1,2,3,4,6,7,8,9 OCDF	0.021	0.026	0.023	0.013	55	69	13	22
PCB 77	106	107	103	30	29	70	2	0
PCB 126	48	48	47	10	21	70	3	0
PCB 169	12	12	12	2.6	22	70	2	1
PCB 81	2.3	2.3	2.3	0.81	36	70	10	3
PCB 105	1972	1974	1945	491	25	69	2	0
PCB 114	120	120	123	33	27	69	2	0
PCB 118	5626	5627	5563	1468	26	69	1	1
PCB 123	64	69	66	29	44	69	11	4
PCB 156	876	878	887	172	19	69	2	0
PCB 157	207	207	203	37	19	69	2	0
PCB 167	469	476	455	113	25	69	5	0
PCB 189	93	93	92	17	19	69	2	0

Consensus statistics

Salmon, 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
PCB 28	725	703	703	873	699	699
PCB 52	1600	1593	1593	1750	1482	1482
PCB 101	6316	6220	6220	6248	5862	5862
PCB 138	10829	10606	10606	11250	10508	10508
PCB 153	15322	15316	15316	14760	14352	14352
PCB 180	4720	4711	4711	4650	4324	4324
PBDE 28	63	62	62	1532	62	62
PBDE 47	1584	1572	1572	1684	1586	1586
PBDE 99	336	333	333	441	337	337
PBDE 100	418	416	416	513	407	407
PBDE 153	93	93	93	185	94	94
PBDE 154	268	262	262	334	261	261
PBDE 183	2.9	2.7	2.9	3.3	2.8	2.9
PBDE 209	24	20	22	1057	21	22
α -HBCD *	3388	3388	3388	3670	3670	3670
β -HBCD *	53	40	40	103	47	47
γ -HBCD *	130	120	120	258	134	134
Tot HBCD *	3820	3820	3820	4184	4184	4184

	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
PCB 28	116	41	41	59	4	0
PCB 52	88	33	33	59	3	0
PCB 101	44	31	31	59	2	0
PCB 138	45	36	36	59	3	0
PCB 153	39	34	34	59	1	0
PCB 180	47	31	31	59	2	0
PBDE 28	573	21	21	36	2	0
PBDE 47	40	21	21	36	1	0
PBDE 99	114	14	14	36	2	0
PBDE 100	96	16	16	36	2	0
PBDE 153	271	11	11	36	2	0
PBDE 154	105	21	21	36	2	0
PBDE 183	83	44	37	36	2	8
PBDE 209	509	50	45	29	9	5
α -HBCD *	24	24	24	12	0	0
β -HBCD *	132	33	33	12	3	0
γ -HBCD *	117	27	27	12	2	0
Tot HBCD *	34	34	34	13	0	0

NDs: Non-detects

* : Indicative value due to few reported values

Consensus statistics

Cheese, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
2,3,7,8 TCDD	0.0063	0.0077	0.0066	0.0036	54	52	10	32
1,2,3,7,8 PeCDD	0.0093	0.010	0.010	0.0045	46	52	12	23
1,2,3,4,7,8 HxCDD	0.0071	0.0080	0.0074	0.0039	52	52	10	28
1,2,3,6,7,8 HxCDD	0.012	0.014	0.012	0.0048	39	52	9	20
1,2,3,7,8,9 HxCDD	0.0078	0.010	0.0084	0.0042	50	52	14	26
1,2,3,4,6,7,8 HpCDD	0.030	0.033	0.032	0.013	41	52	8	12
1,2,3,4,6,7,8,9 OCDD	0.078	0.093	0.085	0.046	54	52	10	13
2,3,7,8 TCDF	0.010	0.012	0.0094	0.0051	54	52	18	20
1,2,3,7,8 PeCDF	0.0052	0.0077	0.0065	0.0036	55	52	13	29
2,3,4,7,8 PeCDF	0.018	0.020	0.019	0.0082	44	52	6	13
1,2,3,4,7,8 HxCDF	0.0090	0.012	0.011	0.0059	55	52	13	20
1,2,3,6,7,8 HxCDF	0.0088	0.010	0.010	0.0054	53	52	8	20
2,3,4,6,7,8 HxCDF	0.0077	0.010	0.0081	0.0042	52	52	14	23
1,2,3,7,8,9 HxCDF	0.0044	0.0071	0.0050	0.0036	72	52	15	36
1,2,3,4,6,7,8 HpCDF	0.012	0.015	0.013	0.0072	55	52	15	16
1,2,3,4,7,8,9 HpCDF	0.0049	0.0085	0.0061	0.0044	72	52	15	37
1,2,3,4,6,7,8,9 OCDF	0.019	0.023	0.017	0.0097	57	52	16	25
PCB 77	0.82	1.0	1.0	0.44	44	52	8	3
PCB 126	0.22	0.25	0.25	0.10	39	52	7	4
PCB 169	0.048	0.057	0.049	0.023	46	52	12	13
PCB 81	0.056	0.066	0.059	0.025	42	52	11	13
PCB 105	8.6	9.1	9.0	2.6	28	52	11	0
PCB 114	1.0	1.1	1.0	0.39	38	52	9	8
PCB 118	36	37	37	11	30	52	8	0
PCB 123	0.55	0.66	0.56	0.26	47	52	13	13
PCB 156	3.1	3.2	3.3	1.2	38	52	7	2
PCB 157	0.62	0.74	0.69	0.26	38	52	12	8
PCB 167	1.54	1.9	1.7	0.64	37	52	10	5
PCB 189	0.24	0.39	0.32	0.18	56	52	11	17

Consensus statistics

Cheese, 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
PCB 28	16	13	13	37	13	13
PCB 52	22	18	18	60	19	19
PCB 101	47	45	45	123	46	46
PCB 138	41	38	38	109	36	36
PCB 153	60	56	56	138	55	55
PCB 180	16	15	15	42	15	14.4
PBDE 28	0.55	0.28	0.30	7.8	0.33	0.38
PBDE 47	15	13	13	207	14	14
PBDE 99	9.5	8.9	8.9	71	9.0	9.0
PBDE 100	2.0	1.7	1.7	45	1.8	1.8
PBDE 153	1.5	1.5	1.4	19	1.6	1.5
PBDE 154	1.00	0.76	0.80	42	0.83	0.87
PBDE 183	1.1	1.0	1.0	2.4	0.96	0.99
PBDE 209	141	140	134	158	147	143
α -HBCD *	10	6.0	6.0	19	7.4	8.1
β -HBCD *	5.0	1.6	0.82	8.5	2.2	0.8
γ -HBCD *	5.3	5.0	5.1	12	3.9	5.1
Tot HBCD *	13	11	11	90	9.8	9.8

	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
PCB 28	136	57	57	43	14	2
PCB 52	190	54	55	43	12	1
PCB 101	222	47	47	43	8	0
PCB 138	216	42	42	43	9	0
PCB 153	201	43	43	43	7	0
PCB 180	253	45	46	43	7	2
PBDE 28	407	69	59	25	9	7
PBDE 47	419	38	38	25	7	0
PBDE 99	315	18	18	25	7	0
PBDE 100	437	31	31	25	8	1
PBDE 153	410	35	34	25	4	3
PBDE 154	470	45	43	25	6	6
PBDE 183	128	36	32	25	8	6
PBDE 209	47	41	43	19	1	2
α -HBCD *	151	60	48	11	3	4
β -HBCD *	110	94		11	4	9
γ -HBCD *	105	90	4	11	4	8
Tot HBCD *	197	40	40	8	3	0

NDs: Non-detects

* : Indicative value due to few reported values

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

TEF ₂₀₀₆	Median pg/g	Mean pg/g	Standard deviation, pg/g	Relative standard deviation, %	Min pg/g	Max pg/g	Reporting laboratories
Beef, fresh weight							
PCDD/PCDF TEQ	0.08	0.11	0.085	79	0.022	0.73	64
Non-ortho PCB TEQ	0.32	0.32	0.066	21	0.092	0.60	62
Mono-ortho PCB TEQ	0.027	0.027	0.0054	20	0.0080	0.049	62
Total TEQ	0.42	0.42	0.15	34	0.10	1.4	64
Sum indicator PCB	2427	2753	2747	100	1.8	21292	54
Sum BDE without BDE 209	24	72	192	264	12	1039	30
Salmon, fresh weight							
PCDD/PCDF TEQ	3.1	4.1	1.1	28	0.14	11	70
Non-ortho PCB TEQ	5.2	5.5	2.4	44	0.23	17	70
Mono-ortho PCB TEQ	0.29	0.30	0.12	40	0.013	1.1	69
Total TEQ	8.6	8.9	3.4	39	0.38	28	71
Sum indicator PCB	40049	39530	15758	40	35	106244	59
Sum BDE without BDE 209	2756	4692	10850	231	1858	67630	36
Cheese, fresh weight							
PCDD/PCDF TEQ	0.034	0.077	0.13	169	0.014	0.83	53
Non-ortho PCB TEQ	0.027	0.065	0.15	237	0.0097	1.0	52
Mono-ortho PCB TEQ	0.0018	0.0051	0.014	273	0.00072	0.090	52
Total TEQ	0.065	0.14	0.23	167	0.031	1.2	53
Sum indicator PCB	204	509	906	178	0.28	4133	43
Sum BDE without BDE 209	34	394	1588	403	18	7971	25

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

TEF ₁₉₉₈	Median pg/g	Mean pg/g	Standard deviation, pg/g	Relative standard deviation, %	Min pg/g	Max pg/g	Reporting laboratories
Beef, fresh weight							
PCDD/PCDF TEQ	0.10	0.11	0.10	95	0.028	0.89	64
Non-ortho PCB TEQ	0.31	0.31	0.063	20	0.089	0.57	62
Mono-ortho PCB TEQ	0.13	0.13	0.027	20	0.039	0.24	62
Total TEQ	0.53	0.54	0.18	34	0.10	1.7	64
Sum indicator PCB	2427	2753	2747	100	1.8	21292	54
Sum BDE without BDE 209	24	72	192	264	12	1039	30
Salmon, fresh weight							
PCDD/PCDF TEQ	4.1	4.1	1.5	38	0.18	15	70
Non-ortho PCB TEQ	5.0	5.3	2.3	43	0.22	15	70
Mono-ortho PCB TEQ	1.4	1.5	0.55	37	0.062	4.8	69
Total TEQ	10	11	4.0	38	0.46	35	71
Sum indicator PCB	40049	39530	15758	40	35	106244	59
Sum BDE without BDE 209	2756	4692	10850	231	1858	67630	36
Cheese, fresh weight							
PCDD/PCDF TEQ	0.038	0.077	0.14	186	0.016	0.87	53
Non-ortho PCB TEQ	0.026	0.062	0.15	245	0.0093	1.0	52
Mono-ortho PCB TEQ	0.0081	0.023	0.065	275	0.0035	0.42	52
Total TEQ	0.073	0.16	0.28	174	0.034	1.5	53
Sum indicator PCB	204	509	906	178	0.28	4133	43
Sum BDE without BDE 209	34	394	1588	403	18	7971	25

Laboratories' Z-scores: Analyte solution

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
1	0.20	0.19	0.35	-0.13	-0.20	0.19	0.17
2	-0.50	-0.50	-0.52	-0.069			
3							
4	-0.021	-0.077	0.58	0.52	0.64	-0.21	-0.26
5							
6	-0.29	-0.29	-0.26	-0.48	-0.13		
7	0.076	0.081	-0.0015	0.12	0.063	0.26	0.12
8							
9							
10							
11	0.11	0.14	-0.14	-0.064	0.015	-1.8	0.078
12							
13							
14							
15	-0.23	-0.29	0.45	0.47	-0.14	-2.3	-0.69
16	-0.050	-0.057	0.077	-0.29	-0.38	-0.32	-0.31
17							
18							
19	-0.37	-0.46	0.69	-0.20	-0.29	1.6	0.40
20	-0.34	0.10					
21							
22	-0.26	-0.29	0.012	0.20	0.24	0.29	0.22
23	0.0069	-0.019	0.33	0.012	0.081	0.13	0.14
24	-0.43	-0.46	-0.17	-0.014	0.081	-1.8	-0.032
25							
26							
27	0.24	0.31	-0.51	-0.42	-0.71	0.29	0.54
28							
29							
30							
31							
32	-0.11	-0.12	0.069	-0.19	0.27	-0.0025	0.045
33	-0.20	-0.25	0.31	-0.015	0.053		
34							
35	0.16	0.18	0.013	-0.082	0.012	-0.27	-0.047
36							
37					-0.10		
38					-0.18		
39	-0.23	-0.29	0.37	0.99	0.70	0.14	0.15
40							
41	-0.16	-0.17	-0.020	-0.59	-0.61		
42	-0.15	-0.19	0.29	0.32	0.29	-1.9	-0.15
43	-0.15	-0.17	0.11	-0.019	-0.081	-1.6	0.30
44	1.1	1.2	-0.22	0.035		3020	4760
45	105	103	120	111			
46	0.23	0.26	0.0011	-1.1	1.2		
47	0.077	0.031	0.64	0.10	0.047		
48							
49							
50	-0.021	-0.057	0.45	-0.16	0.47		
51							
52							
53	20	20	20	-2.3	-2.3		
54					-0.061		
55	0.043	0.016	0.40	-0.14	-0.00066		
56	-0.0033	-0.0032	-0.0028	-0.015	-0.026		
57	-0.030	-0.029	-0.0080	-0.19	0.012	0.078	0.10
58							
59	-0.047	-0.075	0.28	0.072	-0.59	-0.29	-0.35
60	-0.32	-0.36	0.043	0.45			
61	-1.0	-0.98	-0.89	0.26			
62	0.10	0.10	0.11	-0.10	-0.050		
63							
64							
65	-0.35	-0.34	-0.48	-0.42			
66							
67	-0.079	-0.082	-0.023	-0.21	0.22	0.11	-0.28
68							
69							
70	-0.12	-0.14	0.11	-0.20	-0.34	0.022	0.017

Laboratories' Z-scores: Analyte solution (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
71							
72							
73							
74							
75							
76	-4.5		0.59	0.59	0.066		
77	-0.57	-0.54	-0.29	-4.3	-0.22		
78							
79							
80	-0.15	-0.17	0.12	-0.0021	-1.0		
81	0.039	0.038	0.042	0.14	0.15		
82	0.83	0.87	0.43	0.14	0.18	-0.64	0.092
83	0.17	0.16	0.30	-0.21	1.1		
84	0.061	0.046	0.23	0.13			
85	-0.95	-0.57					
86	0.087	0.077	0.16	0.44	0.45	0.45	0.69
87							
88							
89	-0.73	-0.77	-0.17	-0.89			
90	-0.22	-0.26	0.14	0.31	-0.32	-2.4	-0.92
91	0.31	0.31	0.37	-0.035	-0.15		
92	-0.061	-0.082	0.23	-0.22	0.070	-0.15	-0.022
93	-0.15	-0.13	-0.53	0.50	0.0014	-0.38	-0.61
94							
95	-0.23	-0.28	0.30	0.26	0.15		
96							
97							
98	0.010	-0.016	0.30	0.17	0.13	-0.21	-0.34
99	-0.077	-0.051	-0.51	0.49	0.28	-0.41	-0.58
100							
101	-0.071	-0.070	-0.092	-0.0057	-0.036		
102							
103	0.10	0.11	0.022	-0.040	-0.029		
104	-0.71	-0.68	-0.42				
105							
106	3.5	3.2	8.6	-0.21			
107	-0.023	-0.036	0.16	-0.14	0.32		
108	-0.032	-0.076	0.49	0.13	-0.11	-1.5	0.51
109	-0.29	-0.34	0.33	-0.17	0.12		
110	-0.043	-0.060	0.15	-0.020	0.038		
111	-0.15	-0.18	0.20	0.050	-0.71	-0.25	-0.25
112	-0.26	-0.22	-0.58	-0.81	-0.44		
113	-0.52	-0.65	0.96	-0.070	0.23		
114	-0.32	-0.41	0.71	-0.086	0.74	1.6	0.40
115	-0.28	-0.32	0.18	-0.18	-0.27	0.066	-0.18
116	-0.27	-0.35	0.76	-0.041	0.71	1.7	0.29
117							
118	-0.29	-0.33	0.10	0.12	0.30	-0.36	-0.032
119	0.028	0.023	0.070	0.15			

Laboratories' Z-scores: Beef-2015, fresh weight

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
1							
2							
3	0.17	-0.14	0.27	-0.21			
4	-0.33	-0.94	-0.30	0.96	1.8	2.5	0.50
5							
6							
7	0.20	0.74	0.089	0.069	-0.84		
8	-0.22	0.54	-0.56	1.7	1.8	62	229
9							
10							
11	-0.10	-0.78	0.081	-0.40	0.37		
12							
13							
14							
15	-0.86	0.93	-1.2	-1.6	-5.0	-3.7	-0.50
16							
17	1.1	0.44	1.3	0.35	39		
18							
19	0.30	-0.85	0.60	-0.033	0.082	3.2	0.35
20	-3.2	5.1					
21							
22	0.10	2.9	-0.54	0.11	1.1	137	5.0
23	-0.28	-0.26	-0.29	-0.15	-0.38	0.046	-0.15
24							
25							
26	-3.8	-1.4					
27	-0.34	1.3	-0.72	-0.55	-0.010	-2.9	1.6
28							
29							
30	1.2	1.0	1.2	1.6	-0.24		
31							
32	-0.096	0.10	-0.14	-0.066	-1.1	12	0.33
33	-0.075	-0.12	-0.073	0.024	0.96		
34							
35	-0.22	-1.8	0.13	-0.088	-0.46	-3.3	1.0
36	0.094	-0.26	0.20	-0.18	-0.64		
37							
38							
39	0.67	0.70	0.59	1.5	1.3	-2.7	-0.73
40							
41	-0.94	0.026	-1.2	-0.69	-0.69		
42	0.52	-0.063	0.60	1.2	-0.37	-3.1	1.6
43	-0.51	-2.0	-0.17	-0.49	-0.19	-2.1	5.3
44							
45	-0.34	1.7	-0.83	-0.11			
46	2.7	0.14	3.1	4.2	9.2		
47	-0.62	0.13	-0.82	-0.29	-0.095		
48							
49							
50	-0.31	0.54	-0.55	0.12	2.1		
51							
52							
53	-0.51	0.44	-0.64	-1.6	-0.13		
54					0.79	9.1	11
55	0.38	3.1	-0.17	-0.59	-0.60		
56							
57	-0.67	-0.66	-0.68	-0.55	-0.40	1.0	1.6
58							
59	0.55	0.32	0.63	0.33	-0.21	6.1	-0.24
60	11	45	4.4	2.7			
61	0.055	2.5	-0.49	-0.31			
62	0.57	0.20	0.66	0.57	-5.0		
63							
64							
65	-3.5	-3.5	-3.6	-3.5			
66							
67	-0.13	-0.20	-0.048	-0.89	-0.75	1.3	-1.6
68							
69							
70	0.64	0.47	0.74	0.010	0.056	2.4	-0.30

Laboratories' Z-scores: Beef-2015, fresh weight (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
71							
72							
73							
74							
75							
76							
77							
78							
79							
80	-0.016	-0.091	-0.026	0.30	-5.0		
81	0.066	0.15	0.038	0.15	0.27		
82	1.1	2.4	0.81	0.33	0.81	1.3	-0.18
83	-0.22	0.36	-0.34	-0.42	0.14		
84	1.1	3.4	0.66	-0.31			
85	-0.080	-1.1	0.11	0.52			
86	0.23	-0.20	0.32	0.30	0.26	-1.8	-2.3
87							
88							
89							
90	0.16	0.36	0.21	-0.89	-0.78	-3.8	-0.88
91	0.72	0.51	0.84	-0.035	0.76		
92	-0.48	-1.2	-0.34	-0.28	0.0087	-0.33	1.8
93	0.11	0.39	0.046	0.16	0.24	1.9	6.9
94							
95	-0.18	0.56	-0.40	0.33	-5.0		
96							
97							
98	0.32	0.87	0.12	1.2	0.73	1.6	5.9
99	-0.50	-2.5	-0.050	-0.43	-0.34	-3.9	-1.1
100							
101	-0.028	0.27	-0.10	0.016	0.79		
102							
103	0.46	0.26	0.50	0.53	-0.12		
104							
105	0.70	-0.76	1.0	0.72			
106							
107	-0.69	0.069	-1.0	0.35	2.7	-0.80	0.46
108	-1.2	0.74	-1.7	-0.20	-0.65	17	71
109	0.93	0.90	1.1	-1.1	0.62		
110	0.060	1.4	-0.26	0.22	0.75		
111	-0.33	-2.3	0.076	0.38	0.67	0.56	3.3
112							
113	0.61	-0.22	0.87	-0.081	-0.14		
114	-0.35	0.086	-0.45	-0.28	0.26	1.8	-0.21
115							
116	0.31	0.29	0.32	0.30	0.46	2.3	0.10
117	0.094	2.4	-0.44	-0.039	1.0		
118	0.17	0.29	0.12	0.42	0.21	-1.6	0.31
119	-0.84	-0.0033	-1.0	-1.0			

Laboratories' Z-scores: Beef-2015, lipid weight weight

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
1							
2							
3	0.19	-0.12	0.29	-0.19			
4	-0.65	-1.2	-0.62	0.55	1.3	1.9	0.12
5							
6							
7	0.15	0.69	0.042	0.022	-0.88		
8	0.34	1.2	-0.034	2.5	2.6	69	256
9							
10							
11	-0.47	-1.1	-0.30	-0.75	-0.034		
12							
13							
14							
15	-1.4	0.15	-1.7	-2.0	-5.0	-3.9	-1.1
16							
17	0.41	-0.18	0.60	-0.26	34		
18							
19	-0.27	-1.3	-0.0066	-0.57	-0.46	2.3	-0.22
20	-3.4	4.2					
21							
22	0.33	3.2	-0.34	0.34	1.4	144.0	5.5
23	-0.32	-0.31	-0.34	-0.20	-0.43	-0.0049	-0.20
24							
25							
26							
27	-0.17	1.6	-0.56	-0.39	0.17	-2.8	1.8
28							
29							
30	0.90	0.74	0.89	1.4	-0.44		
31							
32	0.22	0.43	0.17	0.25	-0.88	13.00	0.68
33	-0.17	-0.21	-0.17	-0.072	0.84		
34							
35	-0.62	-2.1	-0.29	-0.49	-0.83	-3.4	0.55
36	0.15	-0.21	0.26	-0.13	-0.59		
37	-1.2	1.7			2.3		
38							
39	0.84	0.87	0.76	1.7	1.5	-2.7	-0.60
40							
41	-0.61	0.43	-0.88	-0.35	-0.35		
42	0.55	-0.036	0.63	1.2	-0.35	-3.1	1.6
43	-0.49	-2.0	-0.15	-0.47	-0.17	-2.1	5.3
44							
45	0.28	2.6	-0.28	0.54			
46	1.3	-0.79	1.7	2.5	6.6		
47	-0.56	0.19	-0.77	-0.23	-0.037		
48							
49							
50	0.33	1.3	0.062	0.83	3.0		
51							
52							
53	-1.9	-1.3	-2.0	-2.6	-1.7		
54					0.39	8.2	10.0
55	-0.39	1.9	-0.86	-1.2	-1.2		
56							
57	-0.68	-0.68	-0.69	-0.57	-0.42	1.0	1.5
58							
59	0.43	0.20	0.50	0.21	-0.32	5.9	-0.34
60							
61	-0.17	2.2	-0.70	-0.53			
62	0.55	0.18	0.63	0.55	-5.0		
63							
64							
65	-1.7	-1.6	-1.7	-1.6			
66							
67	-0.65	-0.71	-0.58	-1.3	-1.2	0.66	-2.0
68							
69							
70	0.58	0.41	0.67	-0.047	-0.0022	2.3	-0.35

Laboratories' Z-scores: Beef-2015, lipid weight (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
71	0.0071	-0.068	-0.0022	0.33	-5.0		
72							
73							
74							
75							
76							
77							
78							
79							
80							
81	-0.25	-0.17	-0.27	-0.17	-0.057		
82	1.4	2.7	1.1	0.60	1.1	1.6	0.057
83	0.64	1.3	0.50	0.41	1.1		
84	-0.43	1.3	-0.74	-1.5			
85	-0.14	-1.2	0.051	0.45			
86	0.32	-0.12	0.41	0.39	0.35	-1.7	-2.3
87							
88							
89							
90	0.47	0.68	0.52	-0.65	-0.53	-3.8	-0.6
91	0.66	0.45	0.77	-0.093	0.69		
92	-0.33	-1.0	-0.18	-0.12	0.17	-0.18	2.1
93	0.38	0.68	0.31	0.43	0.51	2.2	7.5
94							
95	-0.90	-0.27	-1.1	-0.46	-5.0		
96							
97							
98	0.61	1.2	0.40	1.5	1.0	1.9	6.5
99	0.31	-2.0	0.84	0.38	0.49	-3.7	-0.38
100							
101	-0.53	-0.26	-0.59	-0.49	0.21		
102							
103	0.52	0.32	0.57	0.59	-0.061		
104							
105	0.72	-0.74	1.1	0.75			
106							
107	3.4	4.9	2.9	5.4	10	3.2	5.6
108	-1.6	0.079	-2.1	-0.76	-1.2	14	63
109	1.1	1.1	1.3	-1.0	0.76		
110	0.080	1.4	-0.24	0.24	0.77		
111	-0.38	-2.3	0.018	0.32	0.61	0.49	3.2
112							
113	-0.058	-0.80	0.17	-0.67	-0.72		
114	0.37	0.87	0.25	0.45	1.1	2.8	0.53
115							
116	0.38	0.35	0.38	0.37	0.52	2.4	0.16
117	-1.2	0.57	-1.6	-1.3	-0.49		
118	0.78	0.91	0.72	1.1	0.82	-1.2	0.94
119	-1.1	-0.32	-1.3	-1.3			

Laboratories' Z-scores: Salmon-2015, fresh weight

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
1	11	13	10	14	8.6	12	12
2							
3	0.12	-0.24	0.32	0.44			
4	0.092	0.50	-0.17	0.49	-0.44	-0.064	-0.13
5							
6	-0.14	-0.22	-0.074	-0.47	0.21		
7	-0.046	0.37	-0.29	-0.22	-0.0050	-0.20	-0.20
8	-0.070	-0.38	0.078	0.60	0.17	-1.3	-1.3
9							
10							
11	-0.019	-0.11	0.025	0.21	0.52	0.49	0.54
12							
13							
14							
15							
16	0.35	0.56	0.21	0.64	-0.55	0.24	0.27
17	0.058	-0.29	0.33	-1.2	1.1		
18							
19	-0.061	-0.079	-0.045	-0.16	0.18	0.15	0.13
20							
21							
22	0.0041	-0.22	0.11	0.48	1.9	53	0.63
23	-0.19	-0.22	-0.17	-0.27	0.44	0.18	0.18
24	-0.16	0.12	-0.37	0.55	0.55	0.39	0.44
25							
26							
27	-0.47	0.50	-1.0	-0.64	-0.18	0.67	0.71
28							
29	-1.7	-0.50	-2.6	0.61			
30	0.99	0.77	1.2	0.41	0.035		
31						117	118
32	0.47	0.59	0.40	0.33		0.31	-0.27
33	-0.12	0.40	-0.44	0.17	1.0		
34							
35	0.67	0.22	0.94	0.49	0.24	0.65	0.66
36	-0.0029	0.027	-0.031	0.17	0.14		
37	-4.2	-3.9			-2.4		
38							
39	0.58	0.20	0.73	1.9	1.4	0.32	0.32
40							
41	-0.96	-0.70	-1.1	-1.0	-0.93		
42	0.63	0.28	0.78	1.6	0.34	-0.59	-0.56
43	-0.33	-0.87	0.086	-2.0	-1.6	-1.6	-1.6
44	-2.0		-0.30	0.16		-0.36	-0.32
45	0.12	0.65	-0.19	0.066			
46	1.5	-0.14	2.4	3.2	5.7		
47	0.34	0.24	0.39	0.34	0.31		
48							
49							
50	-0.90	-0.77	-1.0	-0.31	1.9		
51							
52							
53							
54					0.98	-0.58	-0.72
55	-0.33	-0.36	-0.32	-0.24	-0.25		
56	-0.13	0.21	-0.33	-0.27	-0.76		
57	-0.16	-0.01	-0.24	-0.26	0.11	0.44	-0.057
58							
59	0.24	0.45	0.12	0.17	-0.19	0.023	0.024
60	0.24	-0.050	0.45	-0.55			
61	-0.70	0.00043	-1.1	-0.57			
62	0.40	0.23	0.47	0.73	-5.0		
63							
64							
65	-4.8	-4.8	-4.8	-4.8			
66							
67	-0.22	-0.0039	-0.32	-0.73	-0.36	-1.1	-1.1
68							
69							
70	0.28	0.089	0.42	-0.32	-0.047	0.021	0.0086

Laboratories' Z-scores: Salmon-2015, fresh weight (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
71							
72							
73							
74							
75							
76	5.3	-2.4	9.8	6.4	-2.3		
77							
78							
79							
80	0.0079	-0.30	0.17	0.30	-5.0		
81	0.028	0.27	-0.11	0.053	-0.038	0.27	0.28
82	1.4	1.9	1.1	1.4	1.6		
83	-0.19	0.27	-0.42	-0.83	-1.6		
84	0.15	0.27	0.070	0.34			
85							
86	0.029	-0.18	0.14	0.40	0.49	-0.17	-0.16
87	-2.50	-1.47	-3.1	-1.8	-1.7		
88							
89							
90	-0.43	-0.51	-0.36	-0.81	-1.1	-1.1	-1.1
91	0.60	0.56	0.60	1.0	1.5		
92	-0.31	-0.21	-0.38	-0.14	0.056	0.18	0.19
93	1.1	0.54	1.5	0.34	0.86	0.72	0.72
94							
95	-0.94	-0.82	-1.0	-0.50	-5.0		
96							
97							
98	0.21	-0.085	0.36	0.65	1.6	0.020	-0.0080
99							
100							
101							
102							
103	0.43	0.30	0.49	0.82	-0.069		
104	-0.76	-0.53	-0.66				
105	0.13	0.014	0.18	0.37			
106	7.6	2.9	11	-2.8			
107	-0.037	-0.39	0.18	-0.26	-2.4	-0.35	-0.35
108	-0.73	0.57	-1.6	1.6	-0.024	0.23	0.27
109	0.63	0.67	0.74	-1.6	-0.43		
110	-0.57	-0.23	-0.79	-0.23	-0.22		
111	-0.60	-0.57	-0.61	-0.56	-0.33	-0.47	-0.55
112	-0.27	0.73	-0.91	0.56	0.42		
113	0.54	0.073	0.85	0.020	-0.26		
114	0.91	0.55	1.1	1.0	0.90	0.85	0.75
115	0.24	0.54	0.059	0.29	0.24	0.063	0.029
116	0.41	0.61	0.30	0.39	0.71	0.058	-0.024
117	-0.22	-0.19	-0.24	0.076	0.58		
118	-0.0041	0.28	-0.20	0.55	1.2	0.035	0.039
119	-0.91	-0.63	-1.1	-1.1			

Laboratories' Z-scores: Salmon-2015, lipid weight

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
1	11	12	10	13	8.3	12	12
2							
3	0.038	-0.32	0.23	0.35			
4	-0.44	-0.08	-0.68	-0.090	-0.92	-0.58	-0.64
5							
6	-0.49	-0.56	-0.43	-0.79	-0.16		
7	-0.34	0.053	-0.57	-0.51	-0.30	-0.49	-0.49
8	-0.27	-0.57	-0.13	0.38	-0.043	-1.4	-1.4
9							
10							
11	-0.27	-0.36	-0.22	-0.052	0.25	0.22	0.26
12							
13							
14							
15							
16	1.65	1.9	1.5	2.02	0.54	1.5	1.6
17	0.17	-0.19	0.45	-1.1	1.3		
18							
19	-0.53	-0.55	-0.52	-0.62	-0.31	-0.34	-0.36
20							
21							
22	0.46	0.22	0.57	0.98	2.6	58	1
23	-0.54	-0.57	-0.52	-0.61	0.045	-0.20	-0.20
24	0.01	0.31	-0.21	0.75	0.75	0.58	0.63
25							
26							
27	-0.33	0.67	-0.91	-0.51	-0.022	0.85	0.89
28							
29	-1.9	-0.67	-2.7	0.39			
30	0.94	0.72	1.1	0.37	-0.0056		
31					-5.0	539	544
32	0.72	0.85	0.66	0.58	-5.0	0.56	-0.050
33	-0.26	0.25	-0.57	0.018	0.86		
34							
35	0.44	0.012	0.70	0.27	0.031	0.42	0.43
36	-0.086	-0.056	-0.11	0.086	0.055		
37	-2.7	-1.6			2.8		
38							
39	0.69	0.31	0.85	2.1	1.6	0.44	0.44
40							
41	-0.55	-0.26	-0.72	-0.59	-0.52		
42	3.7	3.2	4.0	5.2	3.3	1.8	1.9
43	-0.036	-0.61	0.40	-1.8	-1.4	-1.4	-1.4
44	-2.02		-0.36	0.09		-0.42	-0.38
45	1.5	2.1	1.1	1.4			
46	1.1	-0.44	1.9	2.7	5.1		
47	-0.12	-0.21	-0.067	-0.11	-0.15		
48							
49							
50	8.6	9.0	8.3	11	18		
51							
52							
53							
54					1.3	-0.36	-0.52
55	-0.62	-0.65	-0.61	-0.54	-0.55		
56	0.43	0.81	0.21	0.28	-0.27		
57	-0.41	-0.26	-0.49	-0.50	-0.15	0.15	-0.31
58							
59	0.14	0.34	0.015	0.064	-0.28	-0.077	-0.08
60							
61	1.2	2.2	0.63	1.4			
62	-1.8	-1.9	-1.8	-1.6	-5.0		
63							
64							
65	-4.1	-4.1	-4.1	-4.1			
66							
67	-0.96	-0.78	-1.0	-1.4	-1.1	-1.7	-1.7
68							
69							
70	0.32	0.13	0.47	-0.28	-0.0064	0.062	0.050

Laboratories' Z-scores: Salmon-2015, lipid weight (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
71							
72							
73							
74							
75							
76	8.4	-1.6	14	9.8	-1.4		
77							
78							
79							
80	0.068	-0.24	0.24	0.37	-5.0		
81	0.032	0.27	-0.11	0.056	-0.035	0.36	0.37
82	1.5	2.0	1.3	1.5	1.7		
83	0.70	1.2	0.42	-0.063	-1.0		
84	-0.62	-0.52	-0.69	-0.47			
85							
86	0.20	-0.024	0.30	0.58	0.67	-0.0057	-0.0038
87							
88							
89							
90	0.39	0.30	0.47	-0.052	-0.39	-0.45	-0.41
91	0.60	0.56	0.60	1.0	1.5		
92	-0.30	-0.20	-0.37	-0.12	0.072	0.20	0.21
93	1.0	0.45	1.4	0.25	0.76	0.63	0.63
94							
95	-0.24	-0.11	-0.35	0.27	-5.0		
96							
97							
98	0.27	-0.026	0.43	0.72	1.7	0.081	0.052
99							
100							
101							
102							
103	-1.9	-1.9	-1.8	-1.6	-2.2		
104							
105	0.67	0.55	0.73	0.94			
106	6.1	2.0	9.0	-3.1			
107	4.9	4.2	5.3	4.5	0.24	4.3	4.3
108	-1.5	-0.40	-2.2	0.46	-0.9	-0.69	-0.65
109	0.94	0.98	1.1	-1.5	-0.18		
110	-0.64	-0.31	-0.86	-0.31	-0.30		
111	-0.54	-0.52	-0.56	-0.50	-0.28	-0.42	-0.49
112							
113	0.21	-0.23	0.50	-0.28	-0.55		
114	1.1	0.71	1.3	1.2	1.1	1.0	0.92
115	-0.61	-0.35	-0.76	-0.56	-0.60	-0.75	-0.78
116	0.39	0.59	0.27	0.37	0.68	0.036	-0.046
117	-2.5	-2.4	-2.5	-2.3	-2.0		
118	0.26	0.56	0.052	0.85	1.5	0.30	0.31
119	-1.1	-0.82	-1.2	-1.2			

Laboratories' Z-scores: Cheese-2015, fresh weight

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
1							
2	6.5	4.2	9.6	1.9			
3	2.2	-0.68	5.7	2.1			
4	4.6	8.7	-0.43	8.2	22	1.0	1.2
5							
6							
7							
8	48	22	72	154	107	243	1440
9							
10							
11	-1.2	-2.0	-0.21	-0.52	0.25		
12							
13							
14							
15							
16							
17							
18							
19	-0.59	-0.66	-0.49	-0.71	-0.18	0.45	1.6
20							
21							
22							
23	0.13	0.76	-0.57	-0.54	-0.64	-0.077	0.57
24							
25							
26							
27							
28							
29							
30	2.6	5.3	-0.52	1.0	-0.57		
31							
32	-0.80	-0.98	-0.62	-0.16		6.5	-1.0
33	1.0	1.9	-0.023	1.2	6.3		
34							
35	-1.5	-1.3	-1.8	-1.9	-0.93	-4.3	-0.69
36							
37	1.1	0.73			-0.092		
38							
39	0.48	0.70	0.18	1.0	0.24	-1.1	-0.29
40							
41	-2.1	-2.3	-1.9	-2.1	-2.2		
42	0.24	0.57	-0.26	2.0	1.0	-3.6	3.2
43	0.94	-1.5	3.8	1.5	6.6	-2.7	8.6
44							
45	17	25	7.1	14			
46	3.0	-0.90	7.3	9.0	39		
47							
48							
49							
50	3.2	3.9	-0.32	43	56		
51							
52							
53							
54					1.1	1.3	11
55	11	2.1	22	1.3	3.2		
56							
57	0.24	1.0	-0.69	-0.21	-0.14	3.5	8.7
58							
59	-0.29	-0.56	0.039	-0.23	0.093	1.4	0.60
60	82	91	72	66			
61	1.1	3.5	-1.8	-0.28			
62	0.0025	-1.0	1.1	1.6	-5.0		
63							
64							
65	-2.0	-1.7	-2.4	-2.3			
66							
67	4.4	6.8	1.8	-0.016	2.4	0.60	-1.1
68							
69							
70	1.3	1.2	1.5	0.017	-0.54	4.1	-0.35

Laboratories' Z-scores: Cheese-2015, fresh weight (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
71							
72							
73							
74							
75							
76	106	8.4	211	287	1.7		
77	78	140	8.6	-0.35	0.47		
78							
79							
80	3.5	5.1	1.4	6.3	-5.0		
81	1.6	2.2	1.0	0.82	2.3		
82	-0.47	0.60	-1.7	-1.6	106	-1.5	-0.36
83	6.2	13	-1.3	-1.2	4.0		
84	9.0	12	5.8	2.6			
85							
86	-0.79	-0.90	-0.67	-0.48	-0.52	-2.3	-1.7
87							
88							
89	1.8	2.5	0.97	1.4			
90	0.15	0.24	0.10	-0.83	-1.2	-4.3	-0.68
91	0.67	-0.31	1.8	1.2	5.6		
92	-0.51	-0.92	-0.030	-0.39	1.3	-1.2	1.3
93	-0.73	-0.76	-0.73	-0.31	0.37	0.85	9.4
94							
95	7.8	14	0.77	2.3	-5.0		
96							
97							
98	0.83	3.0	-1.7	-0.95	-0.050	2.4	6.7
99	5.4	0.51	12	-1.7	-1.2	-2.0	12
100							
101							
102							
103	-0.047	-0.85	0.78	1.9	2.3		
104							
105	-0.71	1.3	-3.0	-2.7			
106							
107							
108	9.3	12	5.7	7.4	9.2	23	160
109	2.5	2.2	2.9	3.5	16		
110							
111	-0.78	-2.5	1.0	2.6	2.1	0.64	2.72
112							
113	1.4	1.1	1.8	-0.034	0.31		
114	-0.20	-0.78	0.46	0.10	0.51	2.5	-0.022
115							
116	-0.19	-0.88	0.60	0.21	1.8	3.7	-0.10
117							
118							
119	3.5	4.7	2.2	2.8			

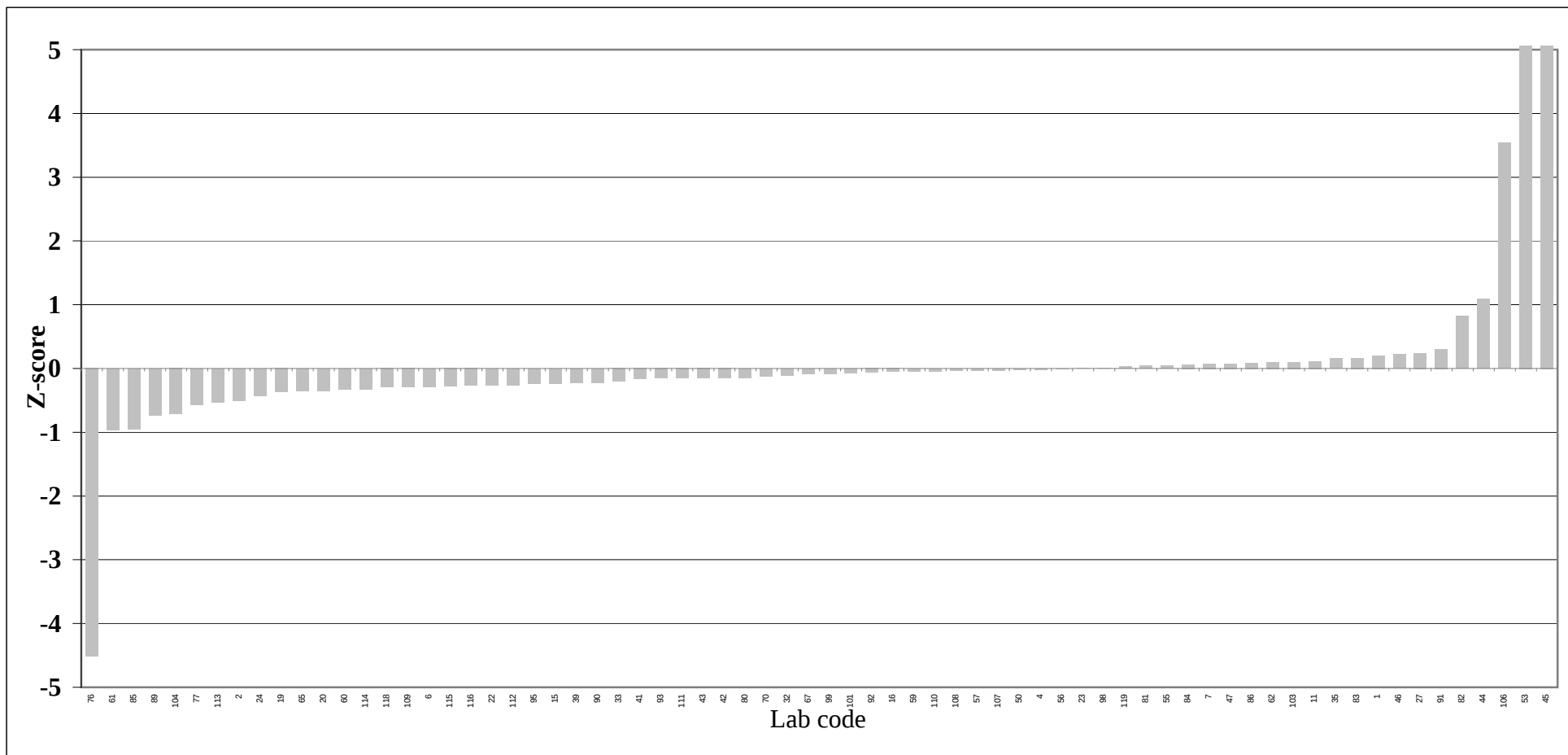
Laboratories' Z-scores: Cheese-2015, lipid weight

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
1							
2	6.3	4.0	9.3	1.7			
3	2.2	-0.68	5.7	2.1			
4	4.3	8.3	-0.56	7.8	21	0.82	1.1
5							
6							
7							
8	56	27	84	179	124	281	1663
9							
10							
11	-0.55	-1.5	0.58	0.22	1.1		
12							
13							
14							
15							
16							
17							
18							
19	-1.1	-1.1	-0.98	-1.2	-0.71	-0.14	0.84
20							
21							
22							
23	-0.14	0.46	-0.80	-0.78	-0.87	-0.33	0.28
24							
25							
26							
27							
28							
29							
30	3.0	5.8	-0.28	1.3	-0.34		
31							
32	2.1	1.8	2.4	3.2		14	1.8
33	1.0	1.8	-0.061	1.2	6.2		
34							
35	0.60	1.0	0.13	0.017	1.6	-3.8	2.0
36							
37	10	9.7			7.6		
38							
39	1.0	1.2	0.67	1.6	0.75	-0.73	0.16
40							
41	-0.37	-0.68	-0.0016	-0.30	-0.50		
42	0.88	1.2	0.31	2.9	1.7	-3.4	4.2
43	0.85	-1.5	3.6	1.4	6.4	-2.7	8.4
44							
45	20	29	8.8	16			
46	1.7	-1.6	5.3	6.6	32		
47							
48							
49							
50	4.3	5.1	0.31	49	64		
51							
52							
53							
54					4.2	4.5	19
55	11	2.1	22	1.3	3.2		
56							
57	0.20	1.0	-0.73	-0.24	-0.17	3.5	8.6
58							
59	-0.22	-0.50	0.11	-0.17	0.16	1.4	0.67
60							
61	-0.29	1.6	-2.5	-1.3			
62	0.12	-0.87	1.2	1.7	-5.0		
63							
64							
65	-1.4	-1.0	-1.8	-1.7			
66							
67	3.1	5.2	0.89	-0.69	1.4	-0.16	-1.7
68							
69							
70	1.3	1.2	1.5	0.036	-0.53	4.2	-0.33

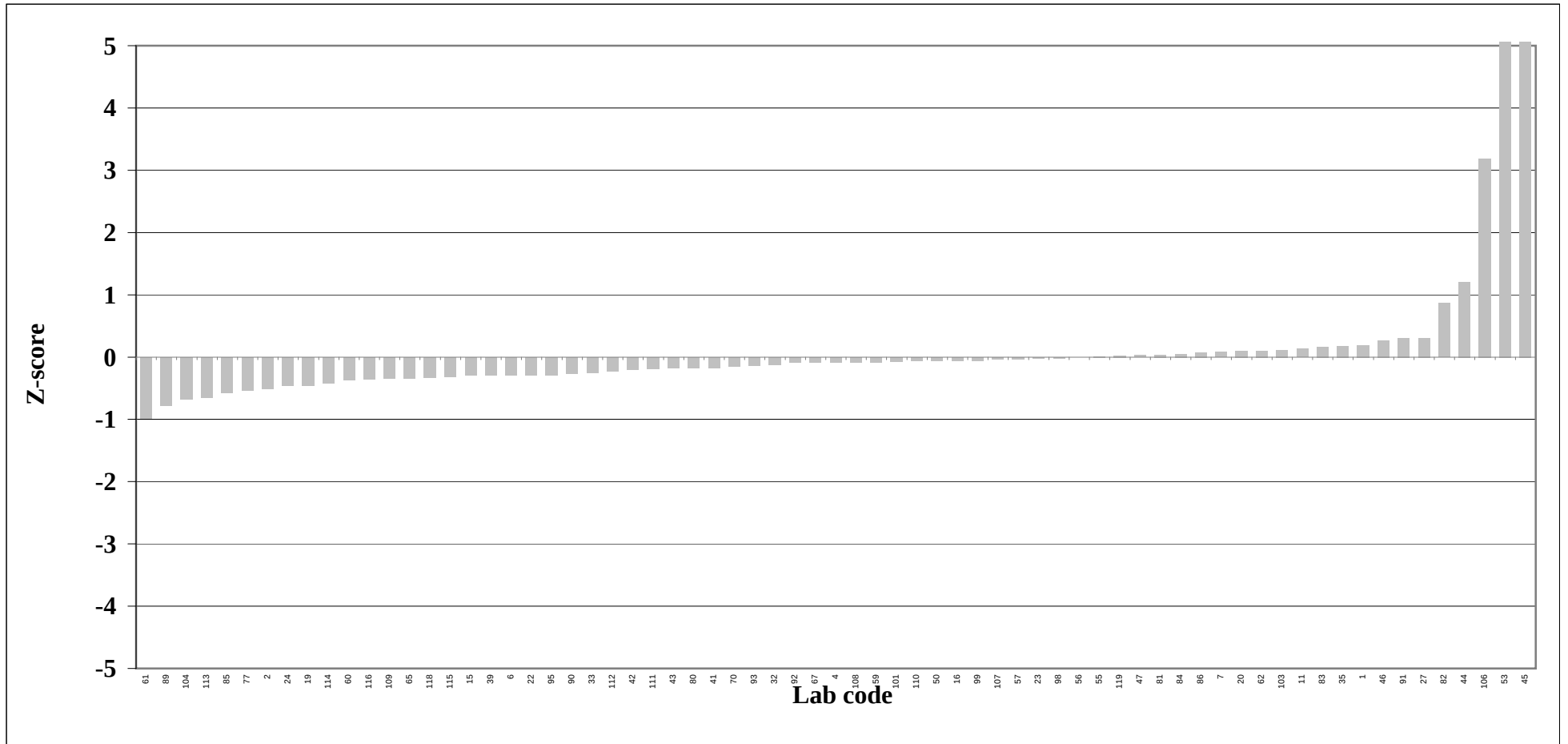
Laboratories' Z-scores: Cheese-2015, lipid weight (continued)

LABCODE	Sum TE	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE with PBDE-209	Sum PBDE without PBDE-209
71							
72							
73							
74							
75							
76	104	8.1	207	281	1.6		
77	63	115	6.2	-1.2	-0.50		
78							
79							
80	3.3	4.9	1.3	6.1	-5.0		
81	1.6	2.2	1.0	0.82	2.3		
82	-0.20	0.93	-1.5	-1.4	113	-1.3	-0.093
83	7.0	14	-1.0	-1.0	4.5		
84	8.3	11	5.2	2.2			
85							
86	-0.36	-0.49	-0.23	-0.019	-0.066	-2.1	-1.4
87							
88							
89	1.6	2.3	0.82	1.2			
90	0.79	0.89	0.73	-0.32	-0.72	-4.2	-0.14
91	0.48	-0.47	1.6	1.0	5.2		
92	-0.99	-1.4	-0.56	-0.88	0.62	-1.6	0.63
93	-0.40	-0.43	-0.40	0.051	0.79	1.3	10
94							
95	7.8	14	0.77	2.3	-5.0		
96							
97							
98	1.0	3.3	-1.5	-0.80	0.13	2.7	7.1
99	8.4	2.1	16	-0.73	-0.13	-1.2	17
100							
101							
102							
103	0.11	-0.71	0.96	2.1	2.6		
104							
105	9.5	16	1.9	2.9			
106							
107							
108	7.8	11	4.5	6.1	7.6	20	142
109	2.5	2.1	2.9	3.5	16		
110							
111	-0.81	-2.5	1.0	2.5	2.1	0.59	2.7
112							
113	0.82	0.58	1.2	-0.47	-0.16		
114	-0.16	-0.74	0.50	0.15	0.55	2.5	0.020
115							
116	-0.10	-0.80	0.71	0.31	1.9	3.9	-0.0090
117							
118							
119	2.9	4.0	1.7	2.3			

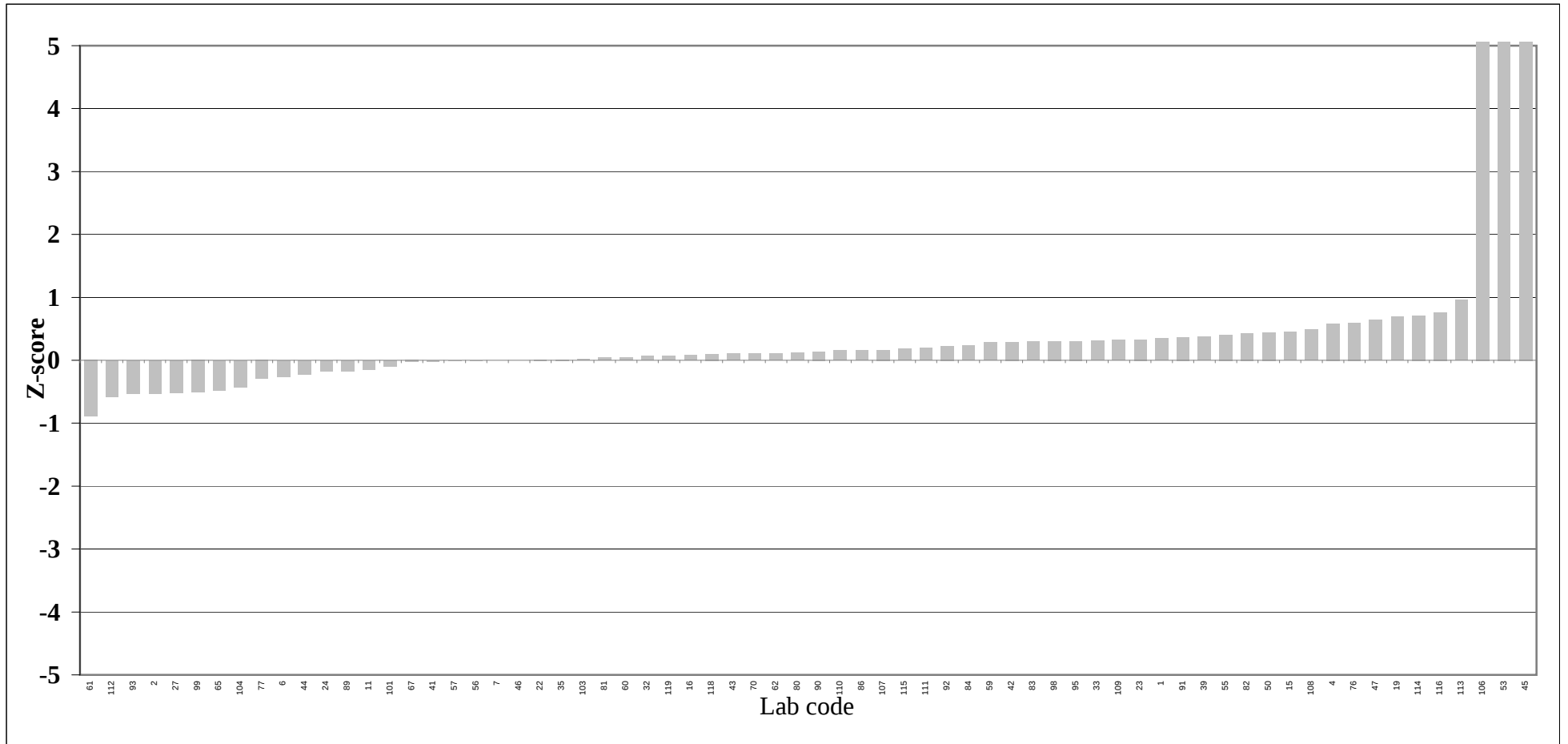
Z-score analyte solution; total TEQ



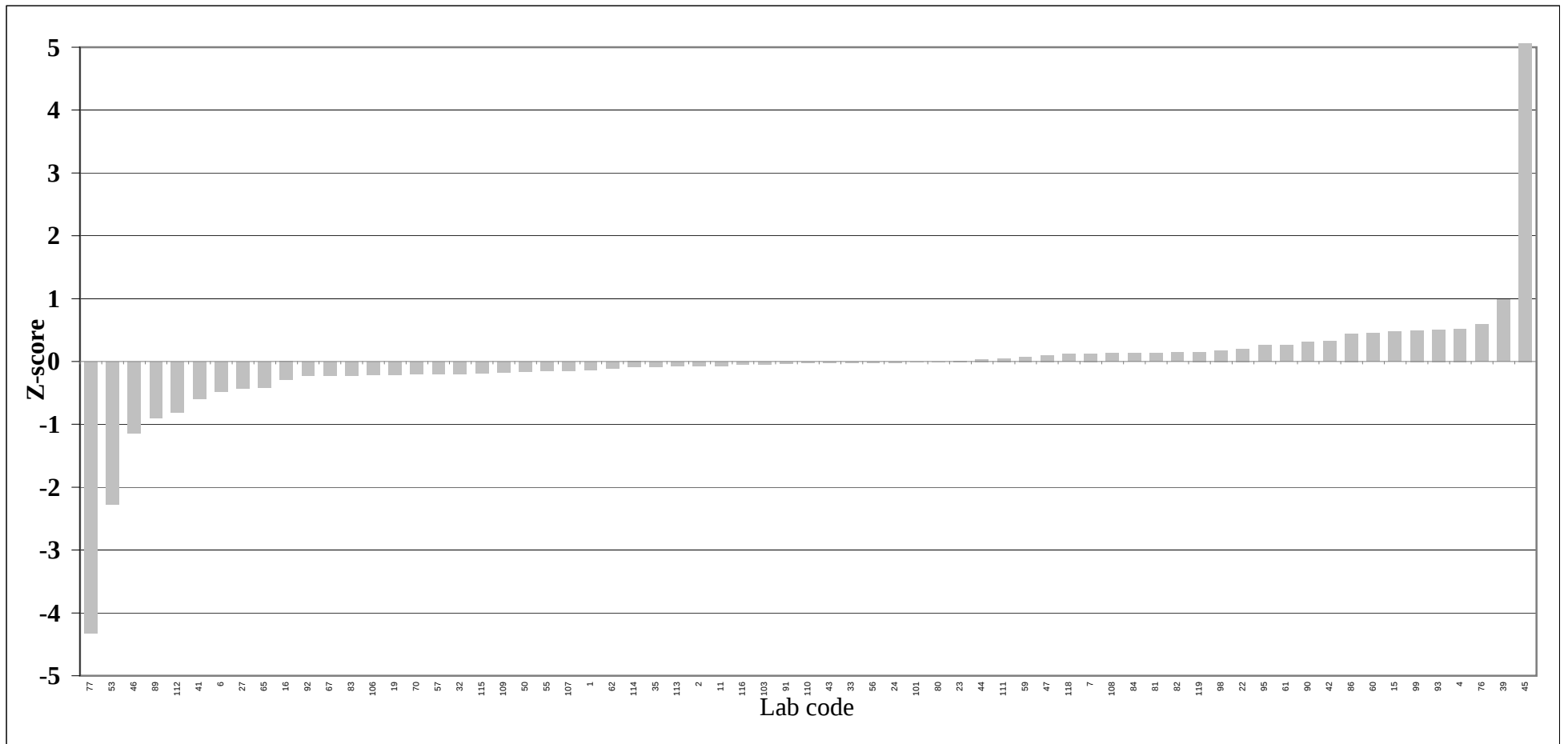
Z-score analyte solution; PCDD/PCDF TEQ



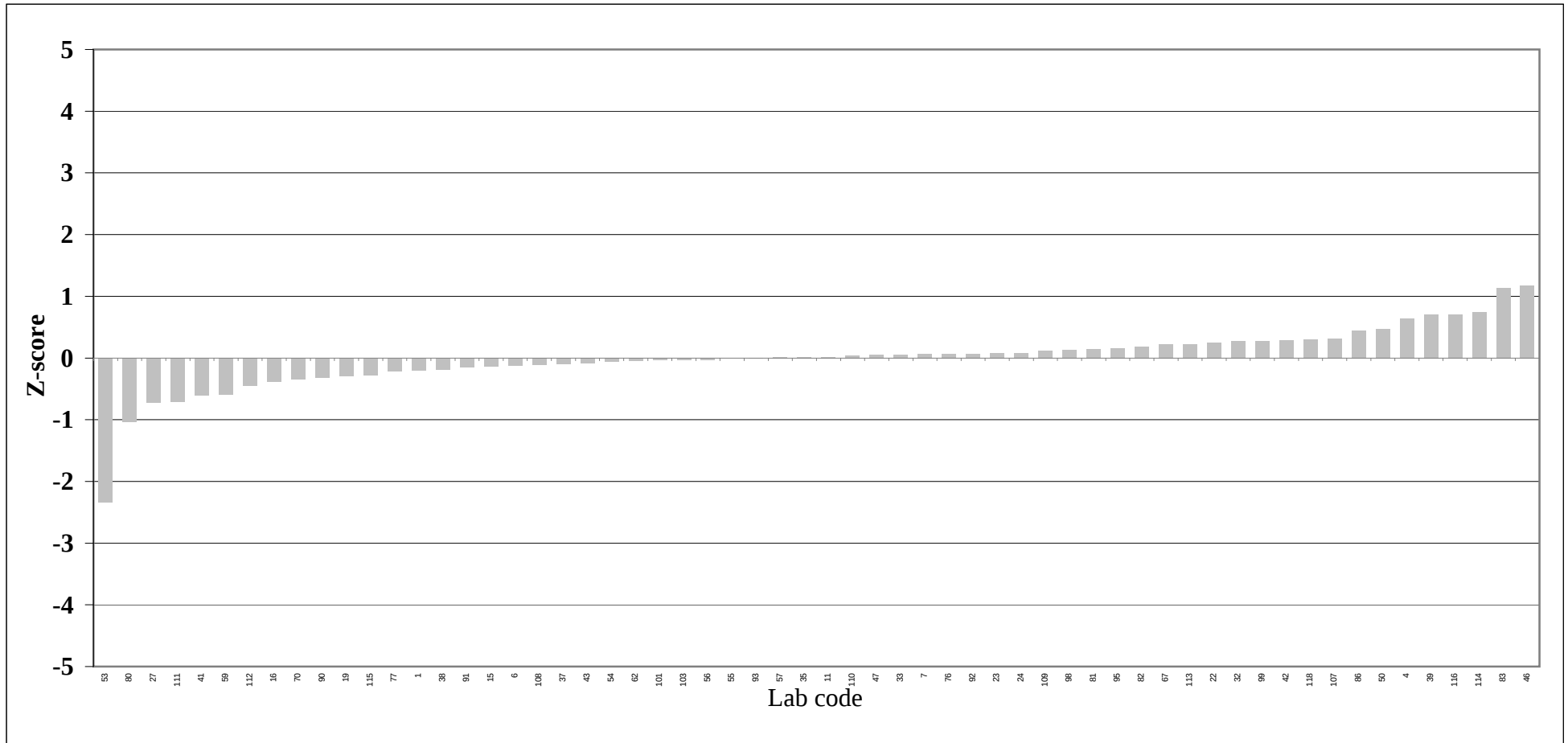
Z-score analyte solution; non-ortho PCB TEQ



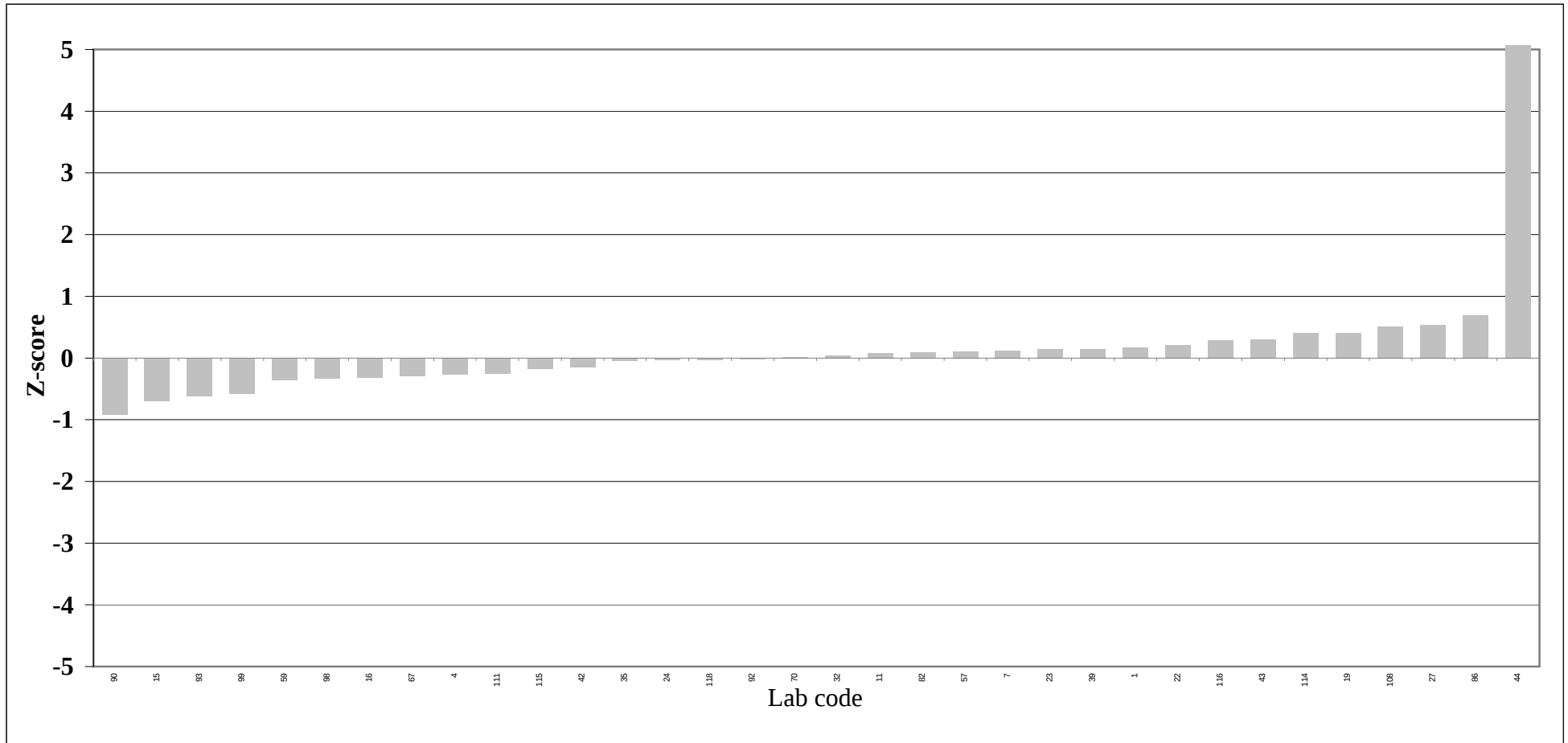
Z-score analyte solution; mono-ortho PCB TEQ



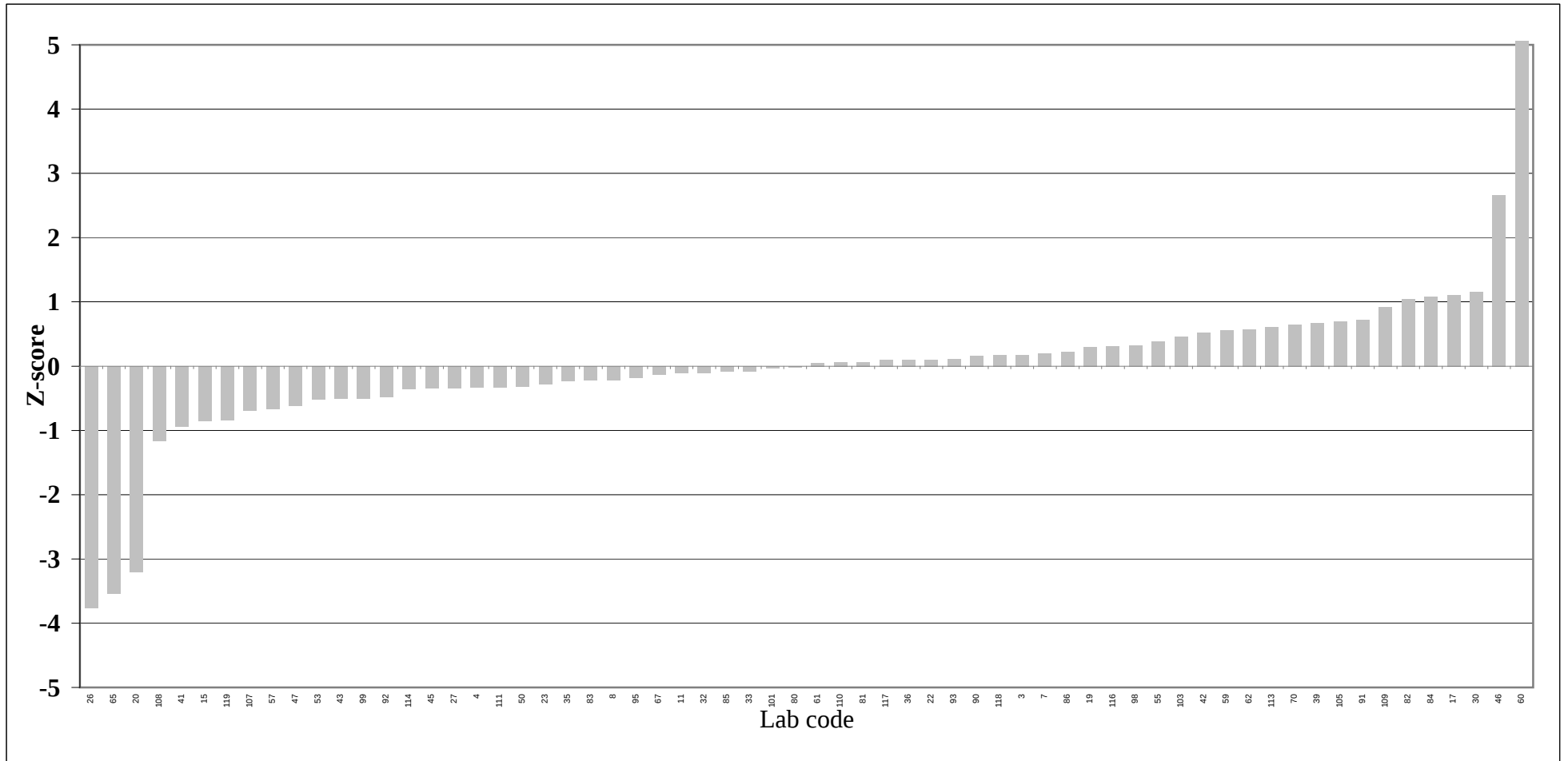
Z-score analyte solution; sum indicator PCB



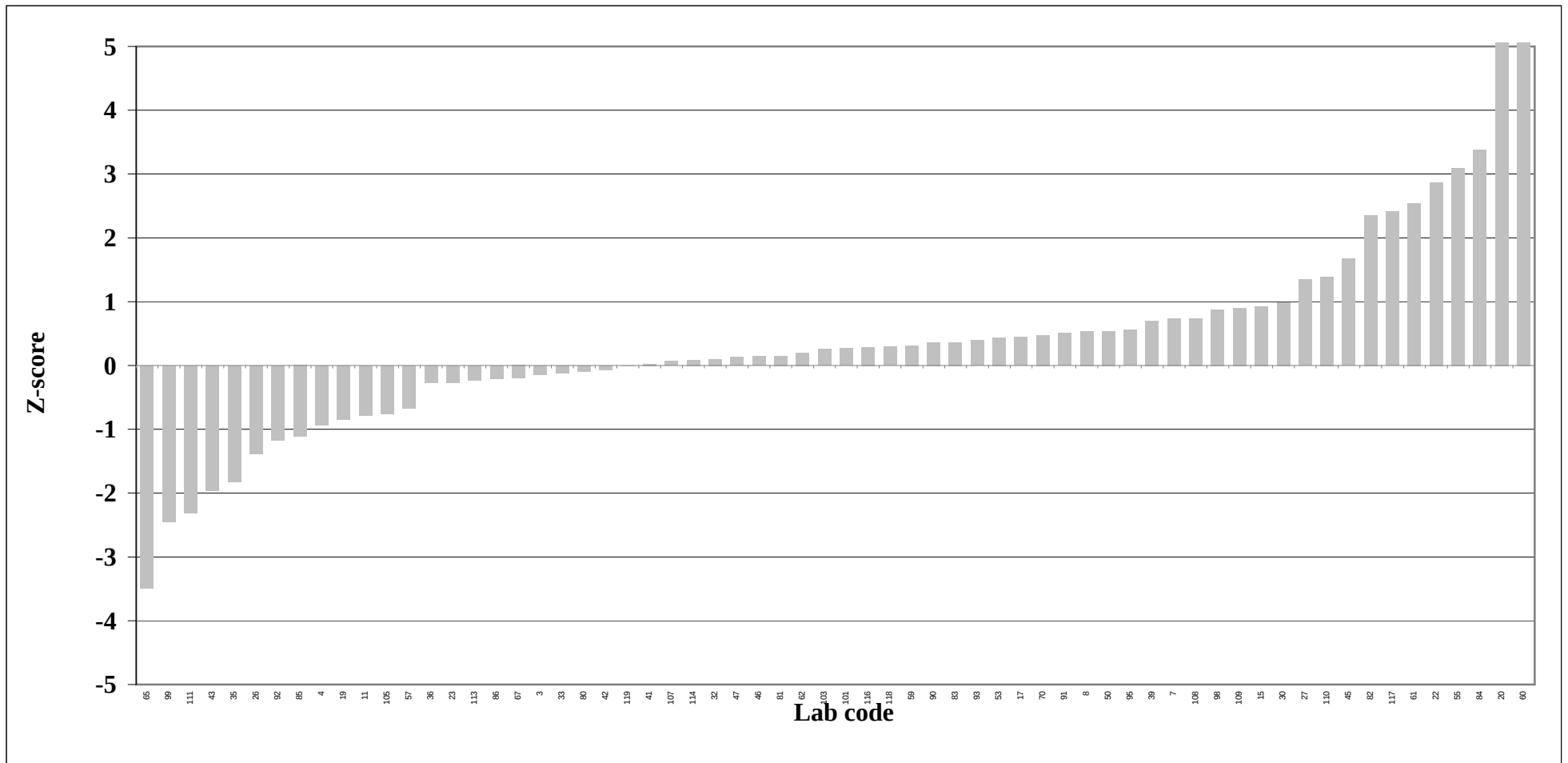
Z-score analyte solution; sum PBDE without PBDE-209



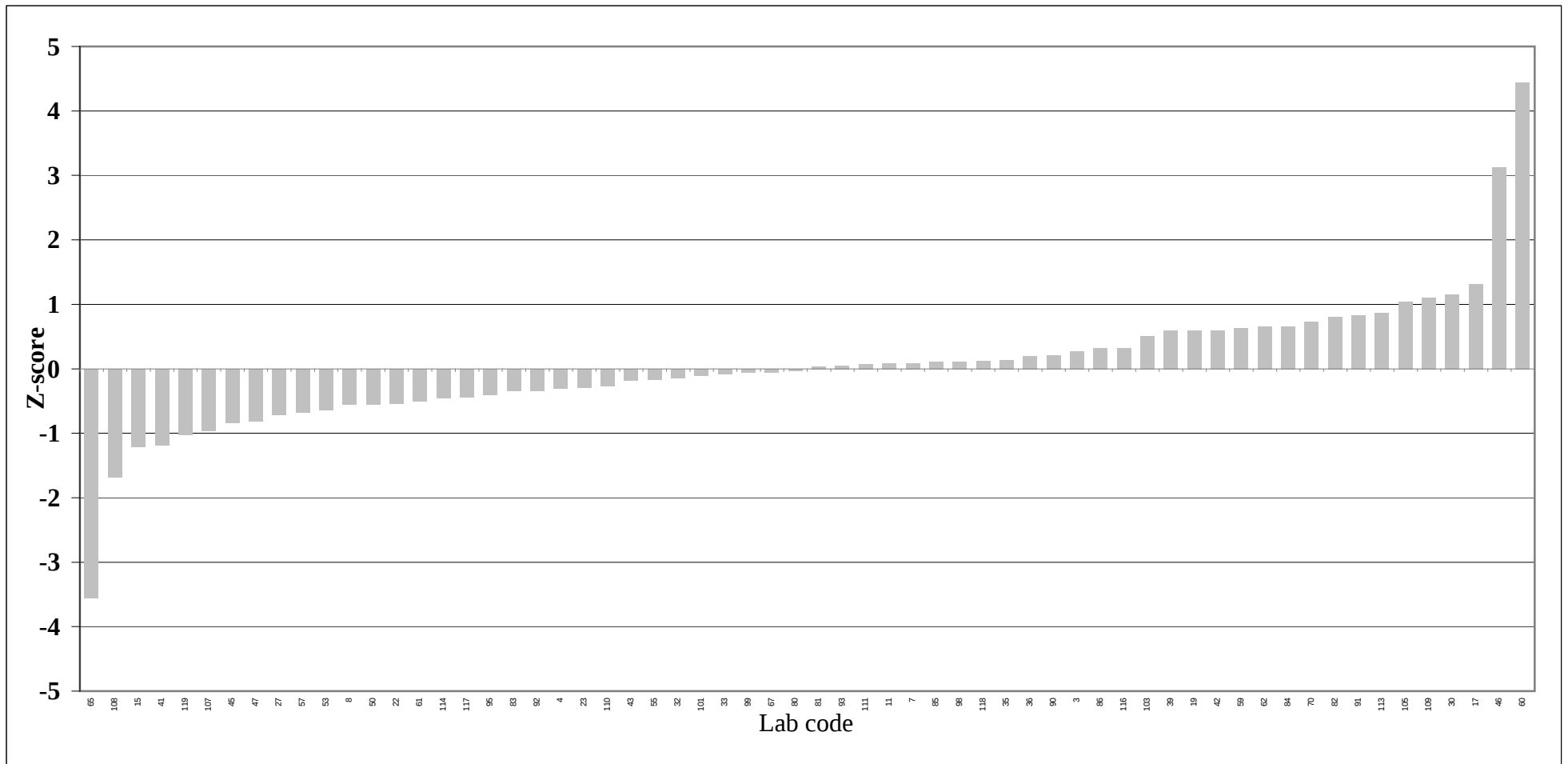
Z-score Beef; total TEQ (fresh weight)



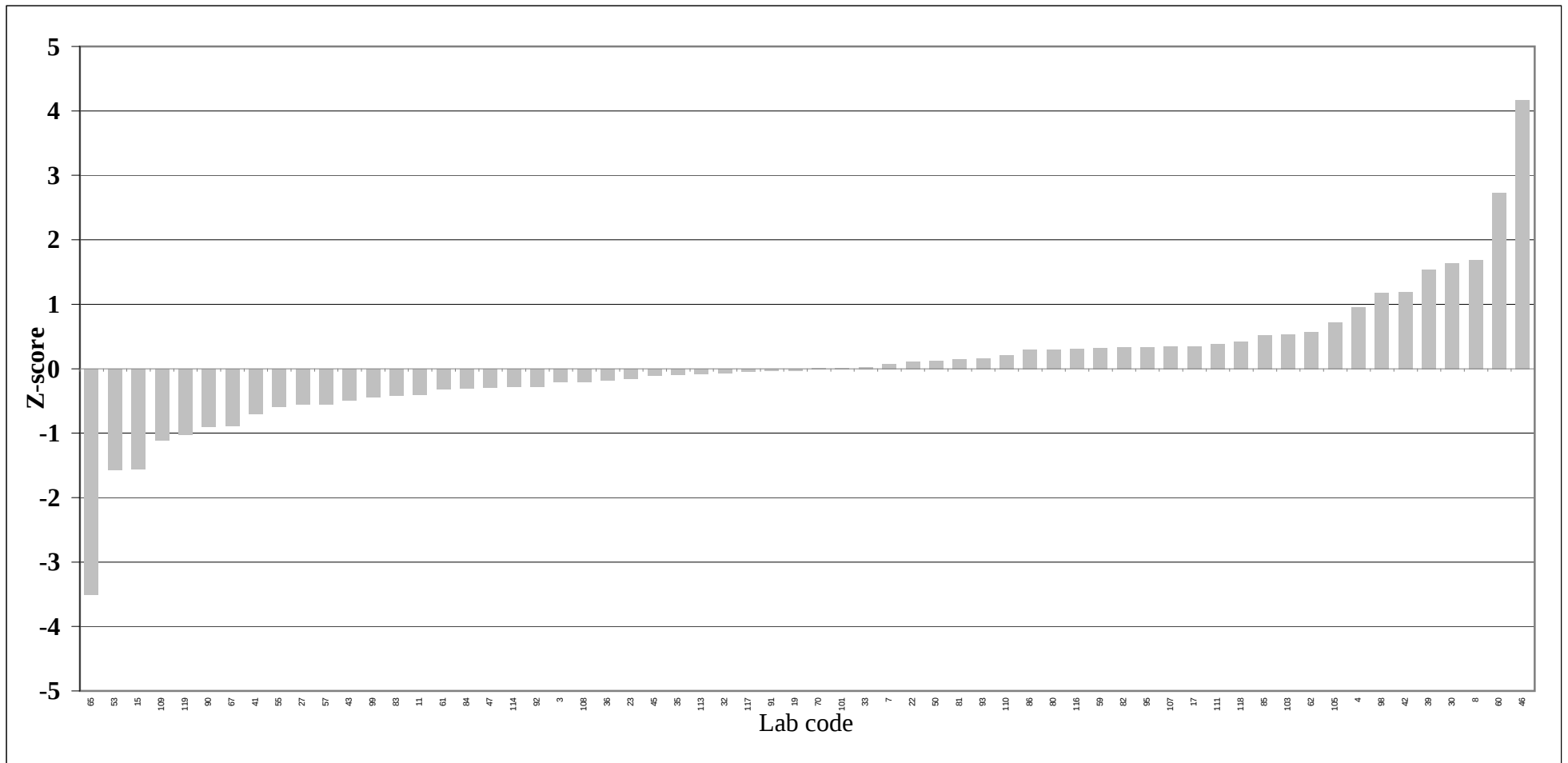
Z-score Beef; PCDD/PCDF TEQ (fresh weight)



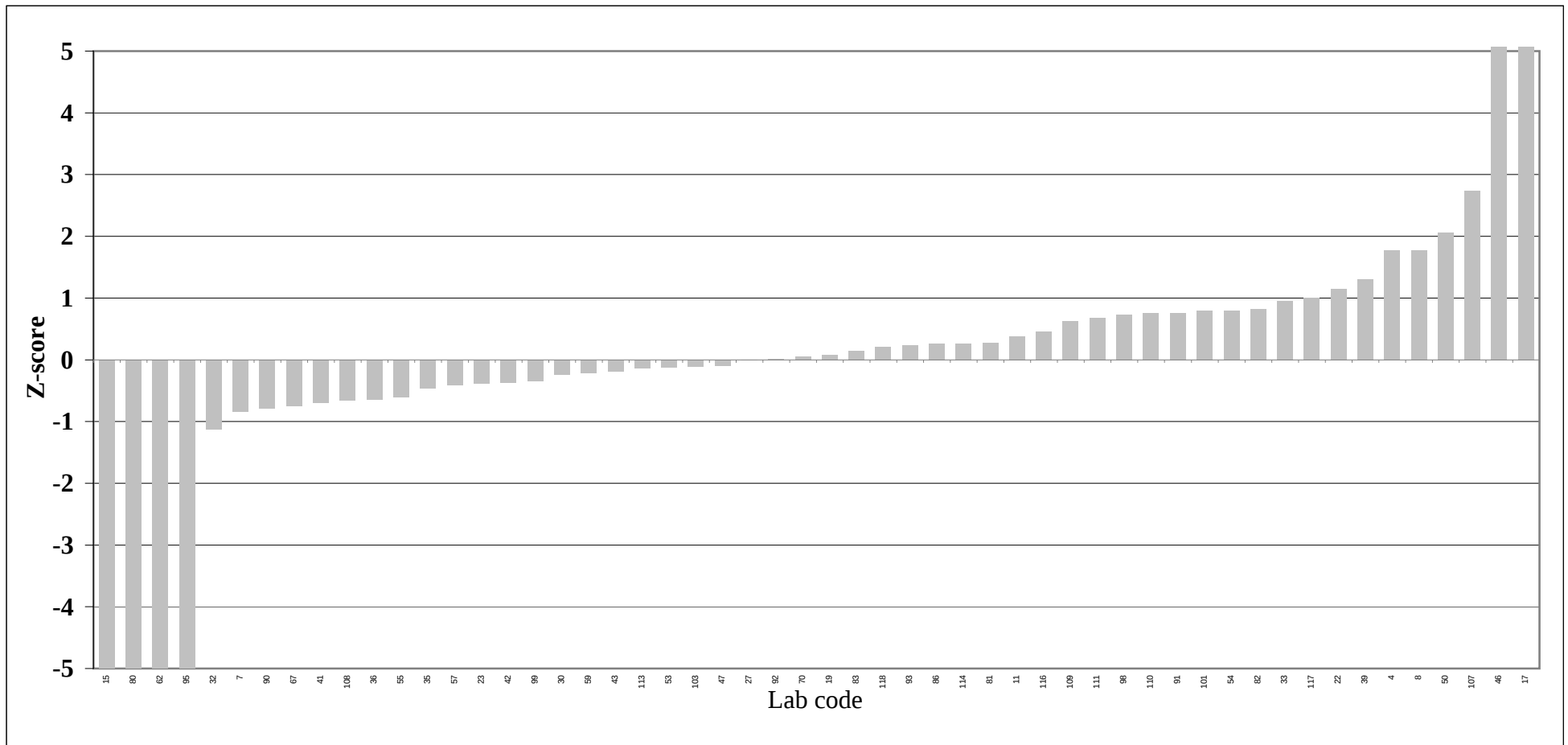
Z-score Beef; non-ortho PCB TEQ (fresh weight)



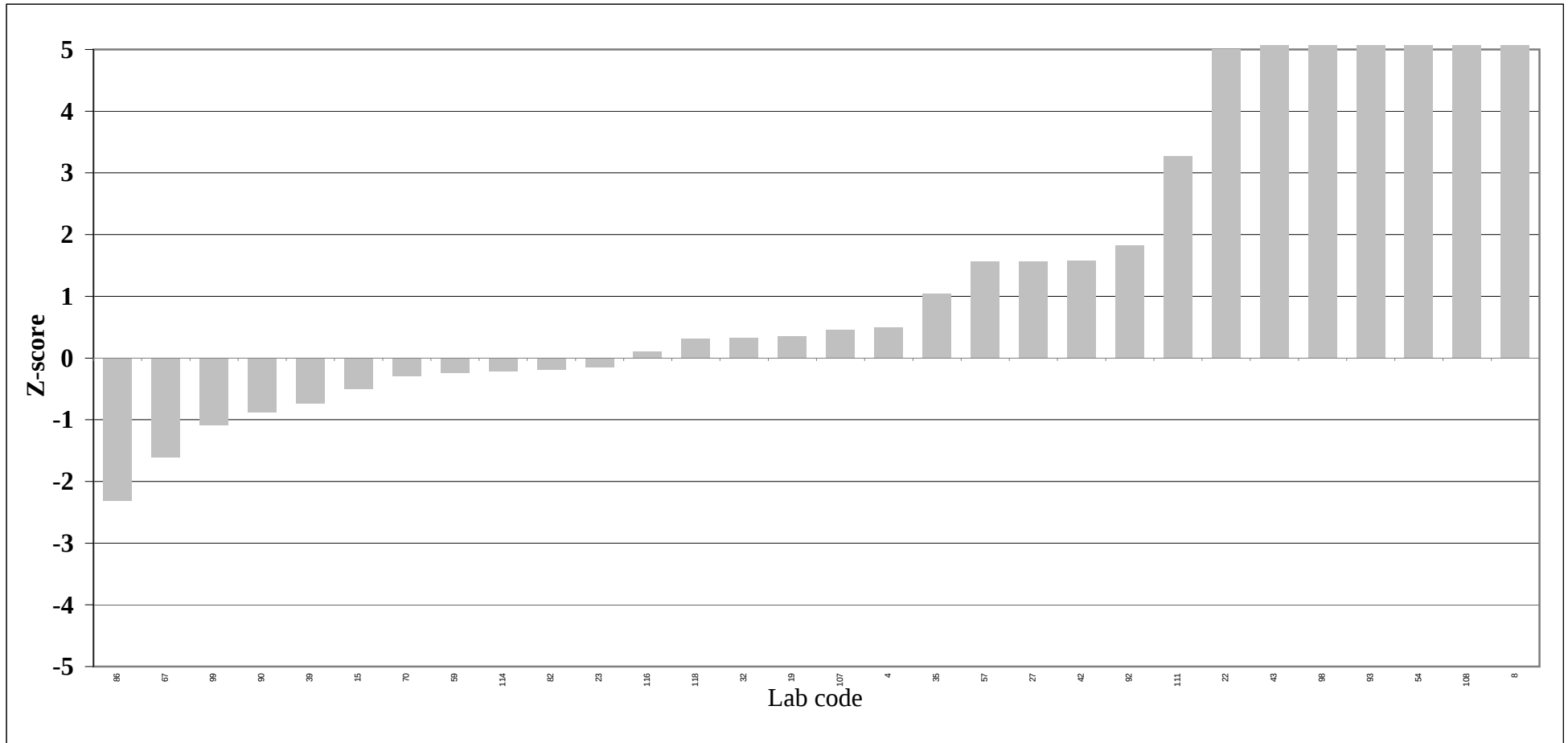
Z-score Beef; mono-ortho PCB TEQ (fresh weight)



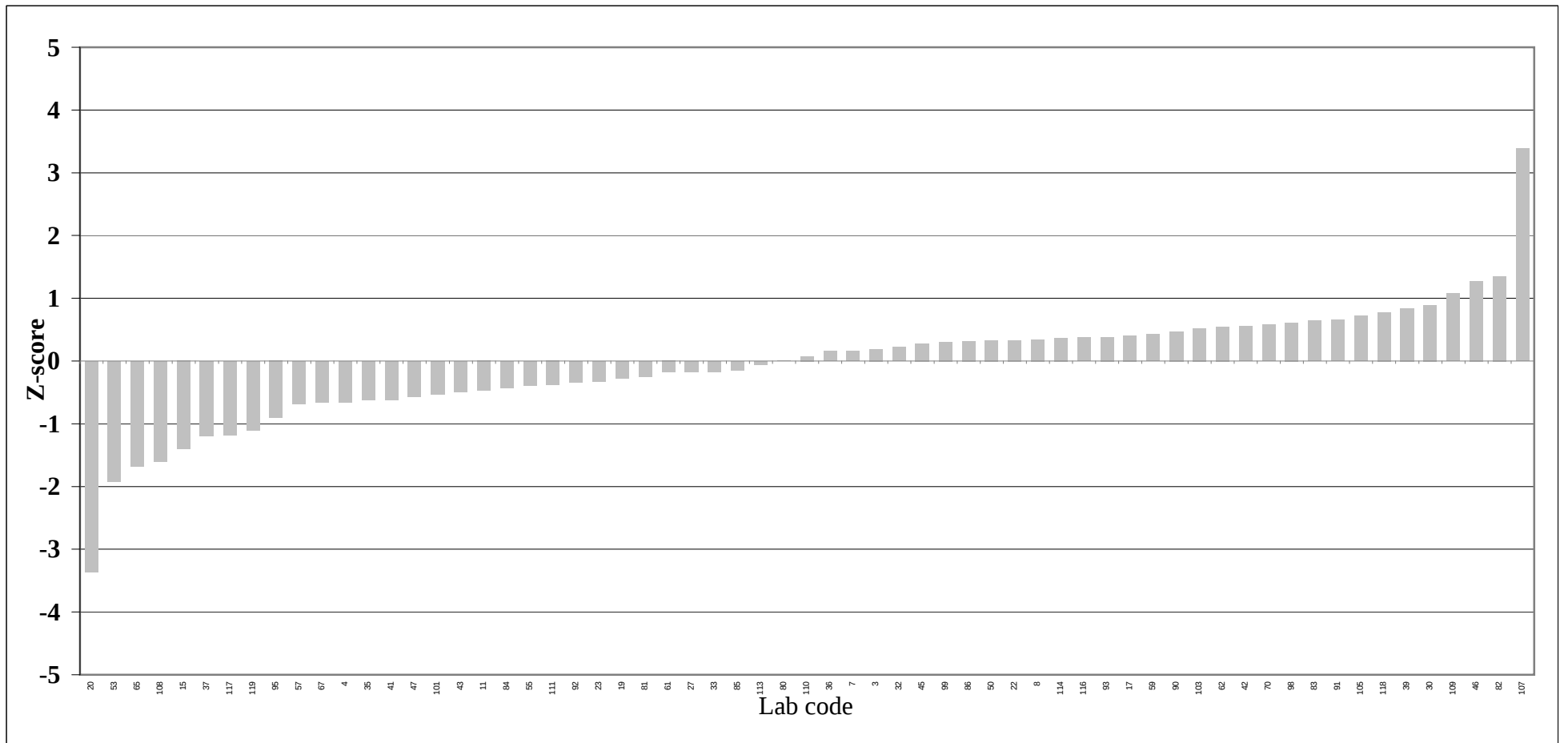
Z-score Beef; sum indicator PCB (fresh weight)



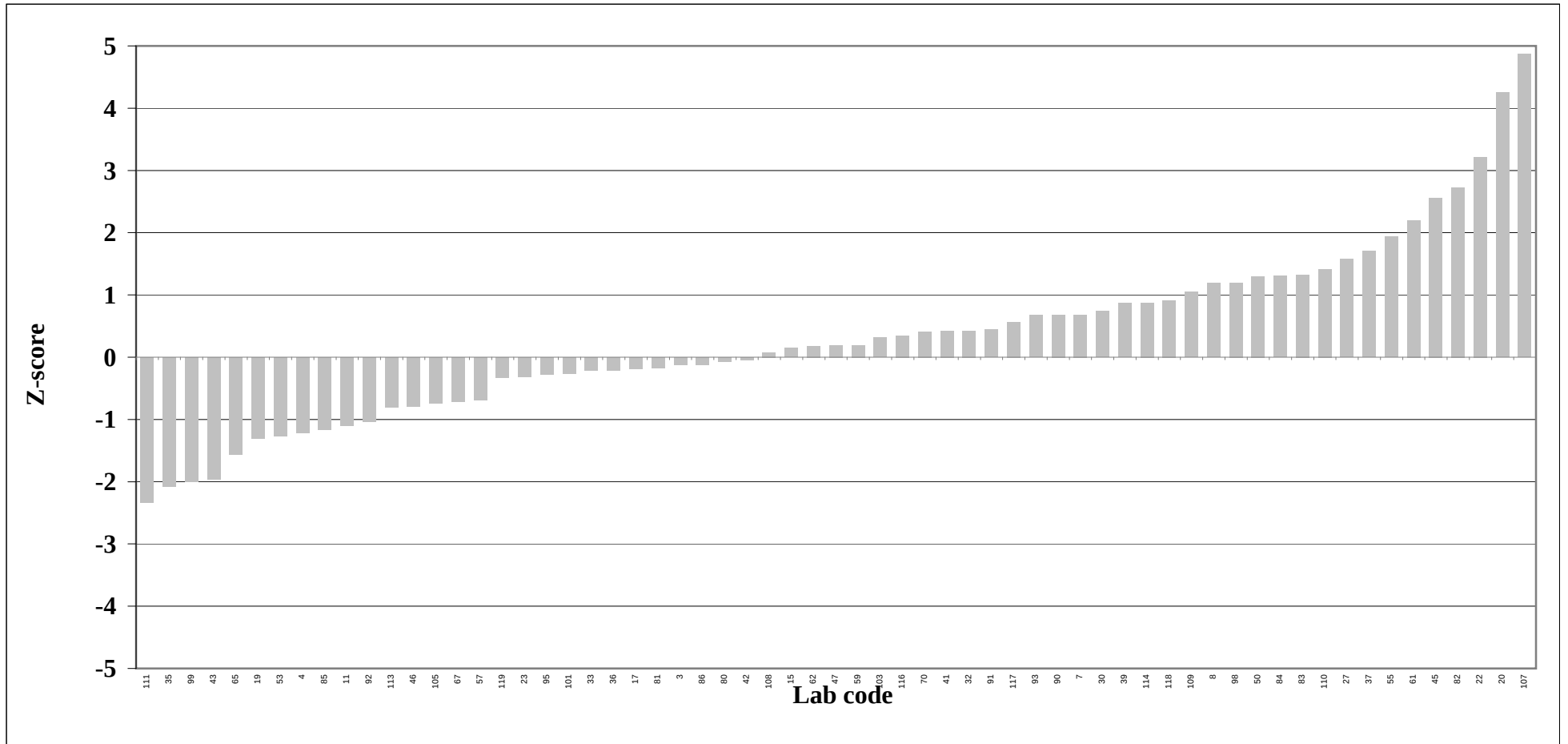
Z-score Beef; sum PBDE without PBDE-209 (fresh weight)



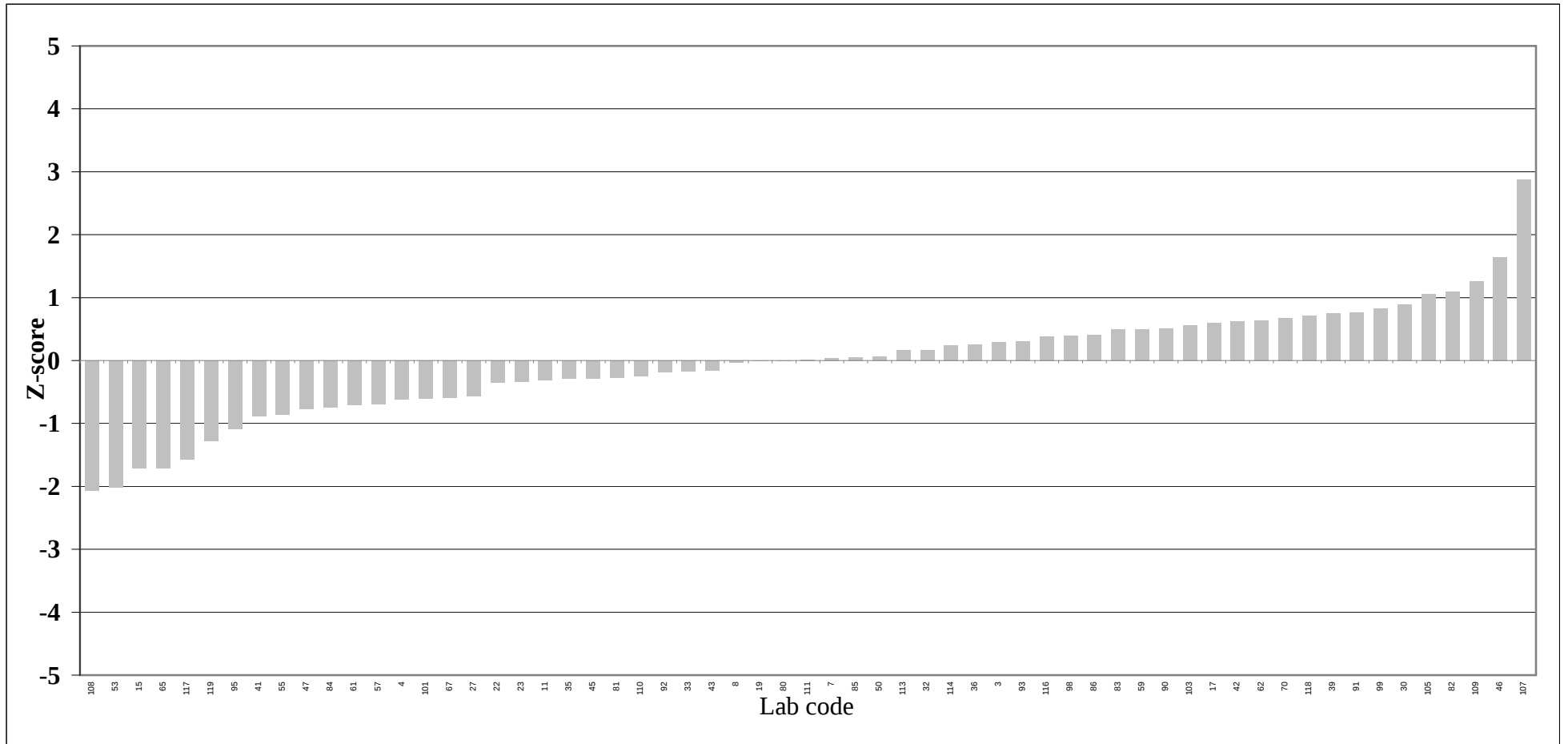
Z-score Beef; total TEQ (lipid weight)



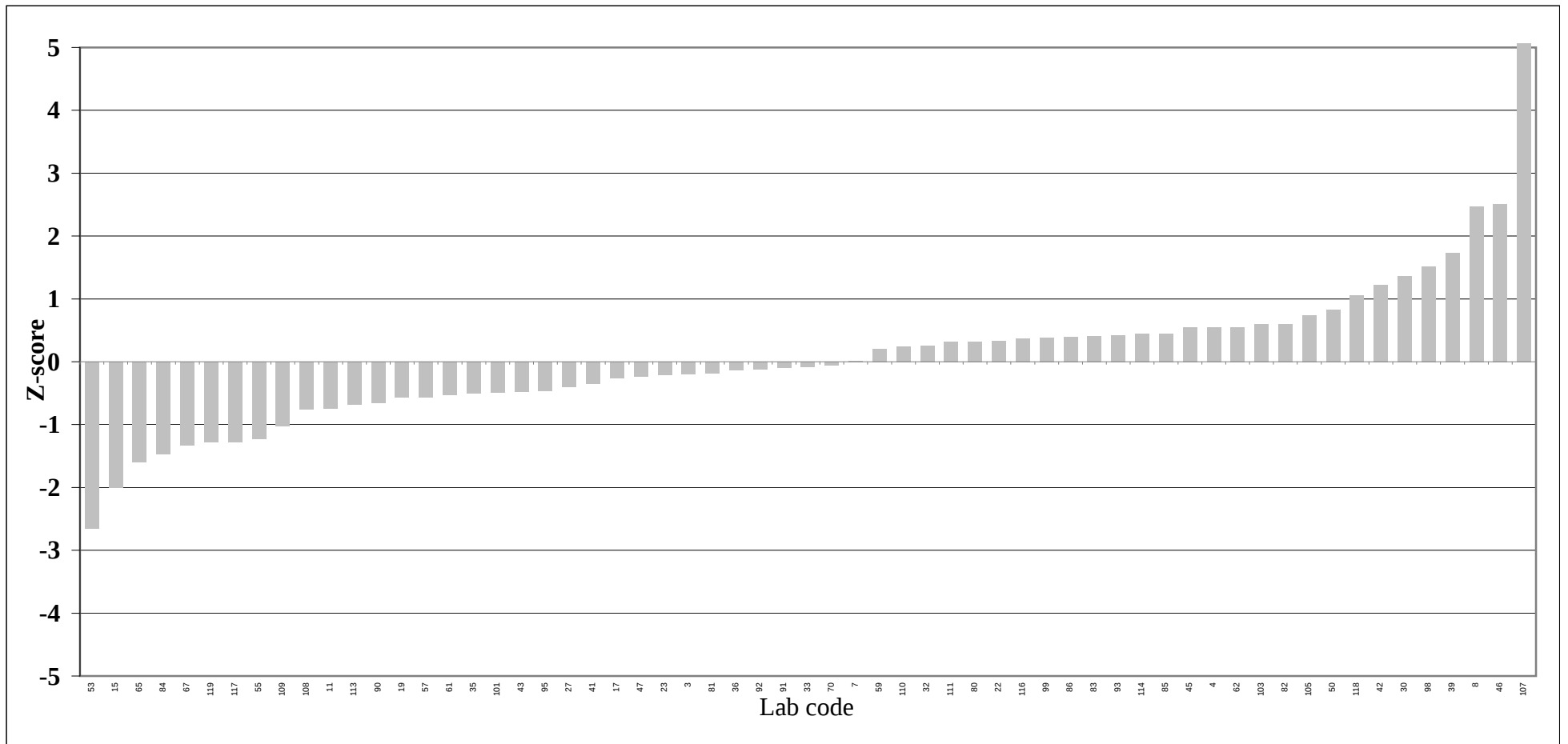
Z-score Beef; PCDD/PCDF TEQ (lipid weight)



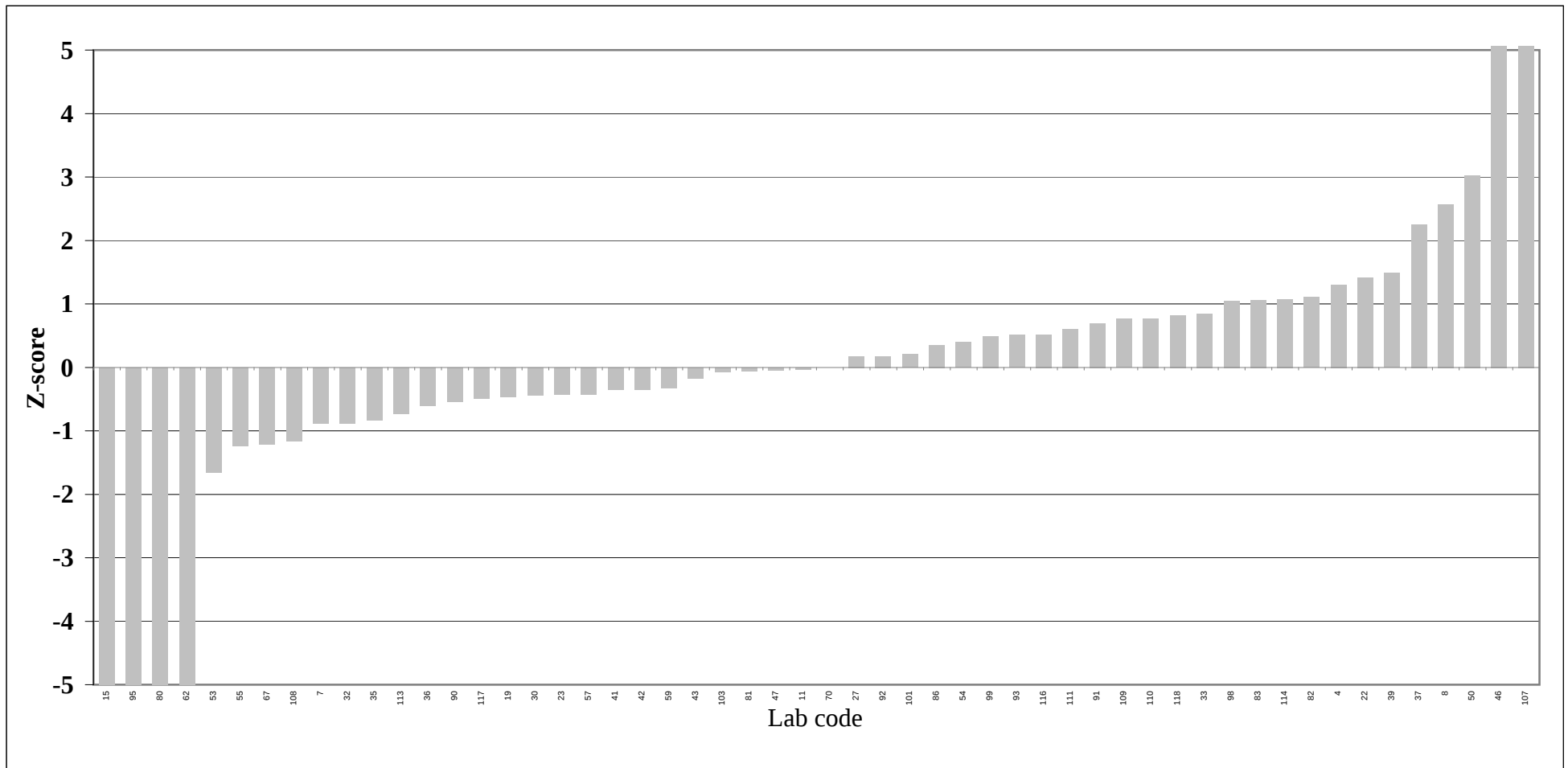
Z-score Beef; non-ortho PCB TEQ (lipid weight)



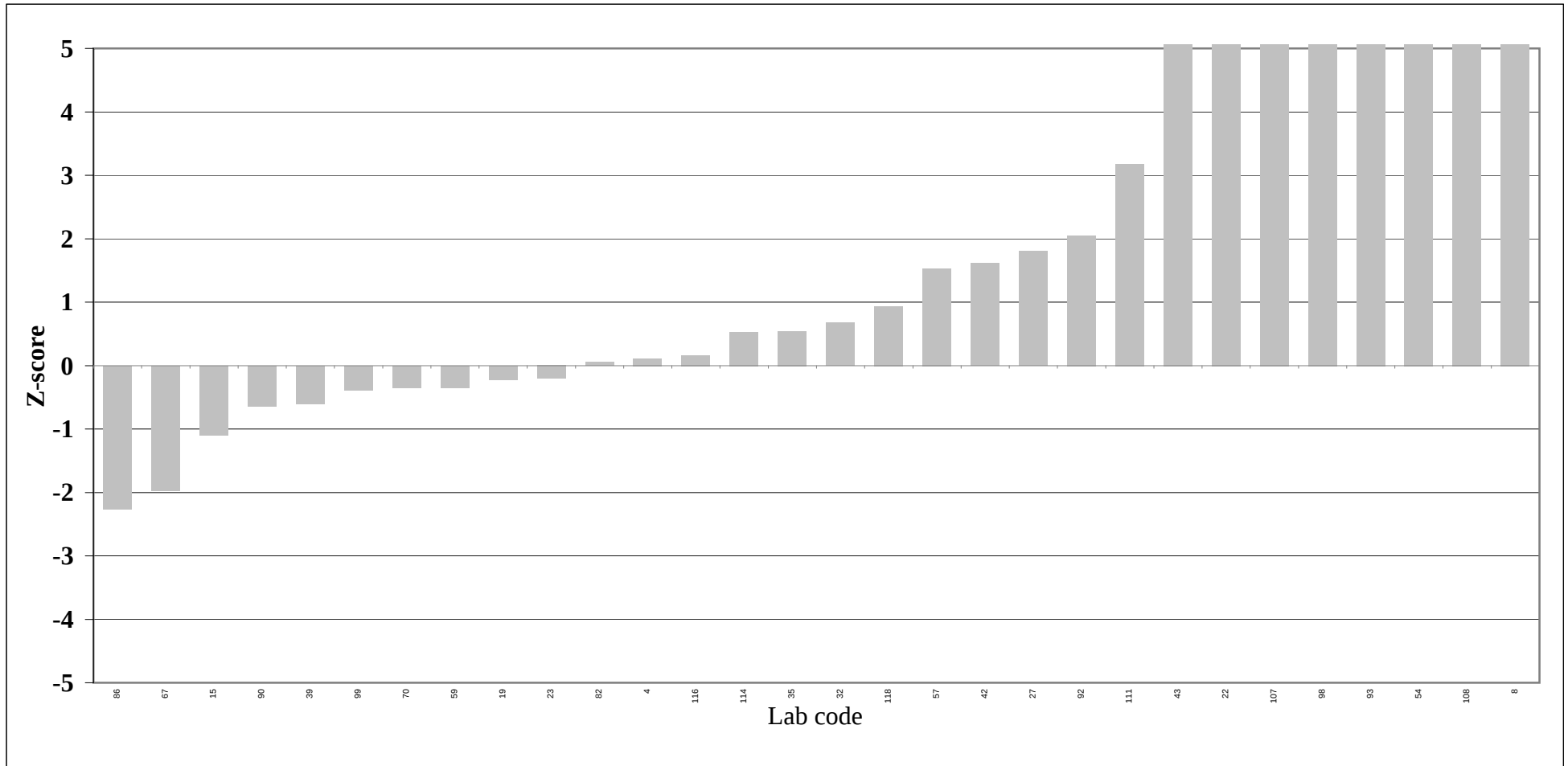
Z-score Beef; mono-ortho PCB TEQ (lipid weight)



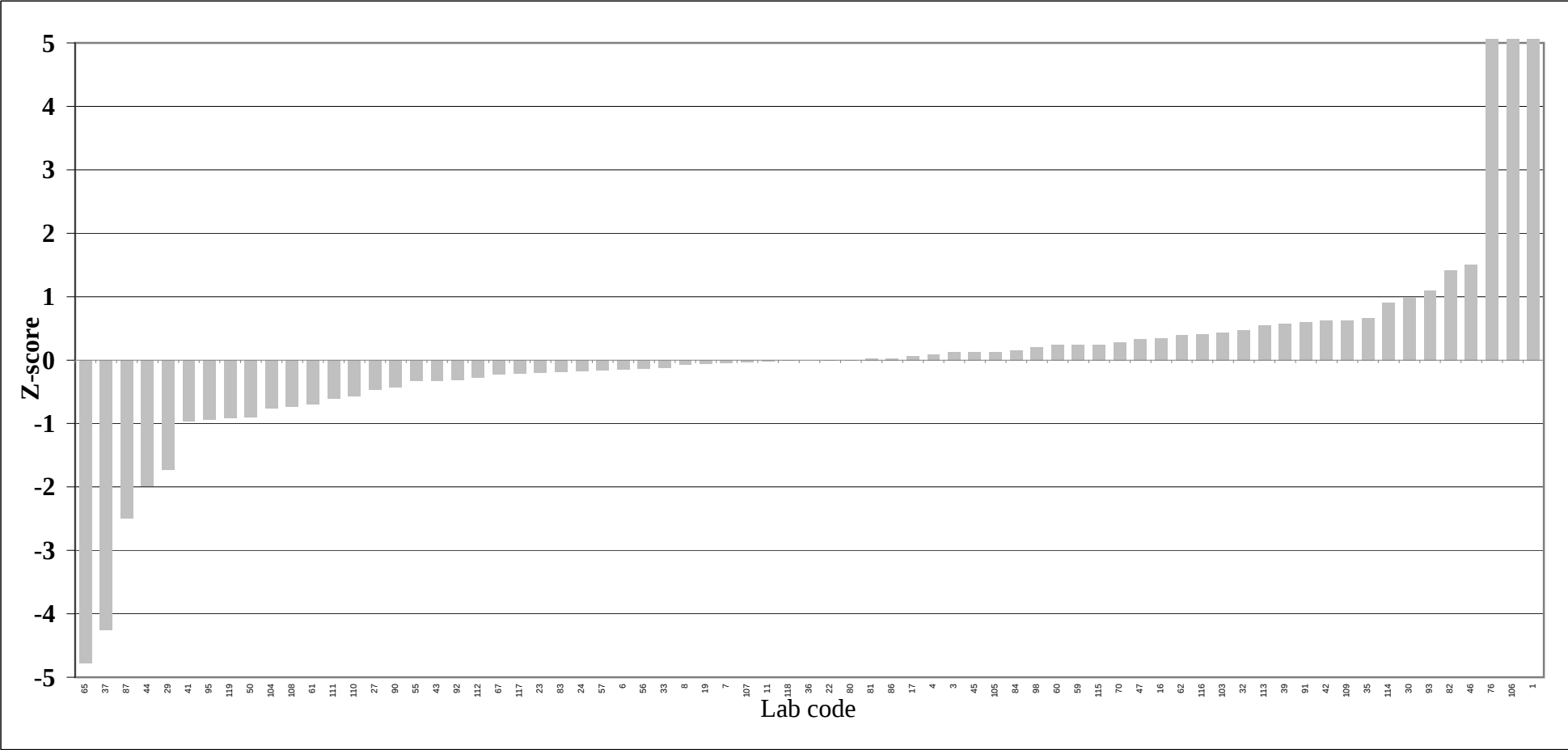
Z-score Beef; sum indicator PCB (lipid weight)



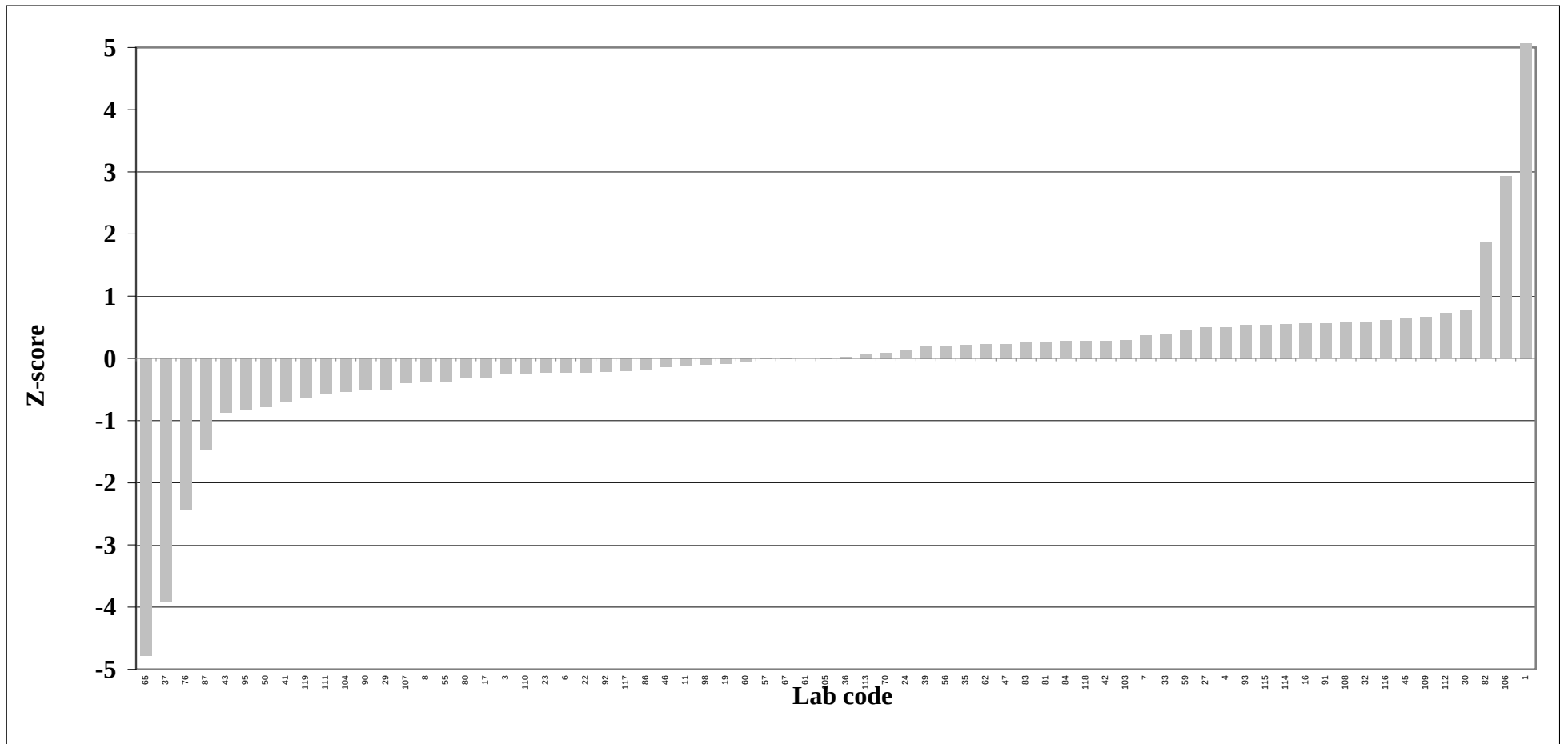
Z-score Beef; sum PBDE without PBDE-209 (lipid weight)



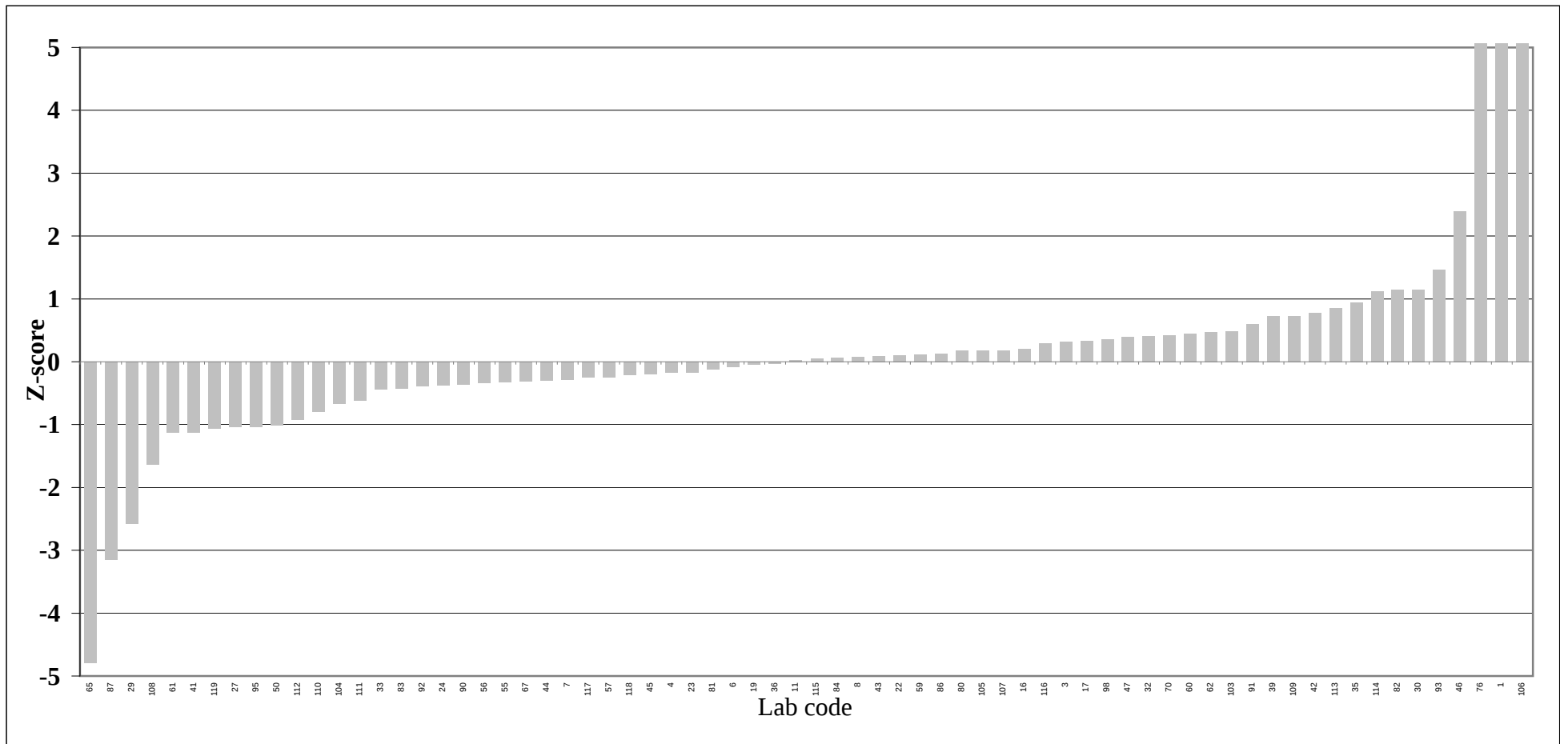
Z-score Salmon; total TEQ (fresh weight)



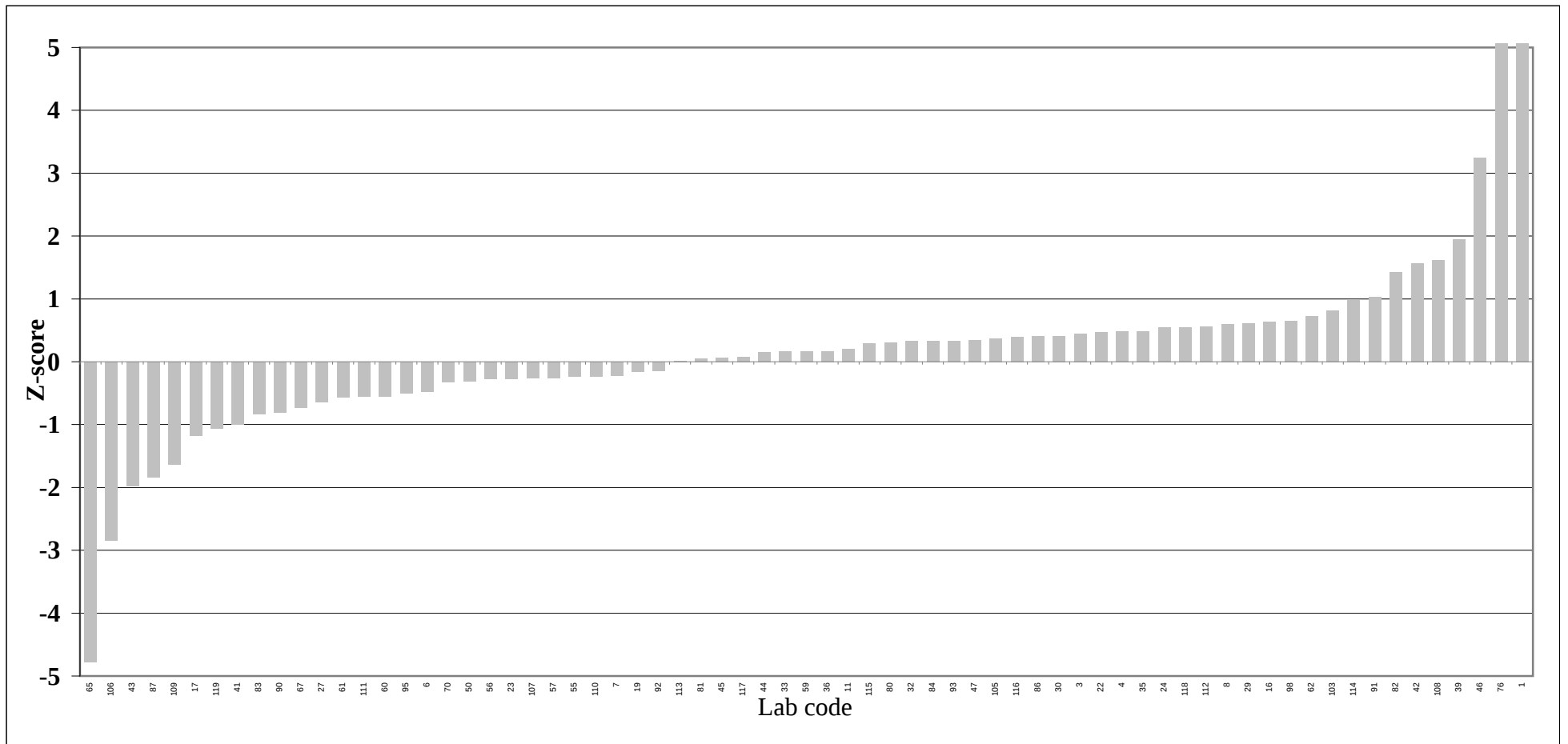
Z-score Salmon; PCDD/PCDF TEQ (fresh weight)



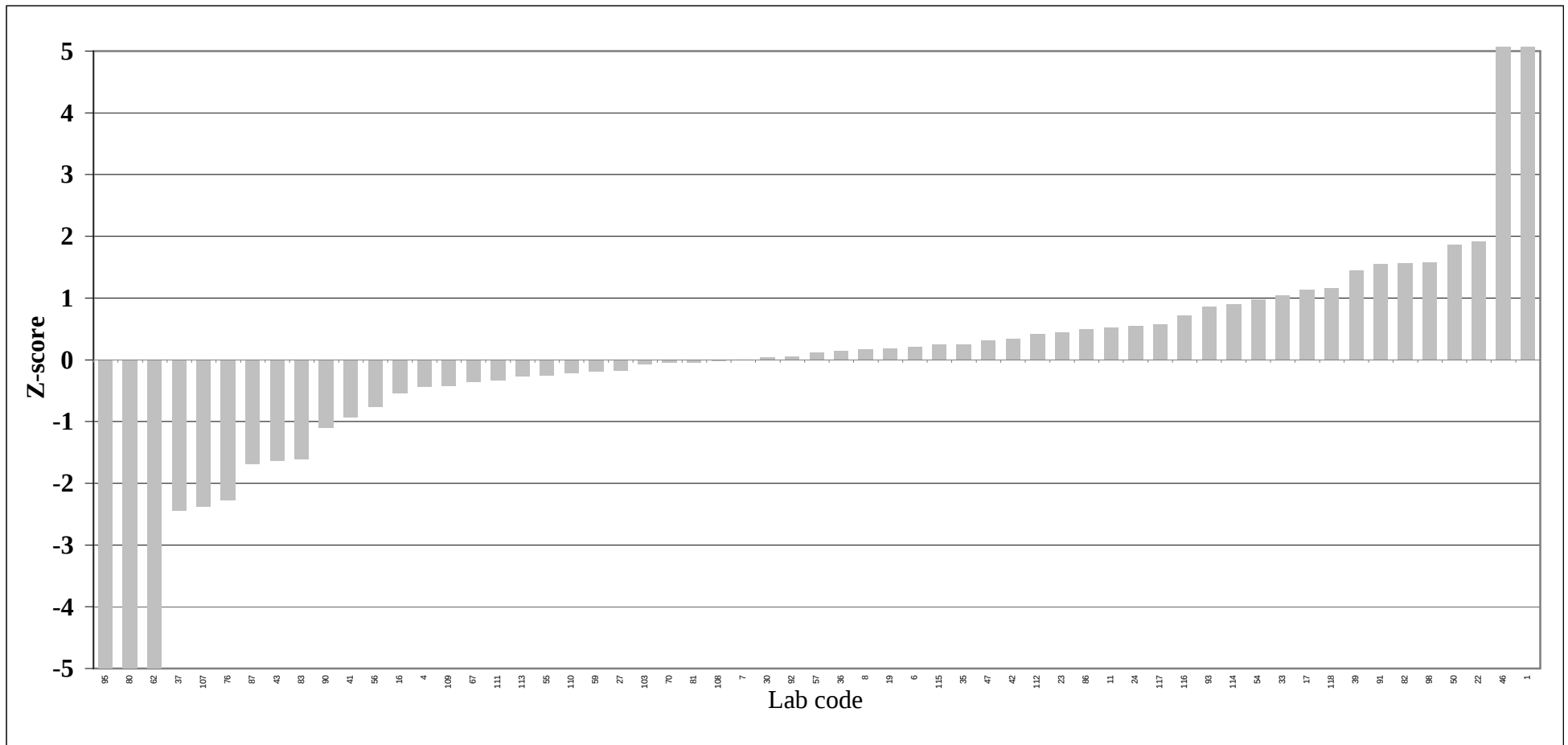
Z-score Salmon; non-ortho PCB TEQ (fresh weight)



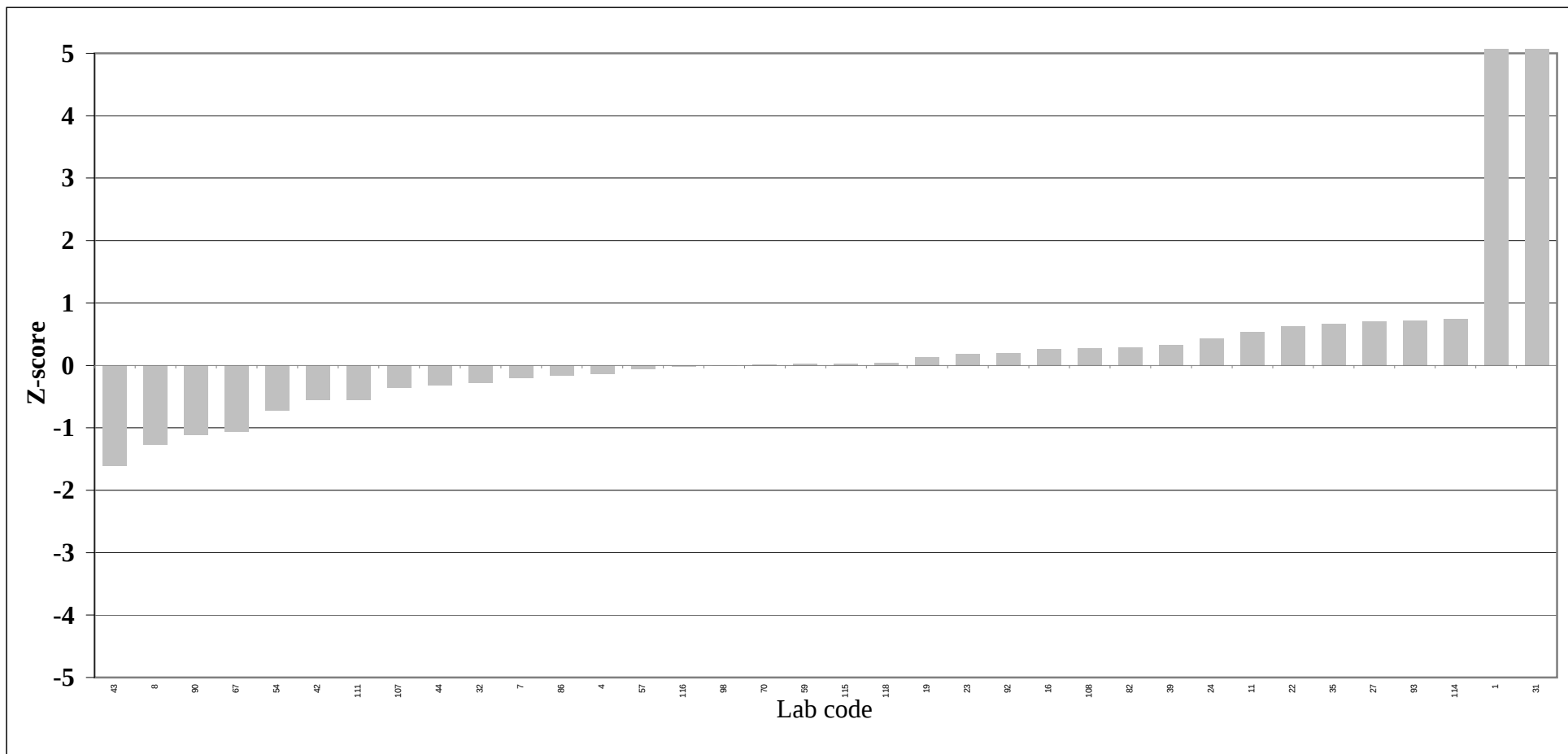
Z-score Salmon; mono-ortho PCB TEQ (fresh weight)



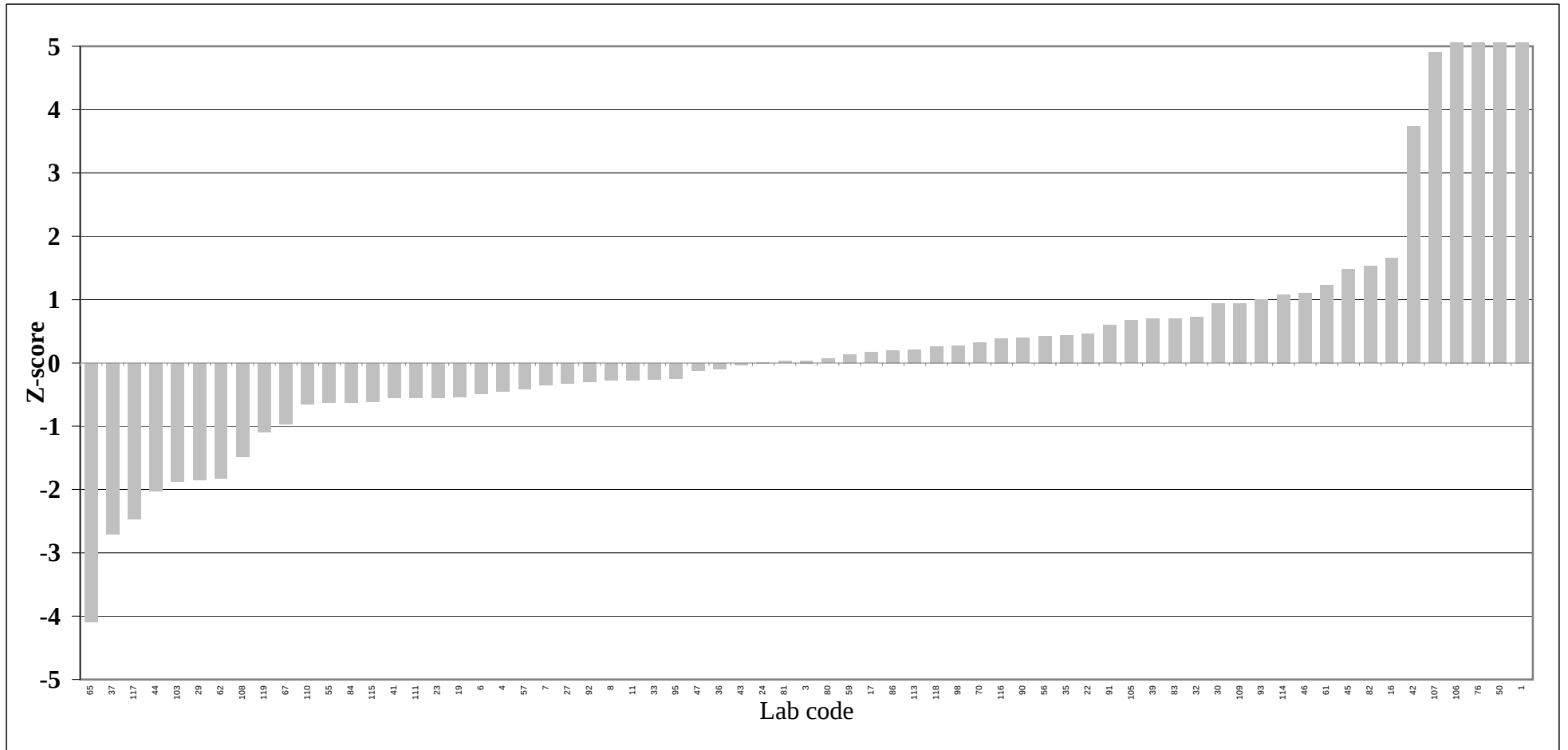
Z-score Salmon; sum indicator PCB (fresh weight)



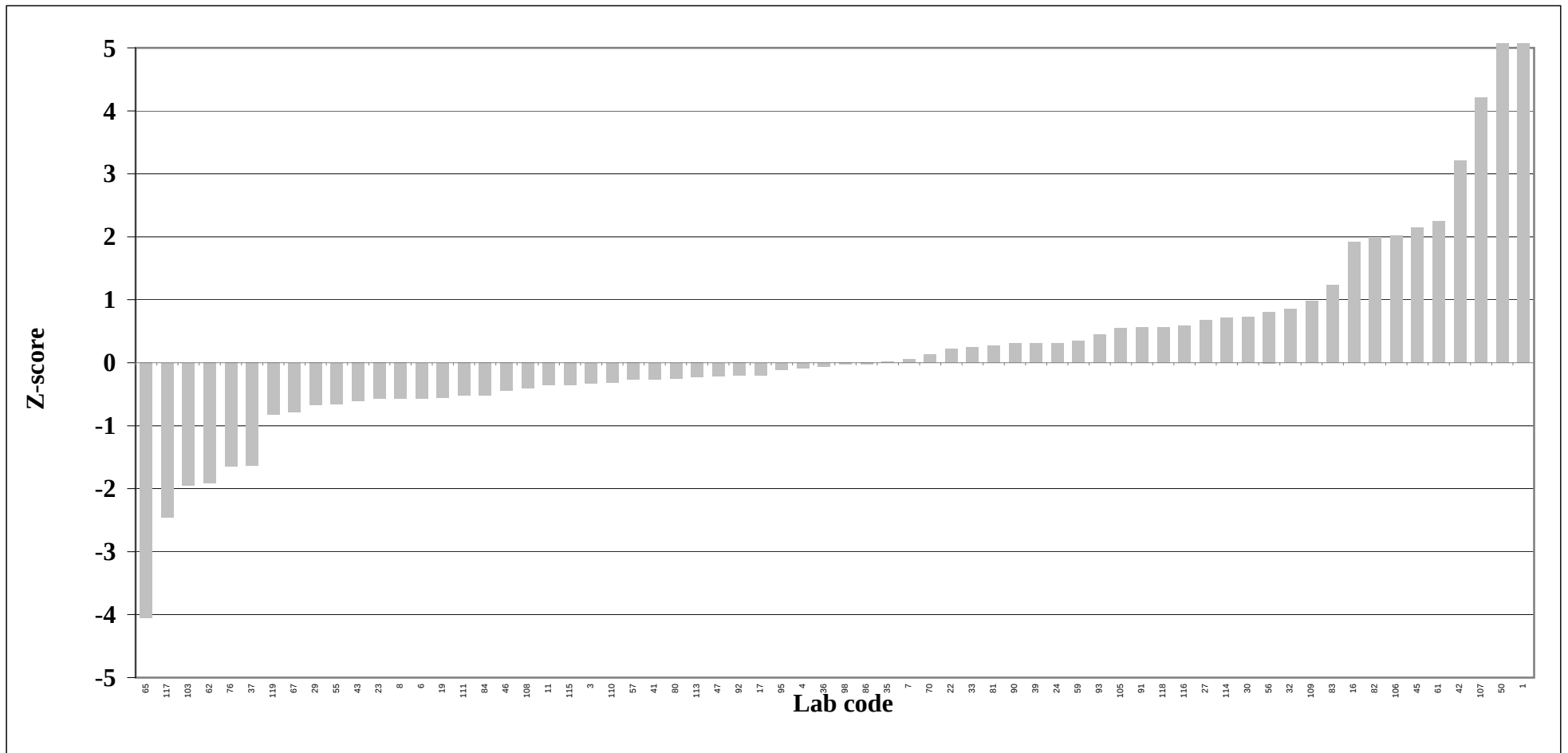
Z-score Salmon; sum PBDE without PBDE-209 (fresh weight)



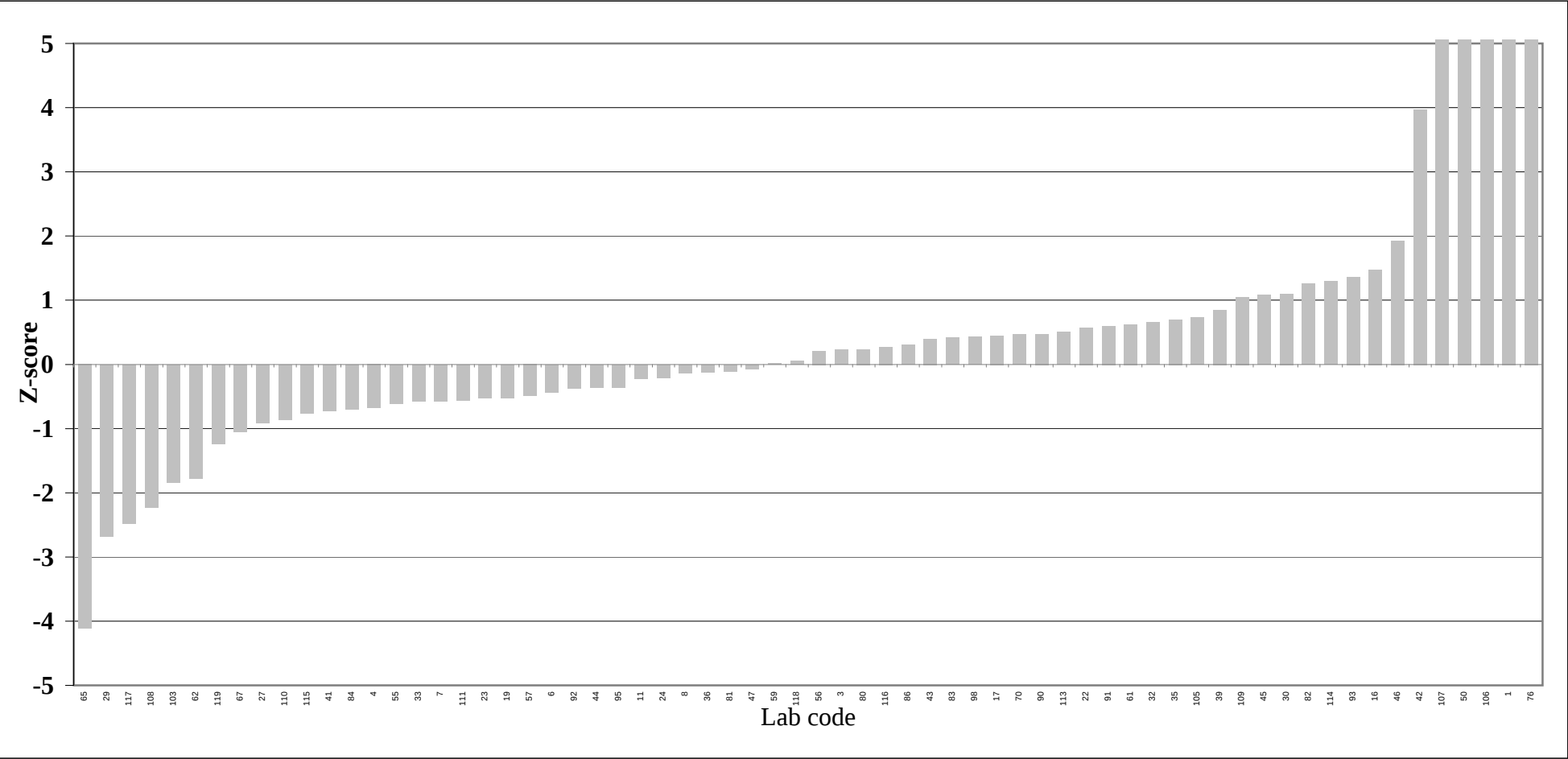
Z-score Salmon; total TEQ (lipid weight)



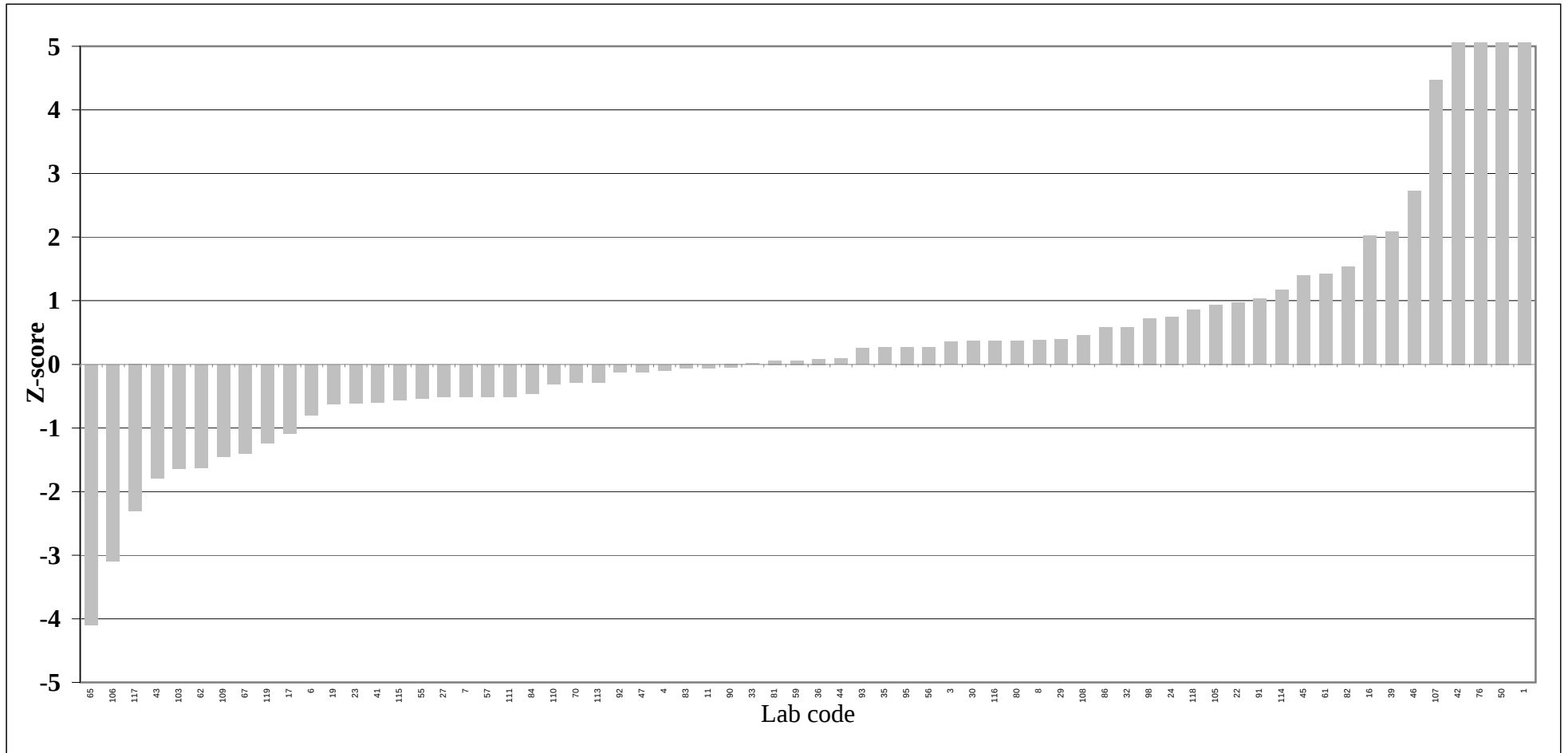
Z-score Salmon; PCDD/PCDF TEQ (lipid weight)



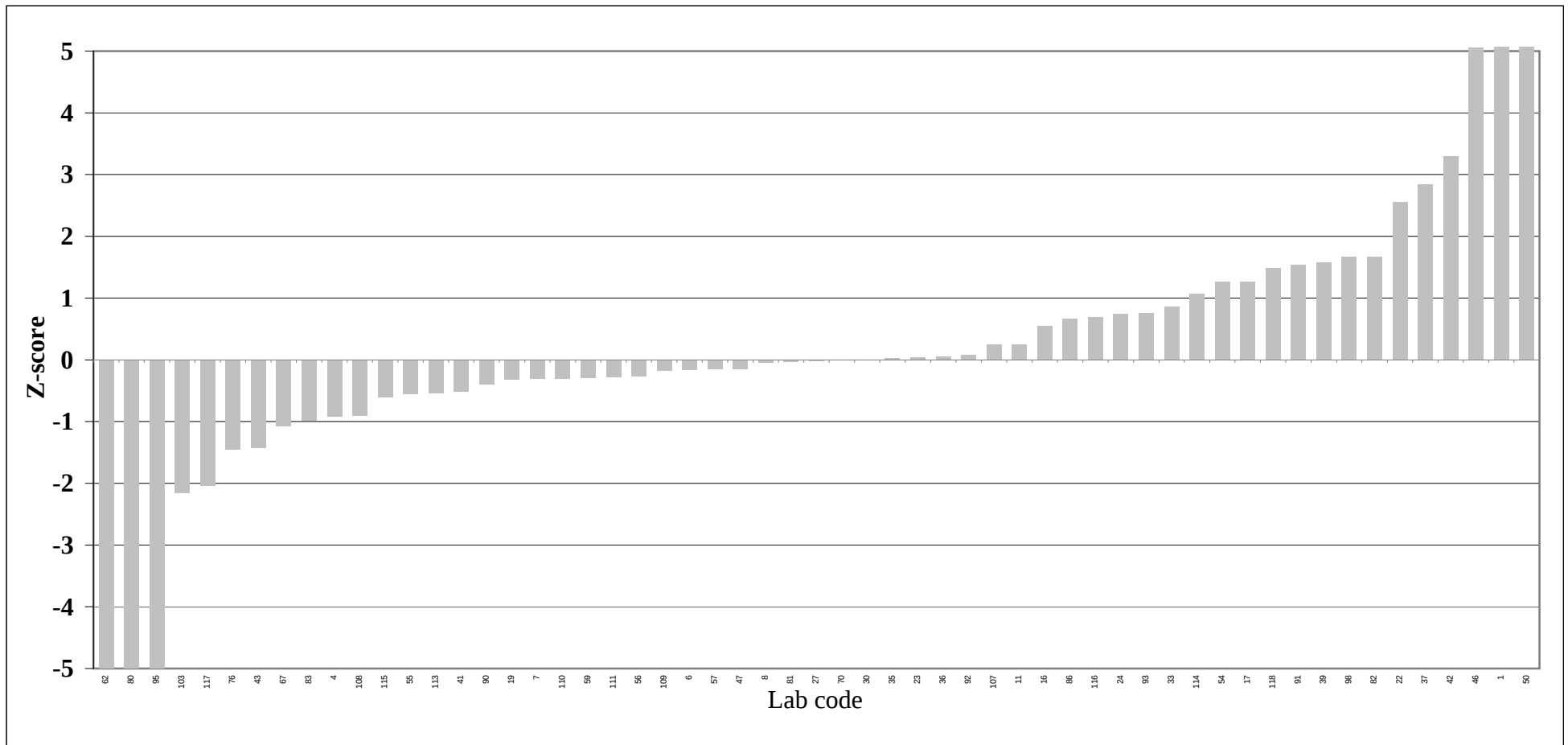
Z-score Salmon; non-ortho PCB TEQ (lipid weight)



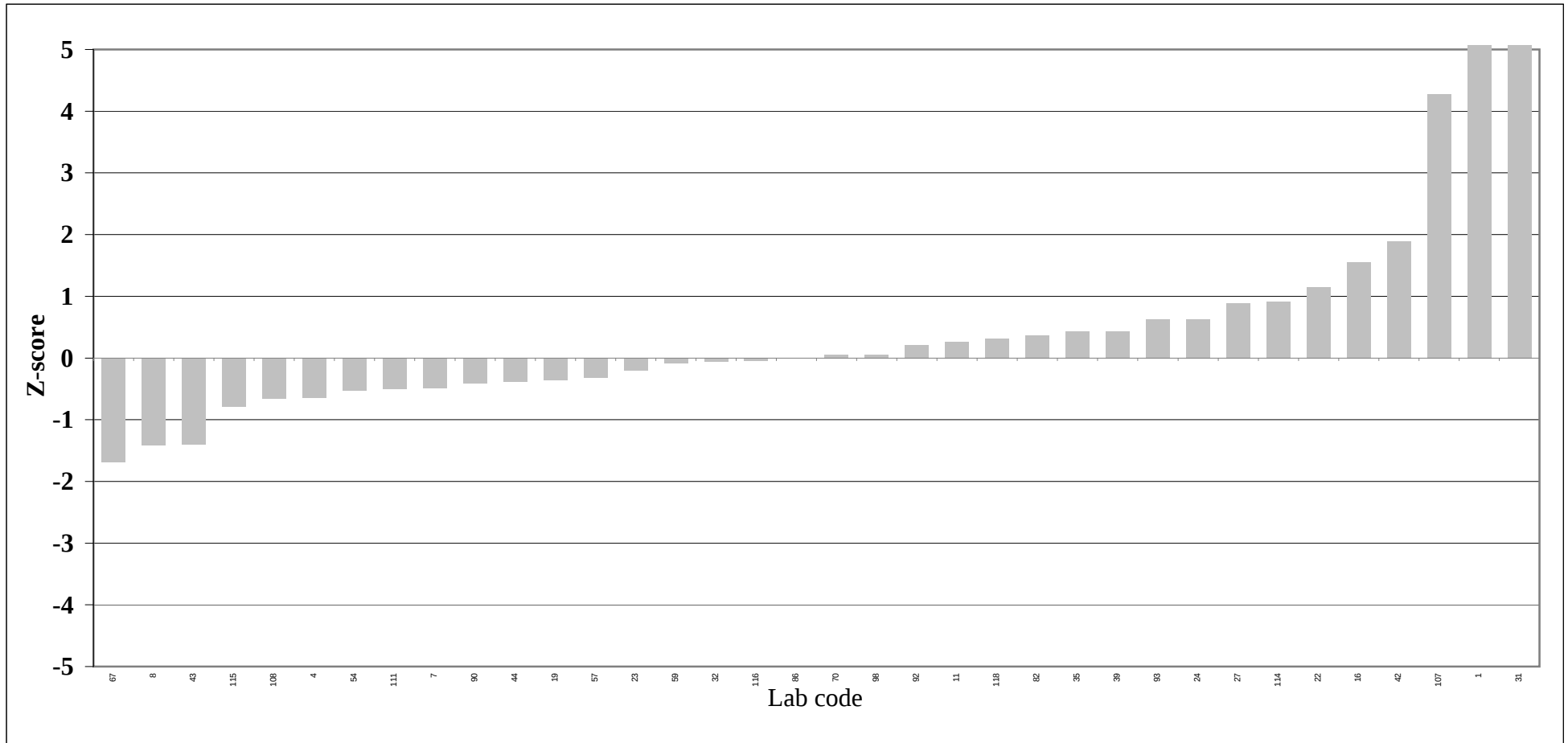
Z-score Salmon; mono-ortho PCB TEQ (lipid weight)



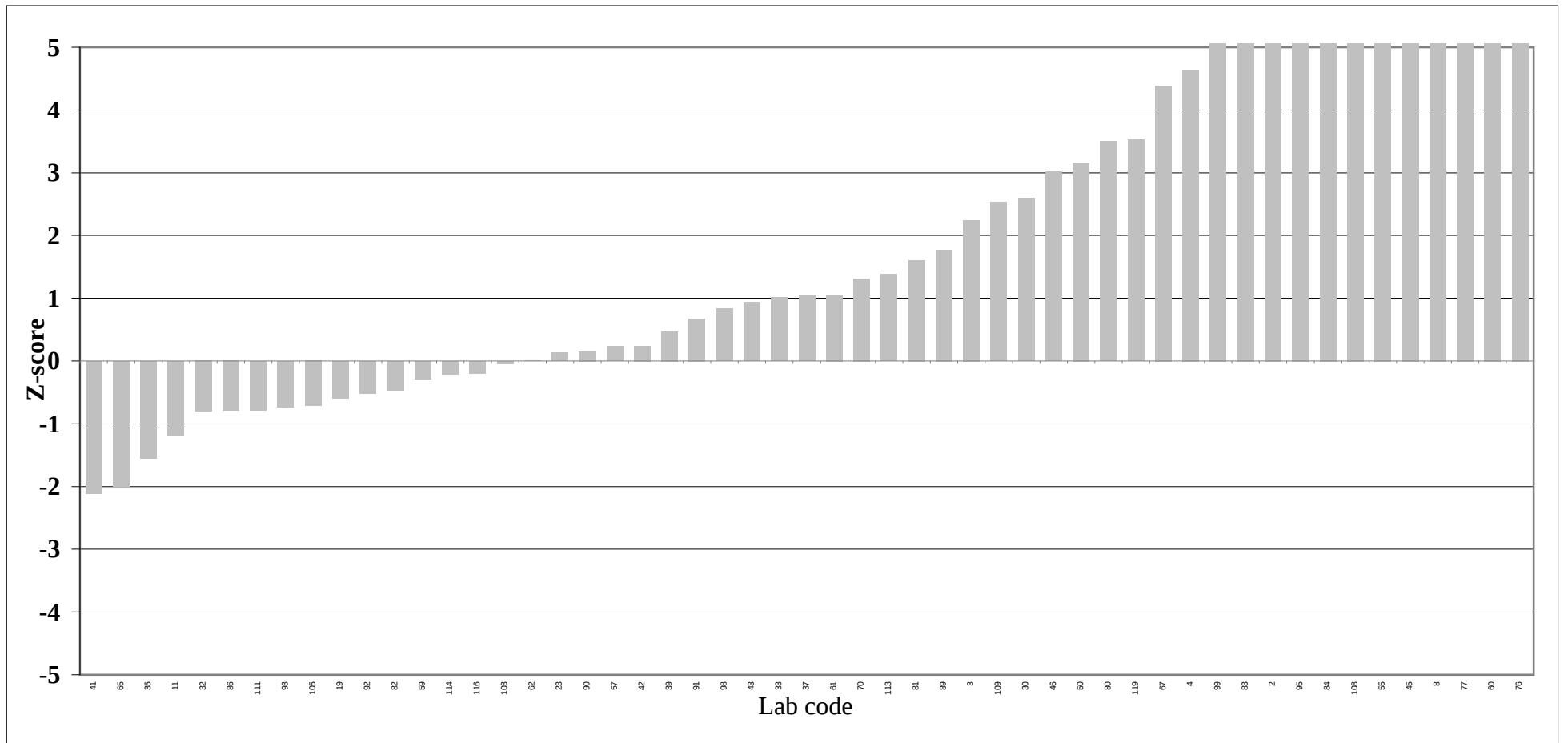
Z-score Salmon; sum indicator PCB (lipid weight)



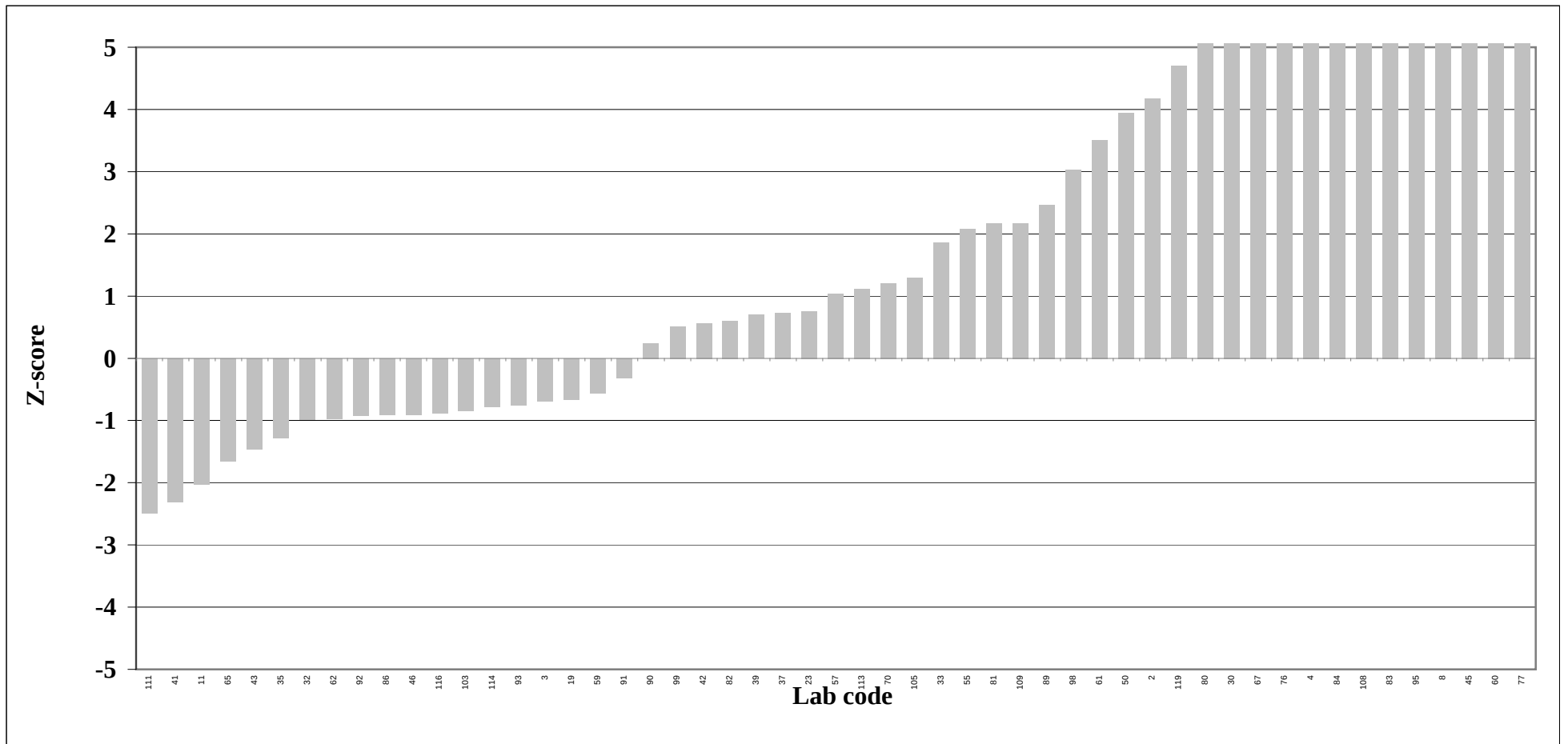
Z-score Salmon; sum PBDE without PBDE-209 (lipid weight)



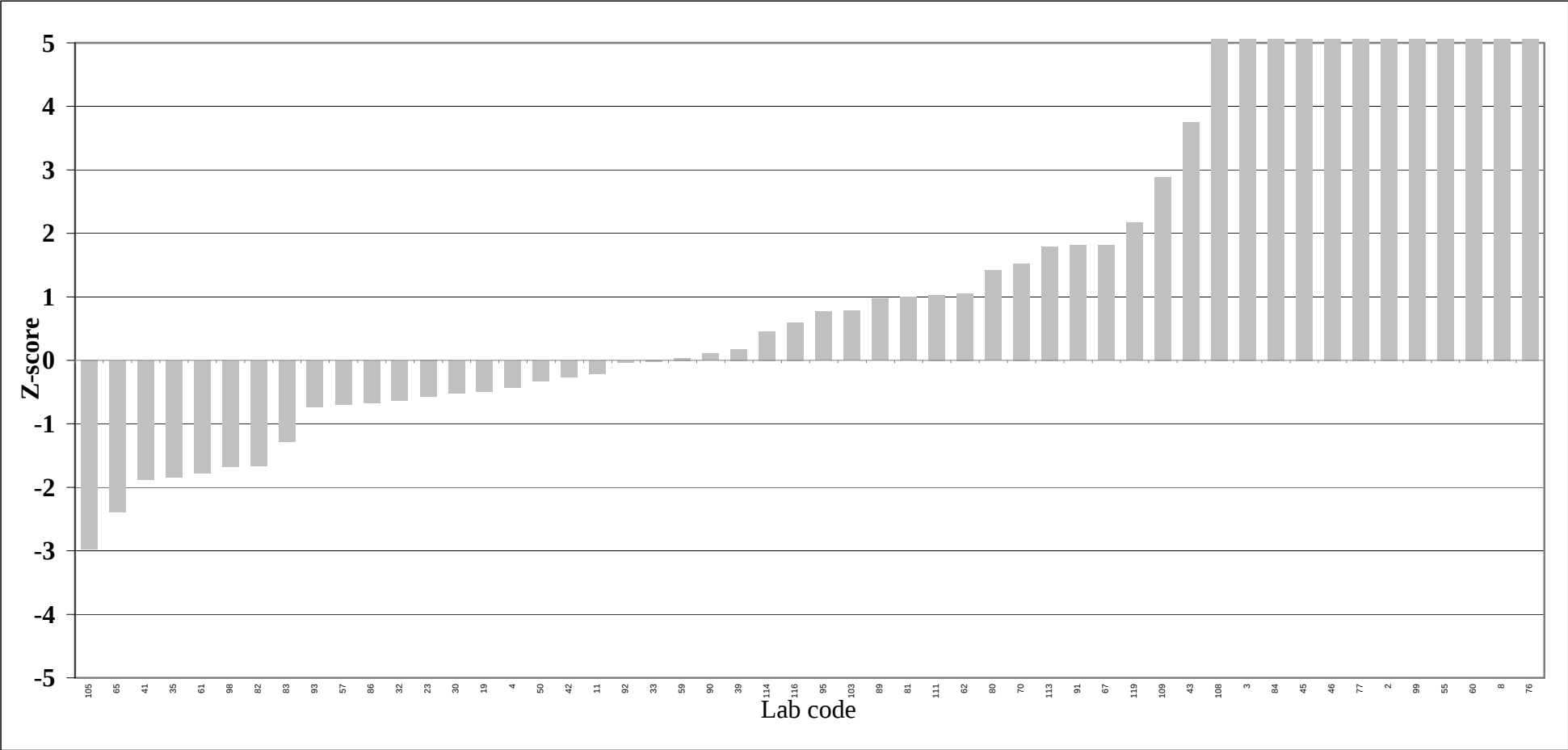
Z-score Cheese; total TEQ (fresh weight)



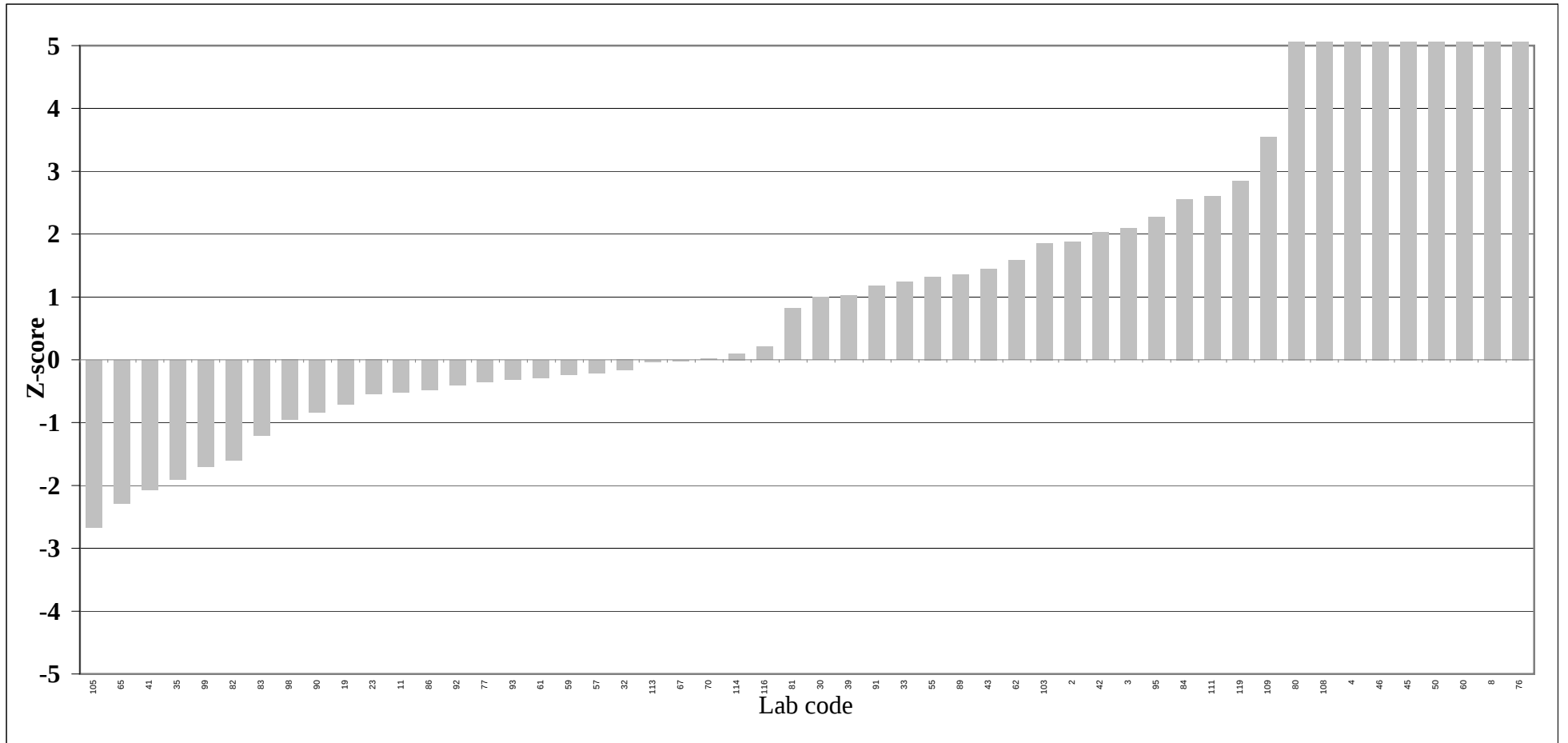
Z-score Cheese; PCDD/PCDF TEQ (fresh weight)



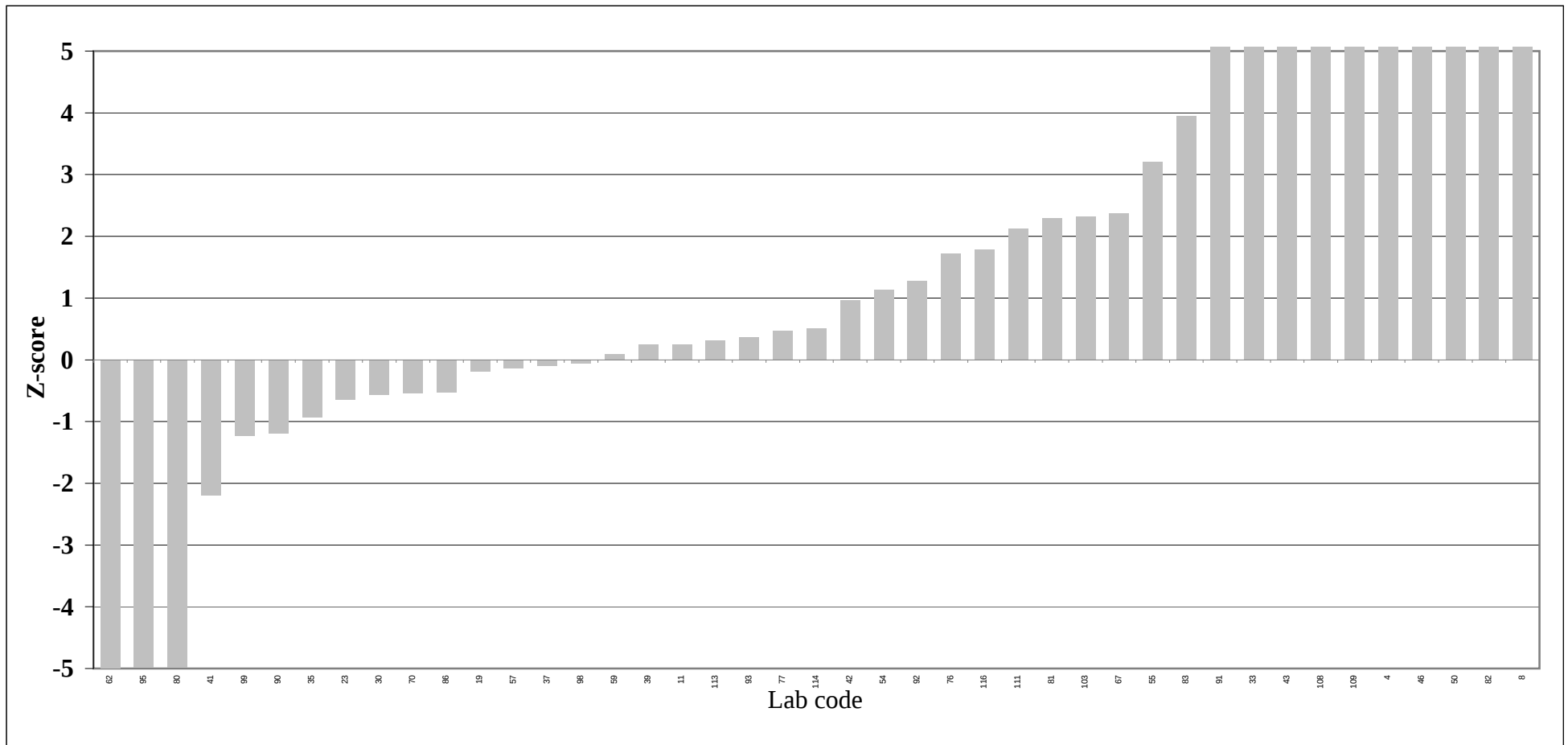
Z-score Cheese; non-ortho PCB TEQ (fresh weight)



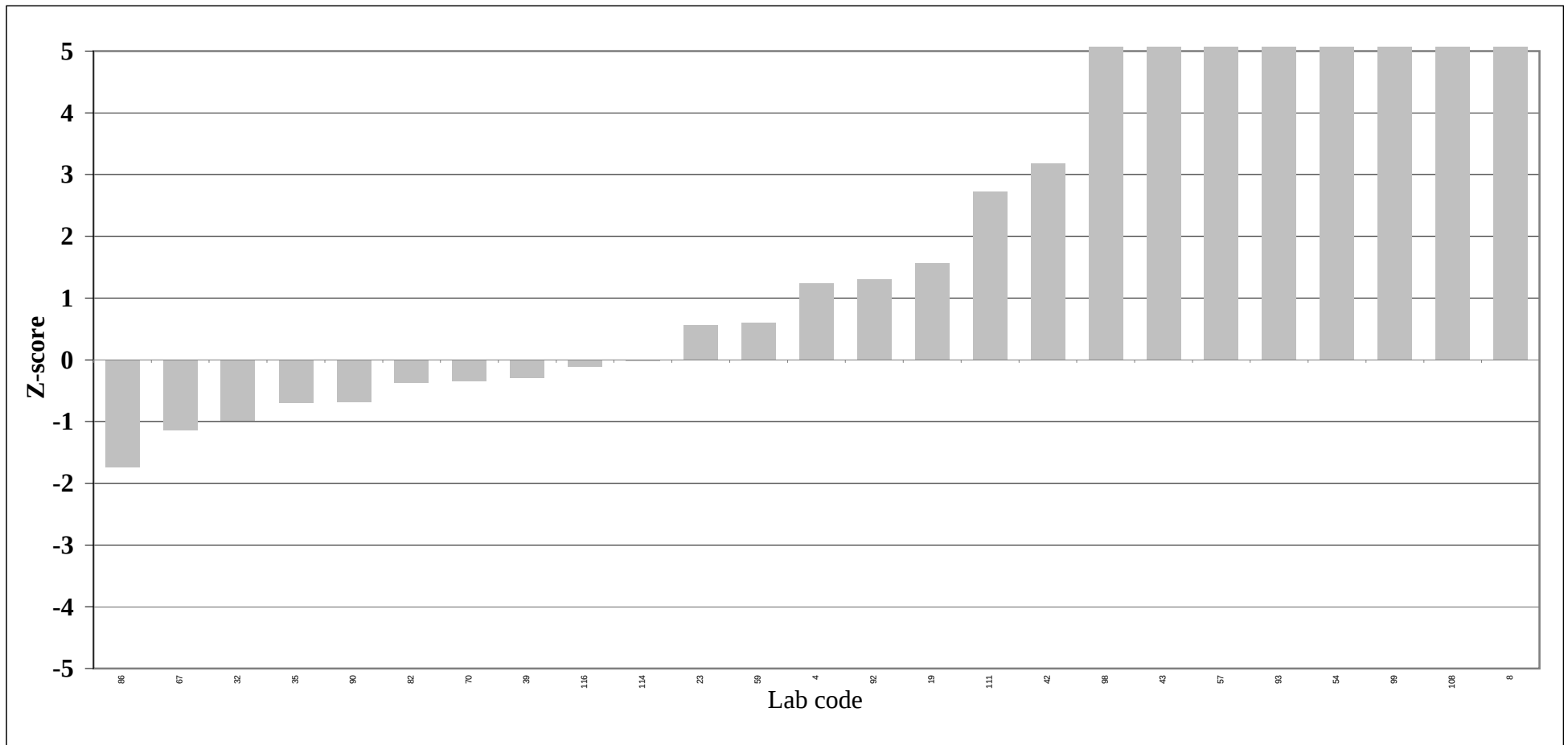
Z-score Cheese; mono-ortho PCB TEQ (fresh weight)



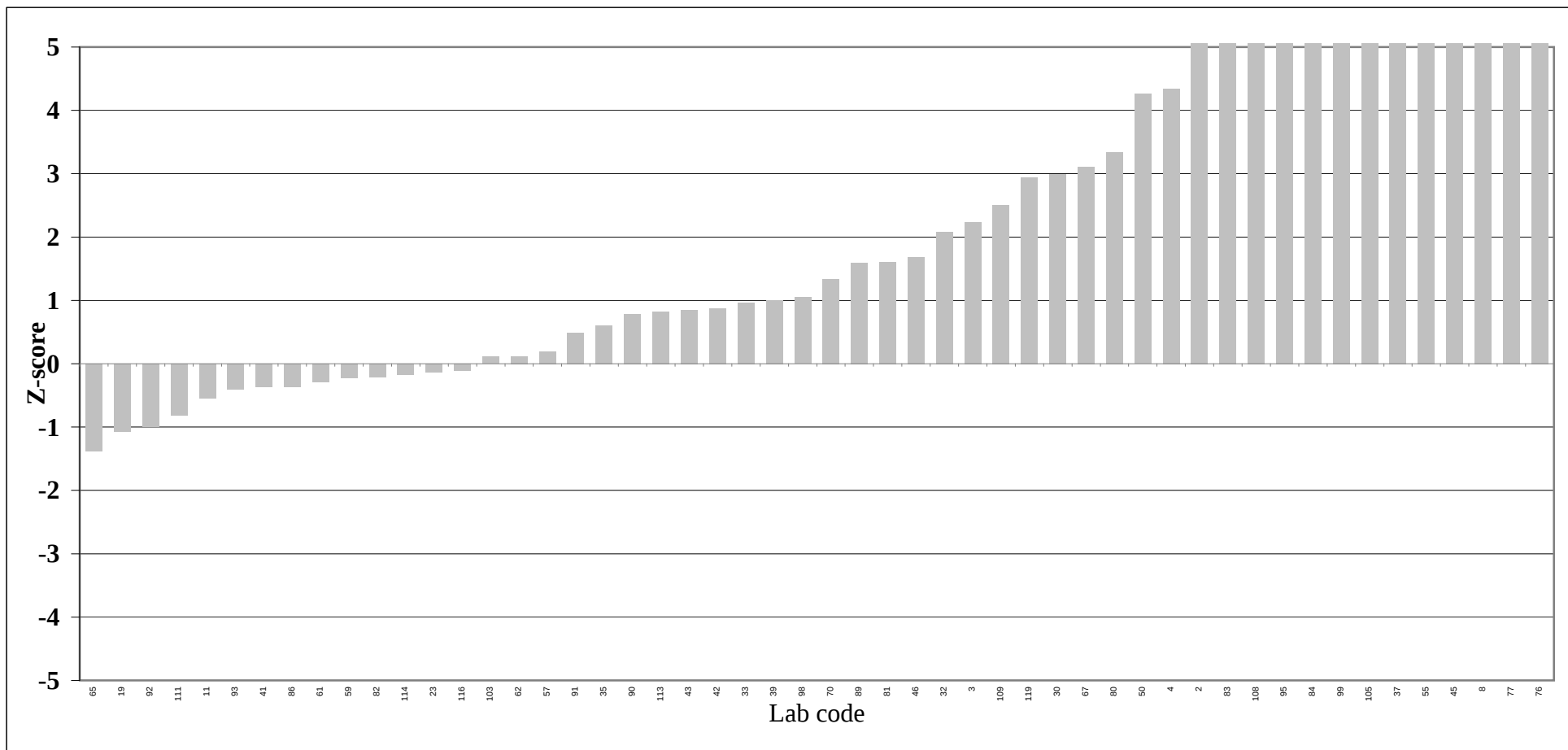
Z-score Cheese; sum indicator PCB (fresh weight)



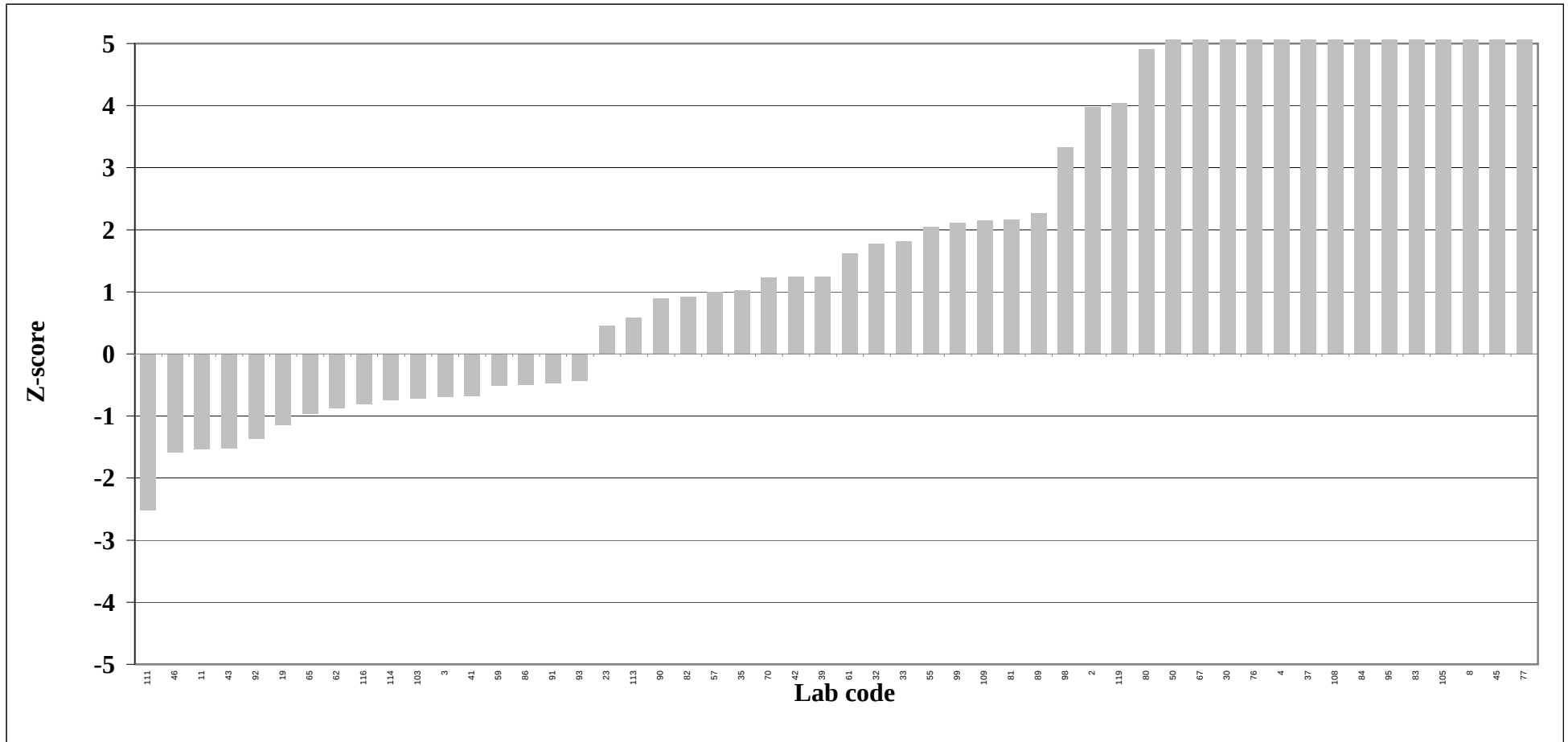
Z-score Cheese; sum PBDE without PBDE-209 (fresh weight)



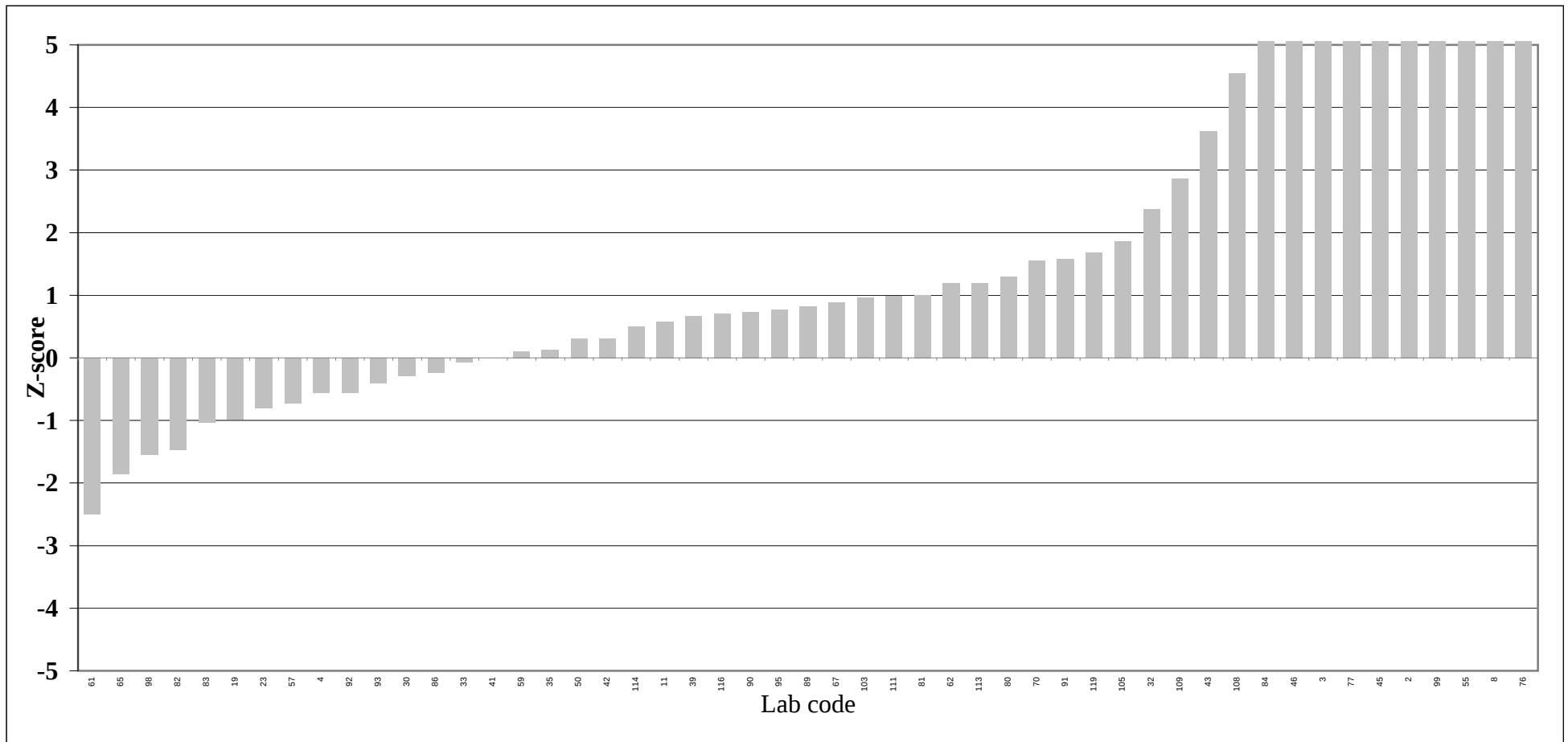
Z-score Cheese; total TEQ (lipid weight)



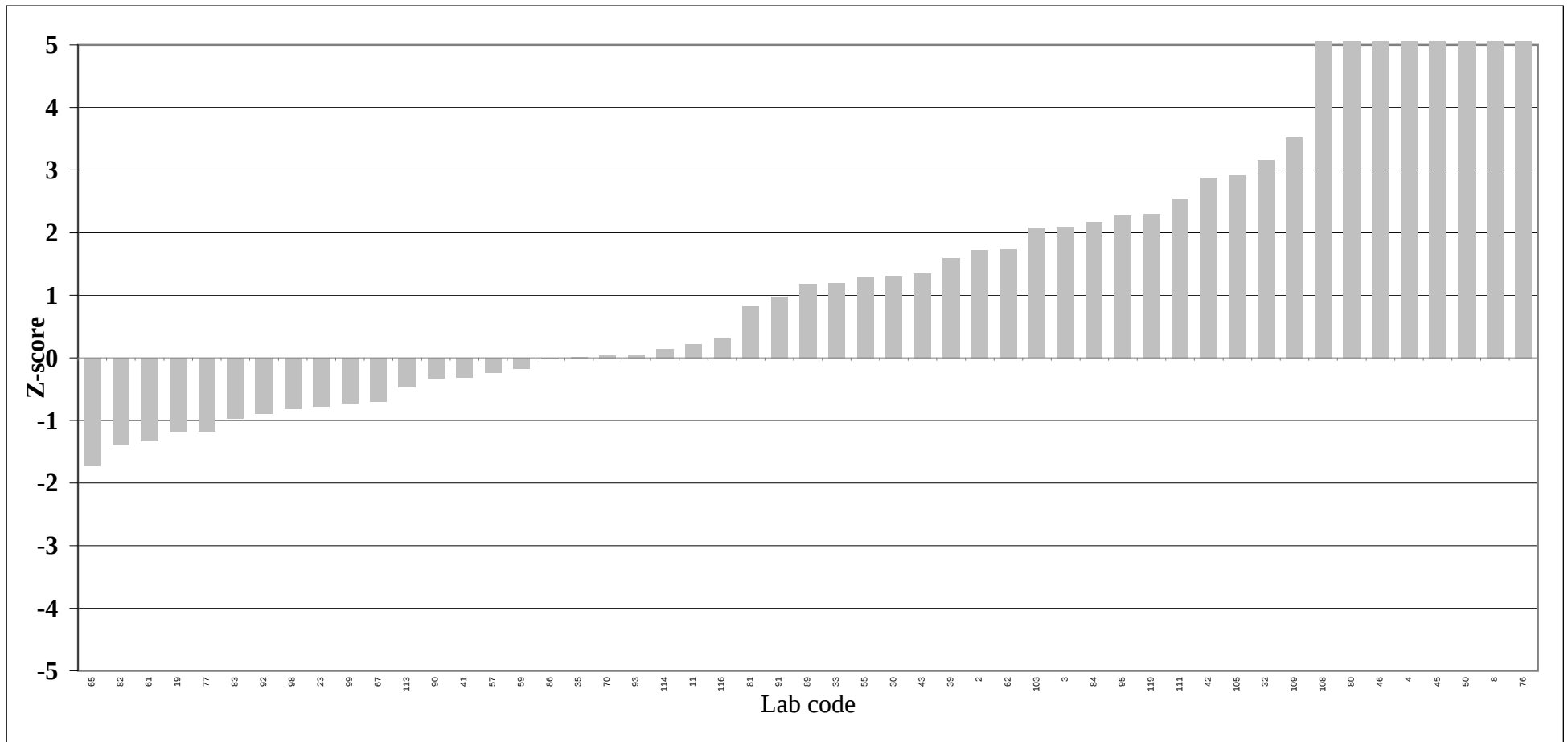
Z-score Cheese; PCDD/PCDF TEQ (lipid weight)



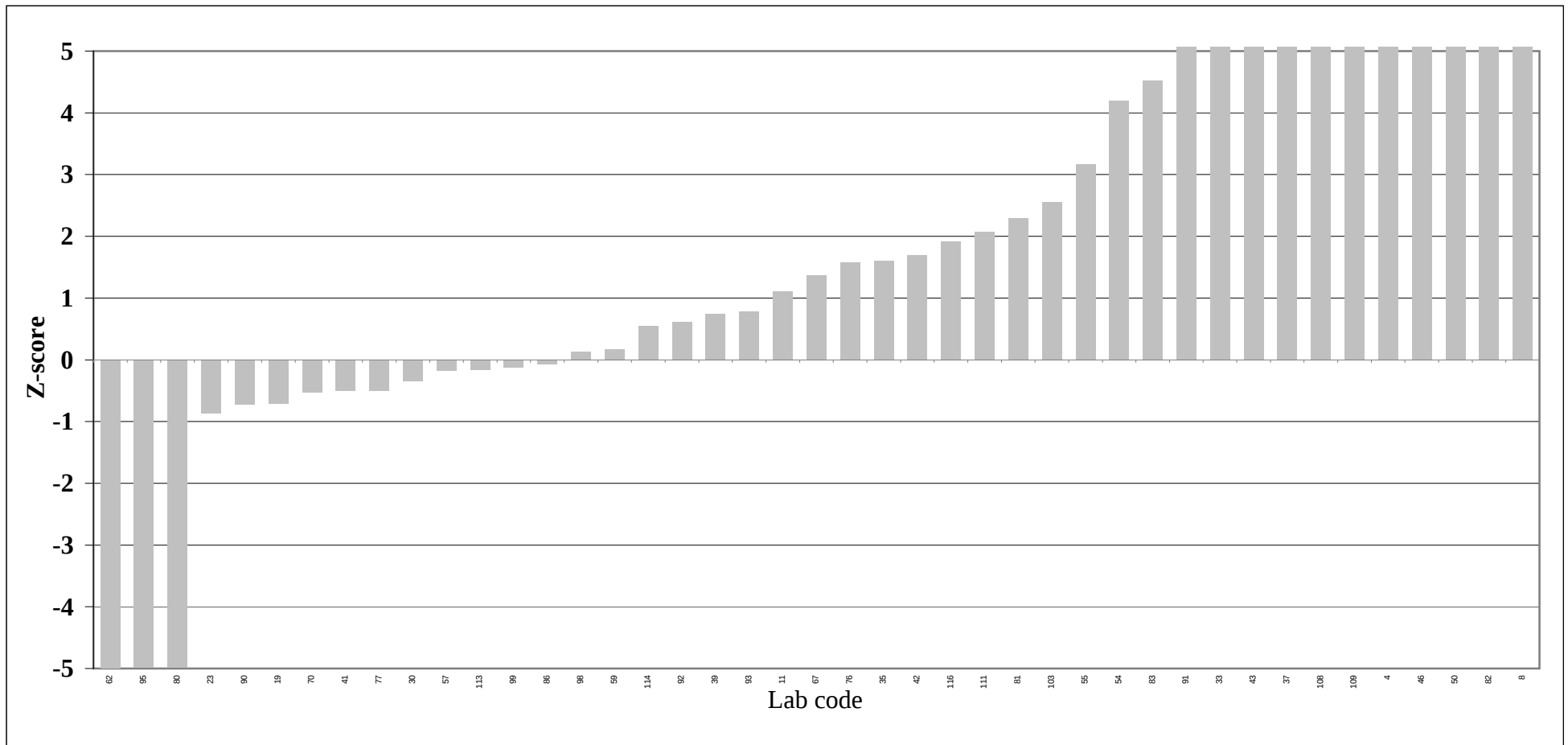
Z-score Cheese; non-ortho PCB TEQ (lipid weight)



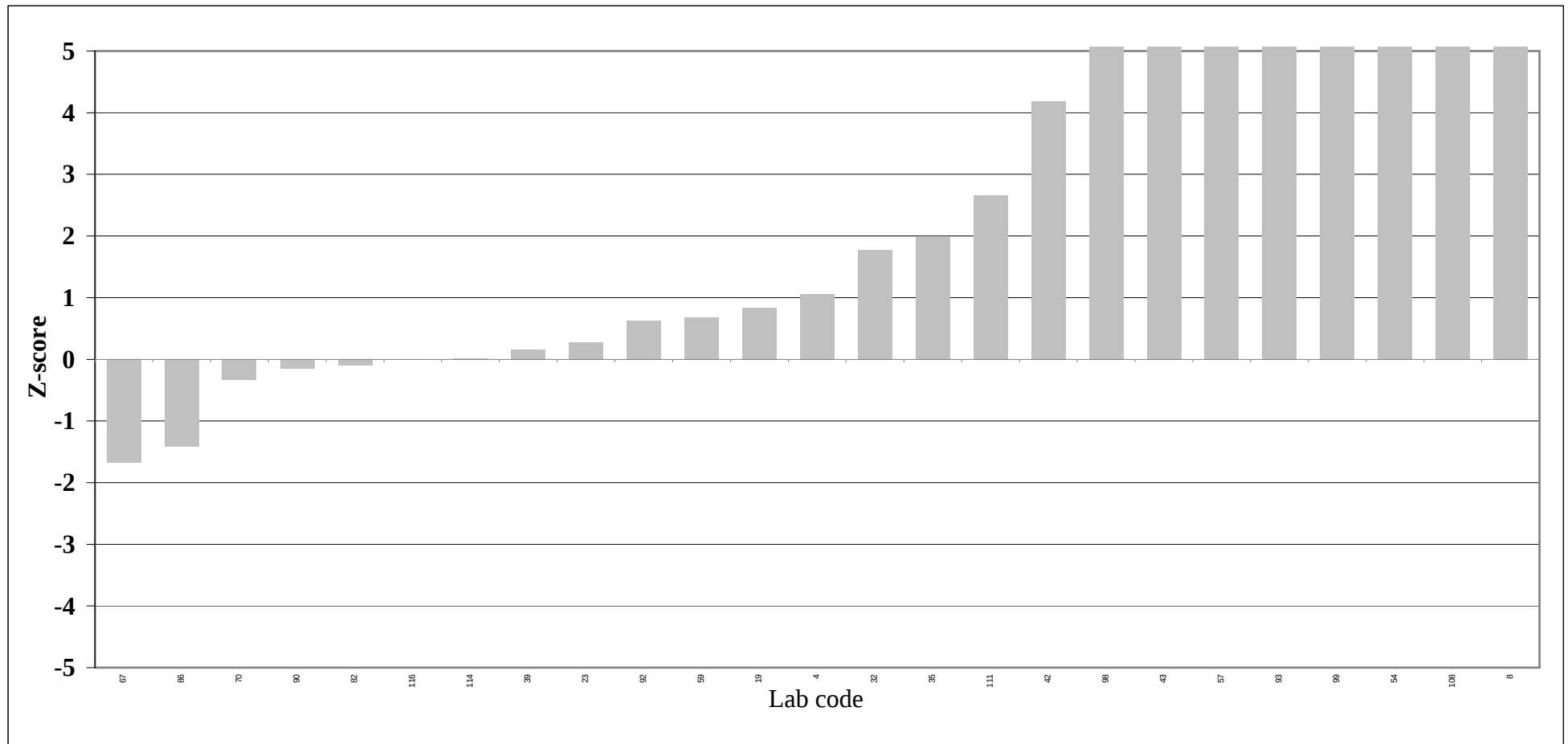
Z-score Cheese; mono-ortho PCB TEQ (lipid weight)



Z-score Cheese; sum indicator PCB (lipid weight)



Z-score Cheese; sum PBDE without PBDE-209 (lipid weight)



Appendix 1:

Presentation of results
for analyte solution

Appendix 1: Presentation of results: Analyte solution

Statistic calculations for PCDDs, PCDFs, dioxin-like PCBs, indicator PCBs, PBDEs and α -HBCD

The analyte solution contained

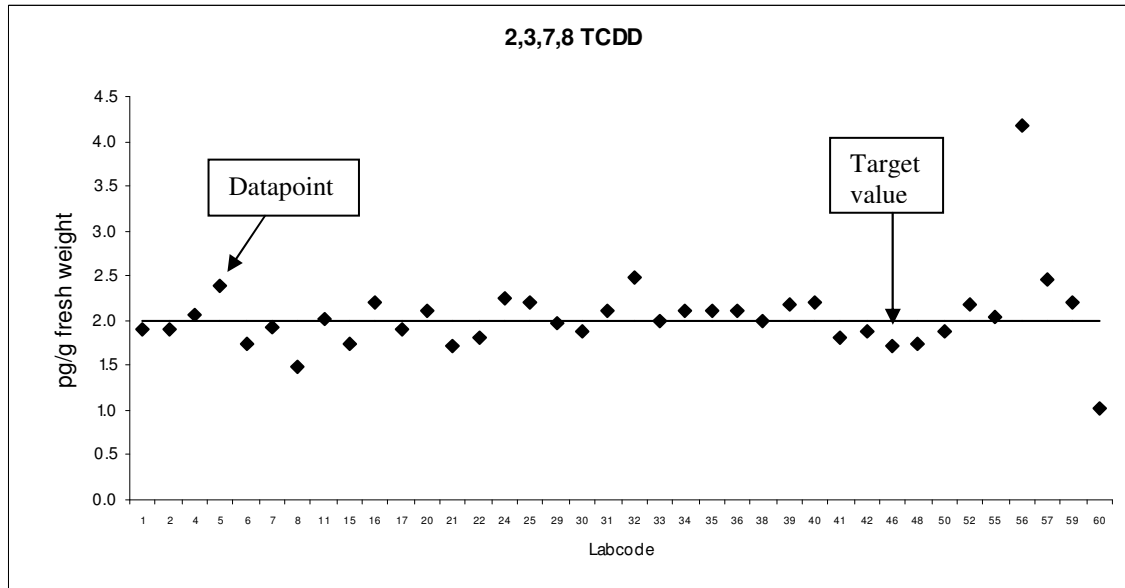
- PCDDs/PCDFs at concentrations of 2:5:10 pg/ μ l for tetra:penta-hexa-hepta:octa chlorinated dibenzodioxins/furans respectively.
- Non-ortho PCBs at concentration of 10 pg/ μ l.
- Mono-ortho PCBs and indicator PCBs at concentration of 100 pg/ μ l.
- PBDE at a concentration of 25 pg/ μ l, except BDE-209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

These concentrations are called the congeners' target value.

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

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

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



Z-Scores of individual congeners

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

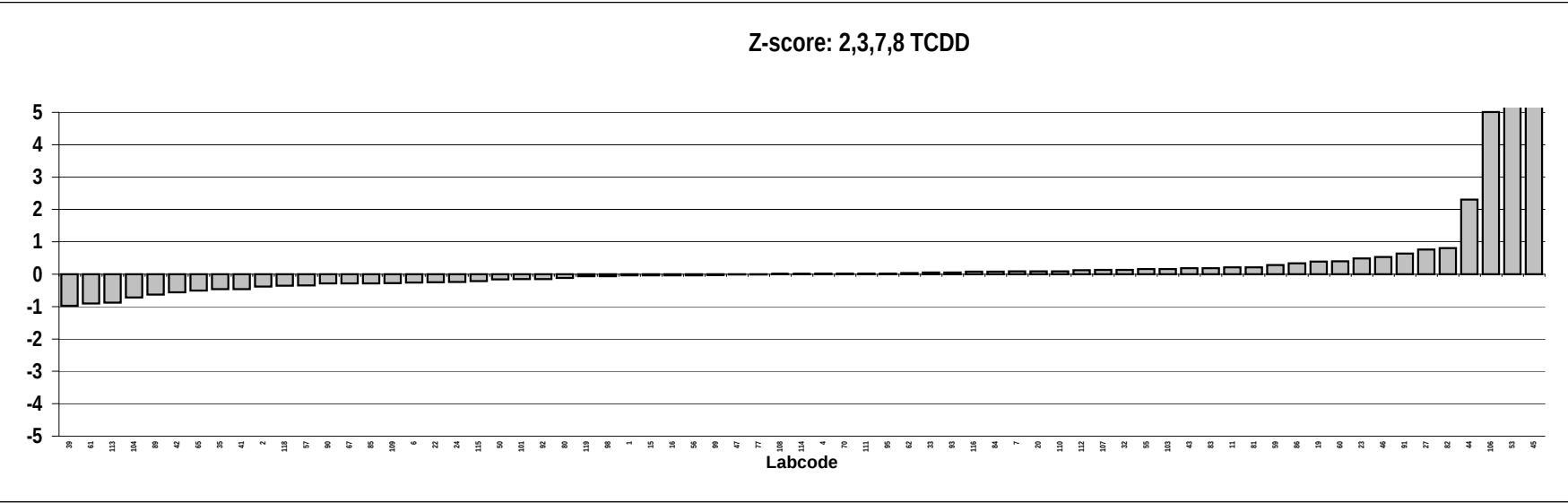
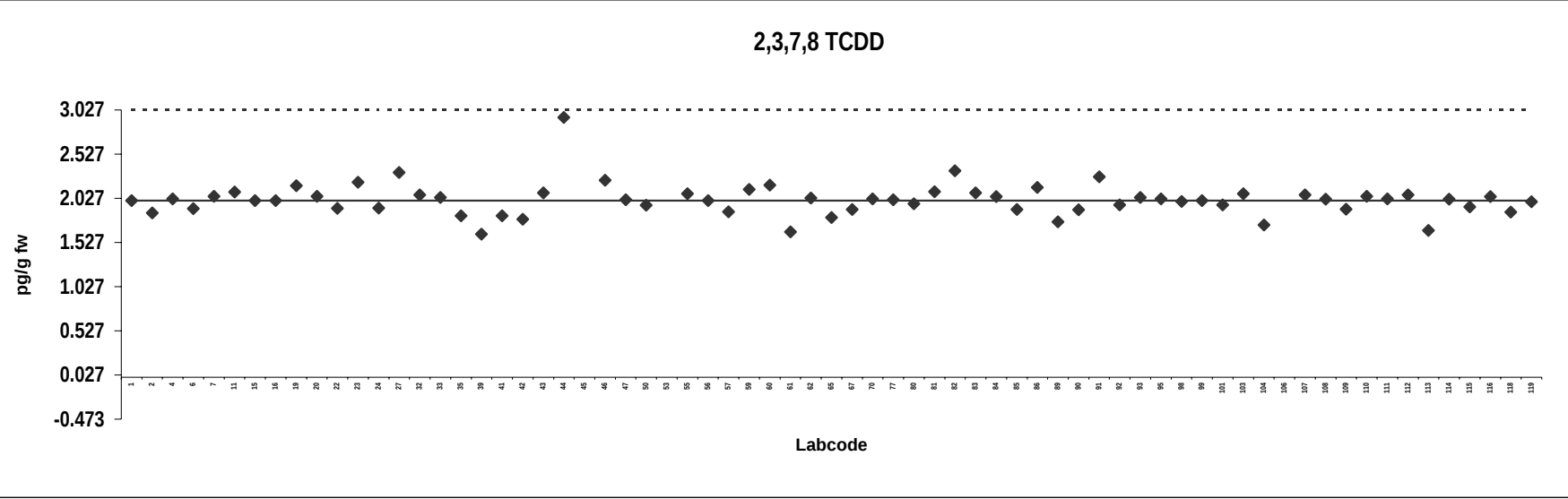
$$z = (x - X)/\sigma$$

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

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.0		89	1.8	
2	1.9		90	1.9	
4	2.0		91	2.3	
6	1.9		92	2.0	
7	2.1		93	2.0	
11	2.1		95	2.0	
15	2.0		98	2.0	
16	2.0		99	2.0	
19	2.2		101	2.0	
20	2.1		103	2.1	
22	1.9		104	1.7	
23	2.2		106	4.0	Outlier
24	1.9		107	2.1	
27	2.3		108	2.0	
32	2.1		109	1.9	
33	2.0		110	2.1	
35	1.8		111	2.0	
39	1.6		112	2.1	
41	1.8		113	1.7	
42	1.8		114	2.0	
43	2.1		115	1.9	
44	2.9		116	2.0	
45	43	Outlier	118	1.9	
46	2.2		119	2.0	
47	2.0				
50	2.0				
53	10	Outlier			
55	2.1				
56	2.0				
57	1.9				
59	2.1				
60	2.2				
61	1.6				
62	2.0				
65	1.8				
67	1.9				
70	2.0				
77	2.0				
80	2.0				
81	2.1				
82	2.3				
83	2.1				
84	2.0				
85	1.9				
86	2.2				

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	0.19
Relative standard deviation, %	9.2
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

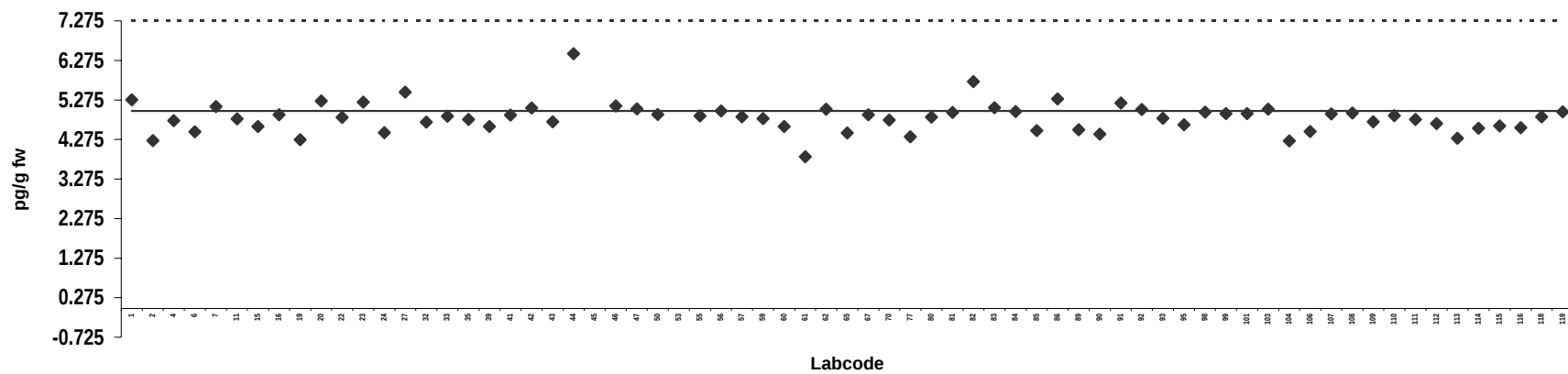


Analyte solution
Congener: 1,2,3,7,8 PeCDD

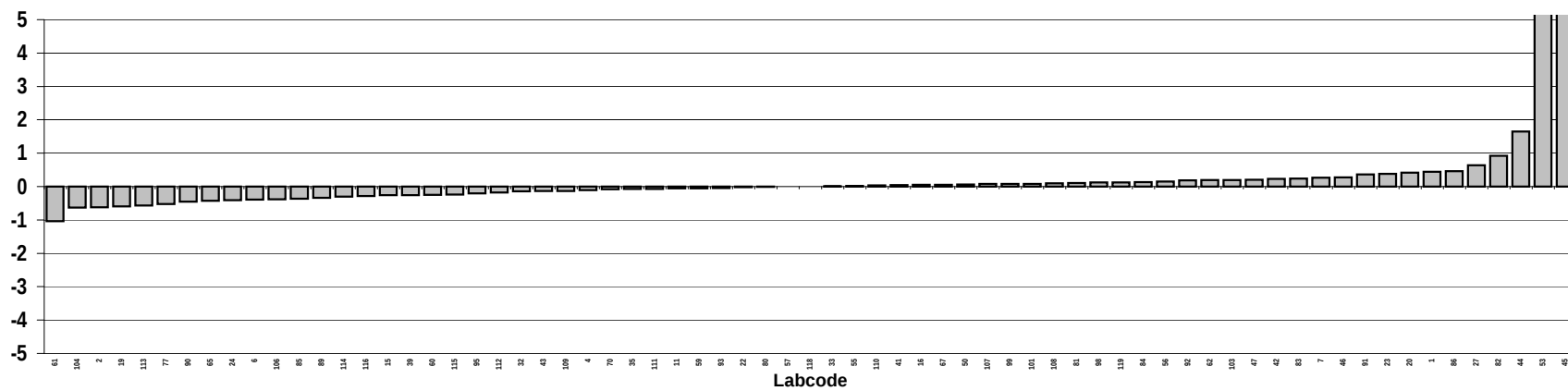
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.3		89	4.5	
2	4.2		90	4.4	
4	4.8		91	5.2	
6	4.5		92	5.0	
7	5.1		93	4.8	
11	4.8		95	4.7	
15	4.6		98	5.0	
16	4.9		99	4.9	
19	4.3		101	4.9	
20	5.3		103	5.0	
22	4.8		104	4.2	
23	5.2		106	4.5	
24	4.5		107	4.9	
27	5.5		108	4.9	
32	4.7		109	4.7	
33	4.9		110	4.9	
35	4.8		111	4.8	
39	4.6		112	4.7	
41	4.9		113	4.3	
42	5.1		114	4.6	
43	4.7		115	4.6	
44	6.4		116	4.6	
45	103	Outlier	118	4.9	
46	5.1		119	5.0	
47	5.1				
50	4.9				
53	25	Outlier			
55	4.9				
56	5.0				
57	4.8				
59	4.8				
60	4.6				
61	3.8				
62	5.0				
65	4.4				
67	4.9				
70	4.8				
77	4.3				
80	4.8				
81	5.0				
82	5.7				
83	5.1				
84	5.0				
85	4.5				
86	5.3				

Consensus statistics	
Consensus median, pg/g	4.8
Median all values pg/g	4.9
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.37
Relative standard deviation, %	7.7
No. of values reported	69
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

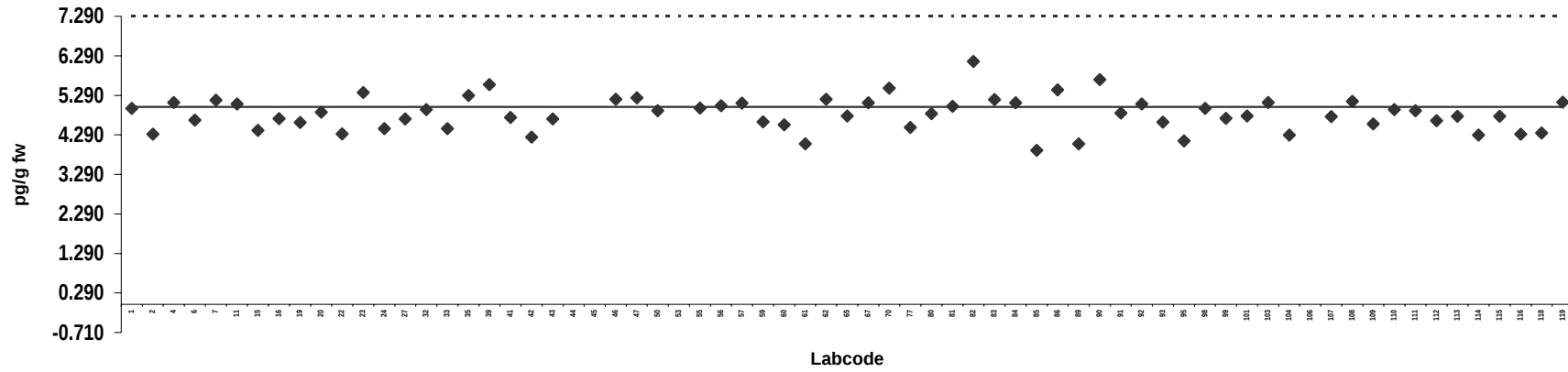


Analyte solution
Congener: 1,2,3,4,7,8 HxCDD

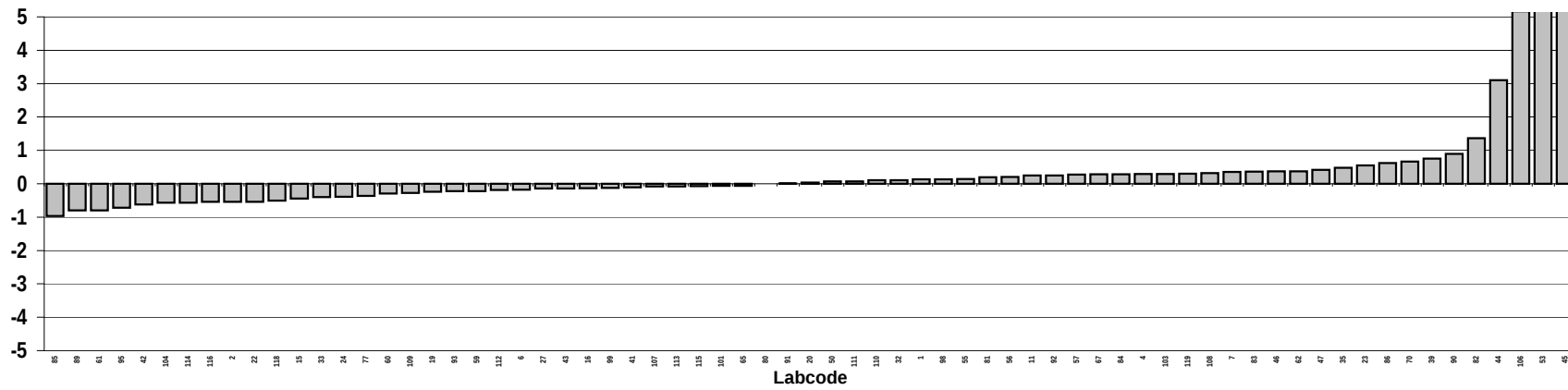
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.0		89	4.1	
2	4.3		90	5.7	
4	5.1		91	4.8	
6	4.7		92	5.1	
7	5.2		93	4.6	
11	5.1		95	4.1	
15	4.4		98	5.0	
16	4.7		99	4.7	
19	4.6		101	4.8	
20	4.9		103	5.1	
22	4.3		104	4.3	
23	5.4		106	9.8	Outlier
24	4.4		107	4.8	
27	4.7		108	5.1	
32	4.9		109	4.6	
33	4.4		110	4.9	
35	5.3		111	4.9	
39	5.6		112	4.6	
41	4.7		113	4.8	
42	4.2		114	4.3	
43	4.7		115	4.8	
44	7.8	Outlier	116	4.3	
45	113	Outlier	118	4.3	
46	5.2		119	5.1	
47	5.2				
50	4.9				
53	26	Outlier			
55	5.0				
56	5.0				
57	5.1				
59	4.6				
60	4.5				
61	4.1				
62	5.2				
65	4.8				
67	5.1				
70	5.5				
77	4.5				
80	4.8				
81	5.0				
82	6.2				
83	5.2				
84	5.1				
85	3.9				
86	5.4				

Consensus statistics	
Consensus median, pg/g	4.8
Median all values pg/g	4.9
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.42
Relative standard deviation, %	8.7
No. of values reported	69
No. of values removed	4
No. of reported non-detects	0

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



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

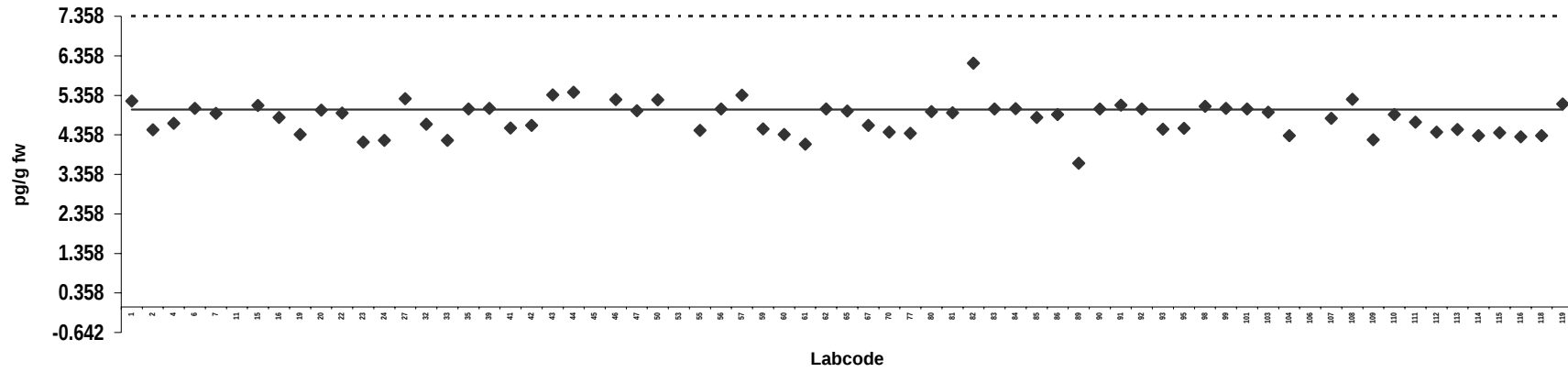


Analyte solution
Congener: 1,2,3,6,7,8 HxCDD

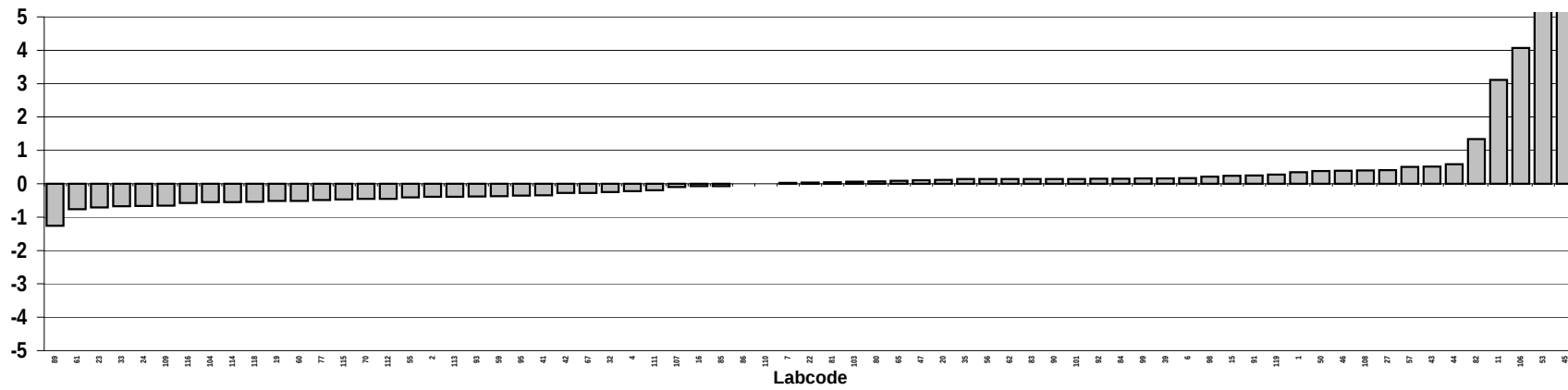
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2		89	3.6	
2	4.5		90	5.0	
4	4.7		91	5.1	
6	5.0		92	5.0	
7	4.9		93	4.5	
11	7.9	Outlier	95	4.5	
15	5.1		98	5.1	
16	4.8		99	5.0	
19	4.4		101	5.0	
20	5.0		103	4.9	
22	4.9		104	4.3	
23	4.2		106	8.8	Outlier
24	4.2		107	4.8	
27	5.3		108	5.3	
32	4.6		109	4.2	
33	4.2		110	4.9	
35	5.0		111	4.7	
39	5.0		112	4.4	
41	4.5		113	4.5	
42	4.6		114	4.3	
43	5.4		115	4.4	
44	5.4		116	4.3	
45	115	Outlier	118	4.3	
46	5.3		119	5.1	
47	5.0				
50	5.2				
53	23	Outlier			
55	4.5				
56	5.0				
57	5.4				
59	4.5				
60	4.4				
61	4.1				
62	5.0				
65	5.0				
67	4.6				
70	4.4				
77	4.4				
80	4.9				
81	4.9				
82	6.2				
83	5.0				
84	5.0				
85	4.8				
86	4.9				

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	0.41
Relative standard deviation, %	8.6
No. of values reported	69
No. of values removed	4
No. of reported non-detects	0

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



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

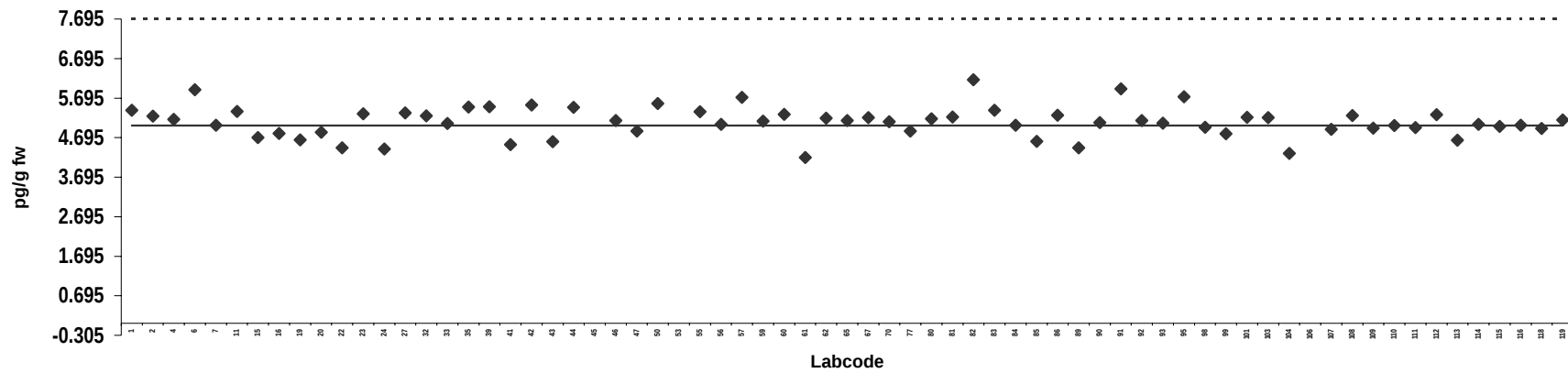


Analyte solution
Congener: 1,2,3,7,8,9 HxCDD

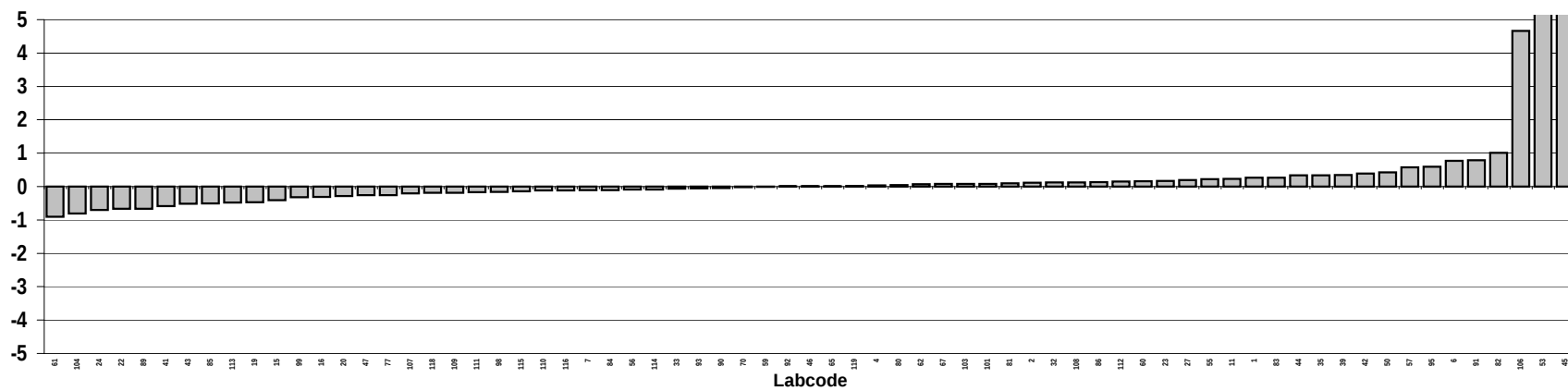
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.4		89	4.4	
2	5.2		90	5.1	
4	5.2		91	5.9	
6	5.9		92	5.1	
7	5.0		93	5.1	
11	5.4		95	5.7	
15	4.7		98	5.0	
16	4.8		99	4.8	
19	4.6		101	5.2	
20	4.8		103	5.2	
22	4.4		104	4.3	
23	5.3		106	9.9	Outlier
24	4.4		107	4.9	
27	5.3		108	5.3	
32	5.2		109	4.9	
33	5.1		110	5.0	
35	5.5		111	5.0	
39	5.5		112	5.3	
41	4.5		113	4.6	
42	5.5		114	5.0	
43	4.6		115	5.0	
44	5.5		116	5.0	
45	119	Outlier	118	4.9	
46	5.1		119	5.1	
47	4.9				
50	5.6				
53	26	Outlier			
55	5.4				
56	5.0				
57	5.7				
59	5.1				
60	5.3				
61	4.2				
62	5.2				
65	5.1				
67	5.2				
70	5.1				
77	4.9				
80	5.2				
81	5.2				
82	6.2				
83	5.4				
84	5.0				
85	4.6				
86	5.3				

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	0.38
Relative standard deviation, %	7.5
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

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



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

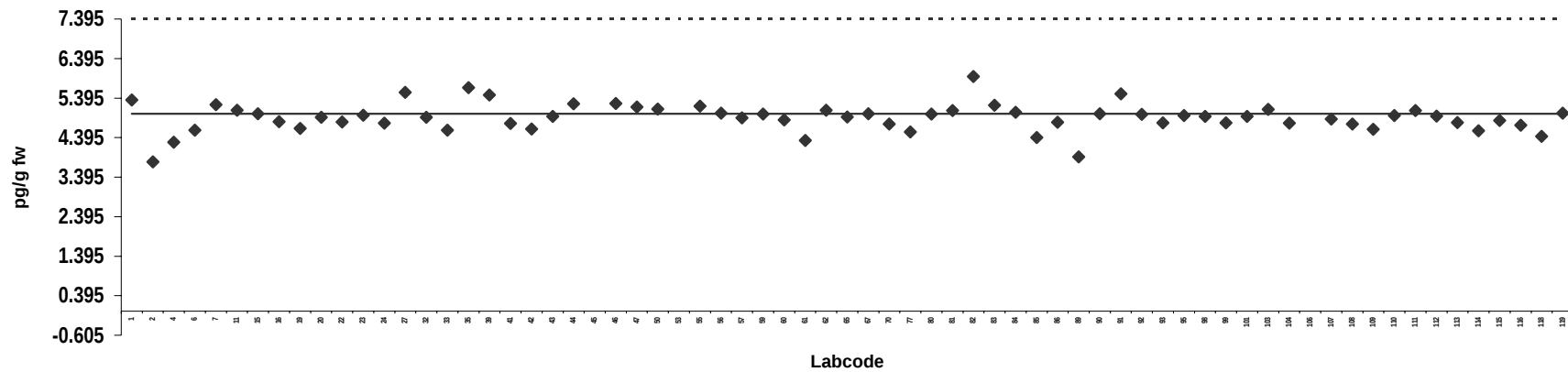


Analyte solution
Congener: 1,2,3,4,6,7,8 HpCDD

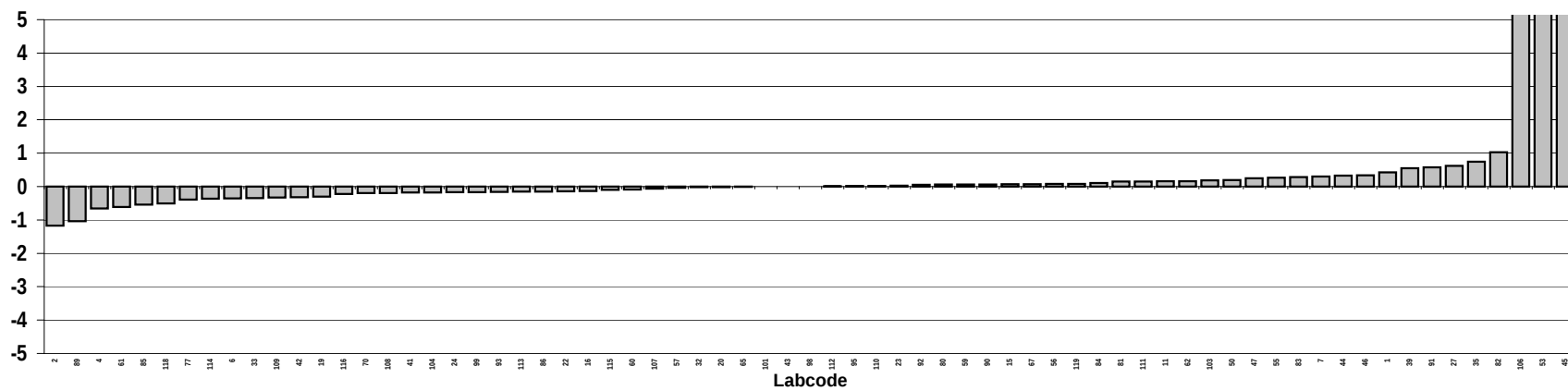
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.4		89	3.9	
2	3.8		90	5.0	
4	4.3		91	5.5	
6	4.6		92	5.0	
7	5.2		93	4.8	
11	5.1		95	5.0	
15	5.0		98	4.9	
16	4.8		99	4.8	
19	4.6		101	4.9	
20	4.9		103	5.1	
22	4.8		104	4.8	
23	5.0		106	11	Outlier
24	4.8		107	4.9	
27	5.5		108	4.7	
32	4.9		109	4.6	
33	4.6		110	5.0	
35	5.7		111	5.1	
39	5.5		112	4.9	
41	4.8		113	4.8	
42	4.6		114	4.6	
43	4.9		115	4.8	
44	5.3		116	4.7	
45	103	Outlier	118	4.4	
46	5.3		119	5.0	
47	5.2				
50	5.1				
53	25	Outlier			
55	5.2				
56	5.0				
57	4.9				
59	5.0				
60	4.8				
61	4.3				
62	5.1				
65	4.9				
67	5.0				
70	4.7				
77	4.5				
80	5.0				
81	5.1				
82	5.9				
83	5.2				
84	5.0				
85	4.4				
86	4.8				

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	0.36
Relative standard deviation, %	7.3
No. of values reported	69
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

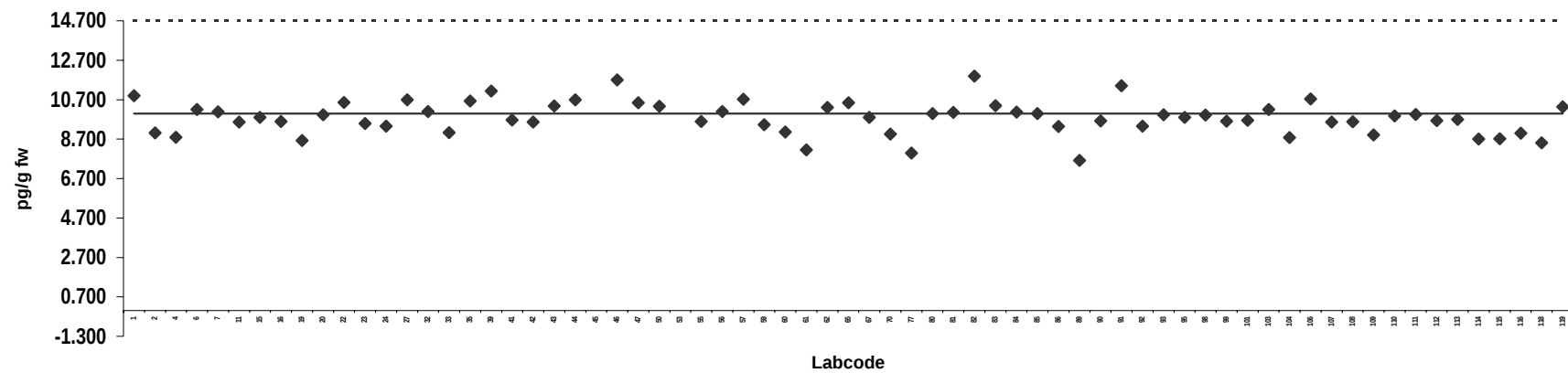


Analyte solution
Congener: 1,2,3,4,6,7,8,9 OCDD

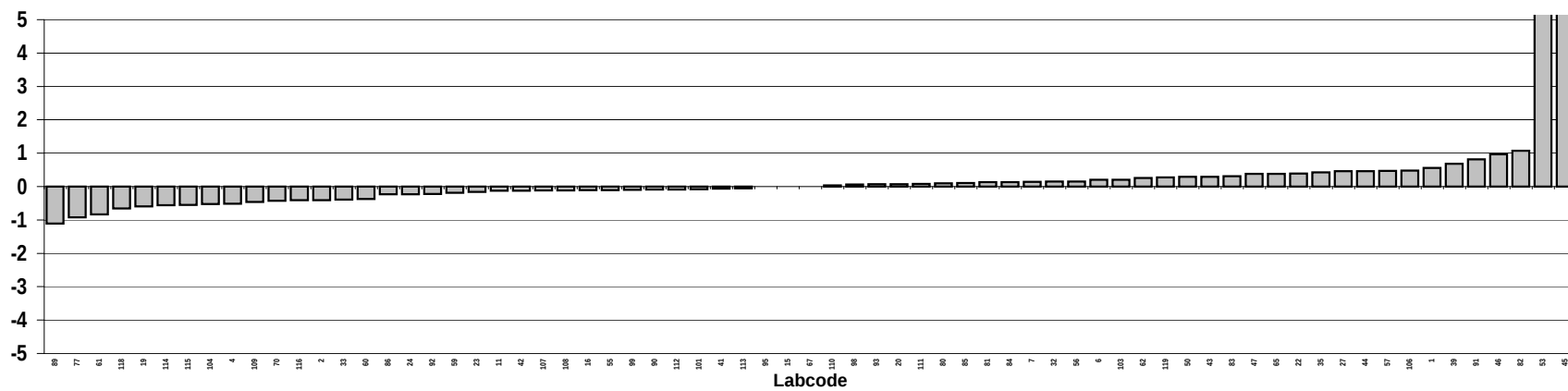
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		89	7.6	
2	9.0		90	9.6	
4	8.8		91	11	
6	10		92	9.4	
7	10		93	9.9	
11	9.6		95	9.8	
15	9.8		98	9.9	
16	9.6		99	9.6	
19	8.6		101	9.7	
20	9.9		103	10	
22	11		104	8.8	
23	9.5		106	11	
24	9.3		107	9.6	
27	11		108	9.6	
32	10		109	8.9	
33	9.0		110	9.9	
35	11		111	10	
39	11		112	9.6	
41	9.7		113	9.7	
42	9.6		114	8.7	
43	10		115	8.7	
44	11		116	9.0	
45	211	Outlier	118	8.5	
46	12		119	10	
47	11				
50	10				
53	47	Outlier			
55	9.6				
56	10				
57	11				
59	9.4				
60	9.1				
61	8.2				
62	10				
65	11				
67	9.8				
70	9.0				
77	8.0				
80	10				
81	10				
82	12				
83	10				
84	10				
85	10				
86	9.3				

Consensus statistics	
Consensus median, pg/g	9.8
Median all values pg/g	9.8
Consensus mean, pg/g	9.8
Standard deviation, pg/g	0.83
Relative standard deviation, %	8.4
No. of values reported	69
No. of values removed	2
No. of reported non-detects	0

1,2,3,4,6,7,8,9 OCDD



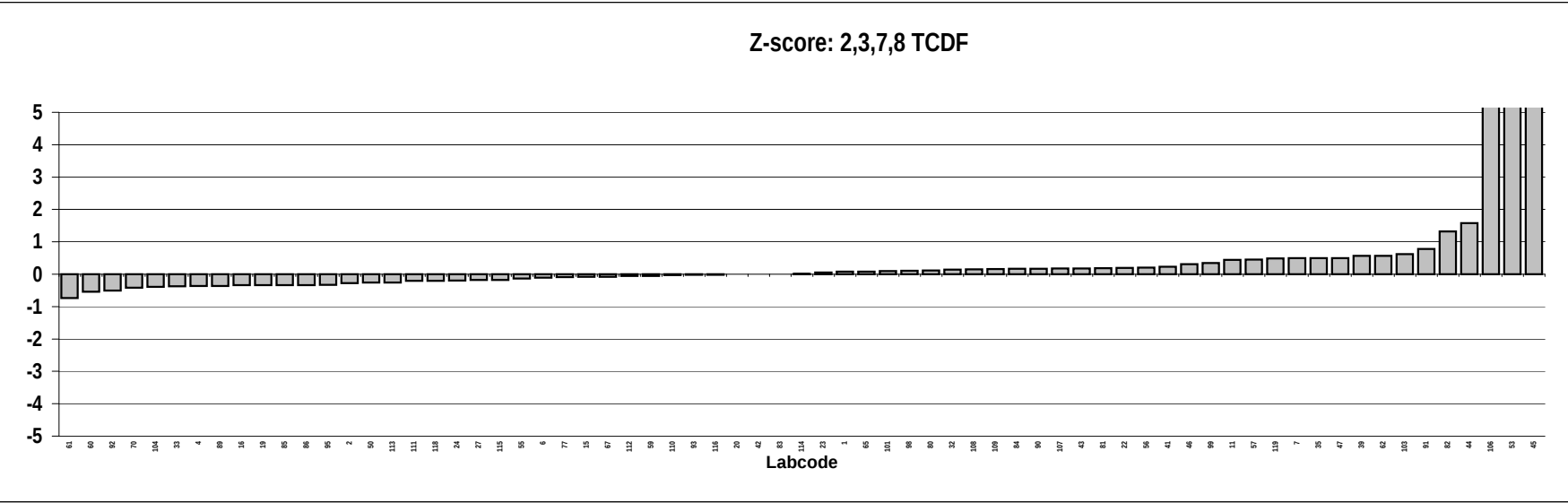
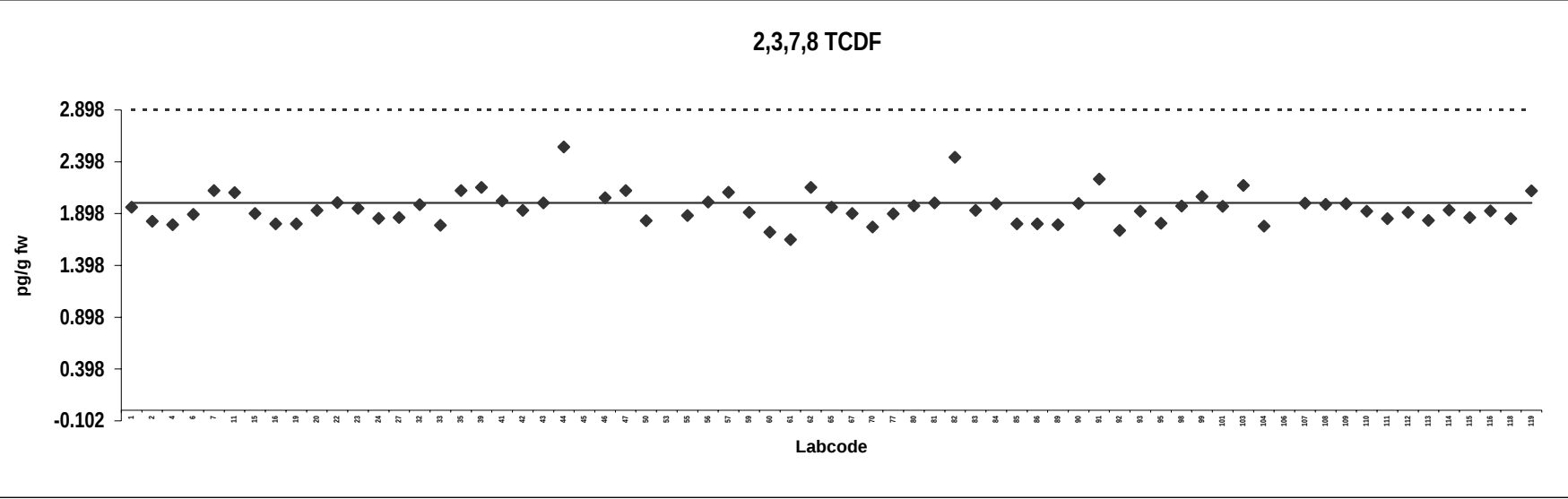
Z-score: 1,2,3,4,6,7,8,9 OCDD



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.0		89	1.8	
2	1.8		90	2.0	
4	1.8		91	2.2	
6	1.9		92	1.7	
7	2.1		93	1.9	
11	2.1		95	1.8	
15	1.9		98	2.0	
16	1.8		99	2.1	
19	1.8		101	2.0	
20	1.9		103	2.2	
22	2.0		104	1.8	
23	1.9		106	10	Outlier
24	1.9		107	2.0	
27	1.9		108	2.0	
32	2.0		109	2.0	
33	1.8		110	1.9	
35	2.1		111	1.9	
39	2.2		112	1.9	
41	2.0		113	1.8	
42	1.9		114	1.9	
43	2.0		115	1.9	
44	2.5		116	1.9	
45	44	Outlier	118	1.9	
46	2.1		119	2.1	
47	2.1				
50	1.8				
53	10	Outlier			
55	1.9				
56	2.0				
57	2.1				
59	1.9				
60	1.7				
61	1.6				
62	2.2				
65	2.0				
67	1.9				
70	1.8				
77	1.9				
80	2.0				
81	2.0				
82	2.4				
83	1.9				
84	2.0				
85	1.8				
86	1.8				

Consensus statistics	
Consensus median, pg/g	1.9
Median all values pg/g	1.9
Consensus mean, pg/g	2.0
Standard deviation, pg/g	0.16
Relative standard deviation, %	7.9
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

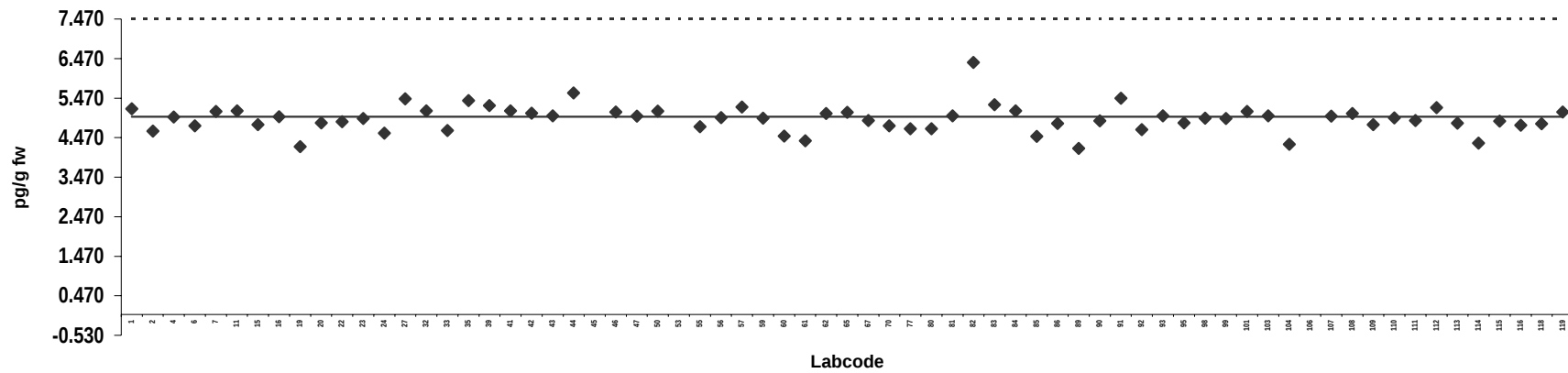


Analyte solution
Congener: 1,2,3,7,8 PeCDF

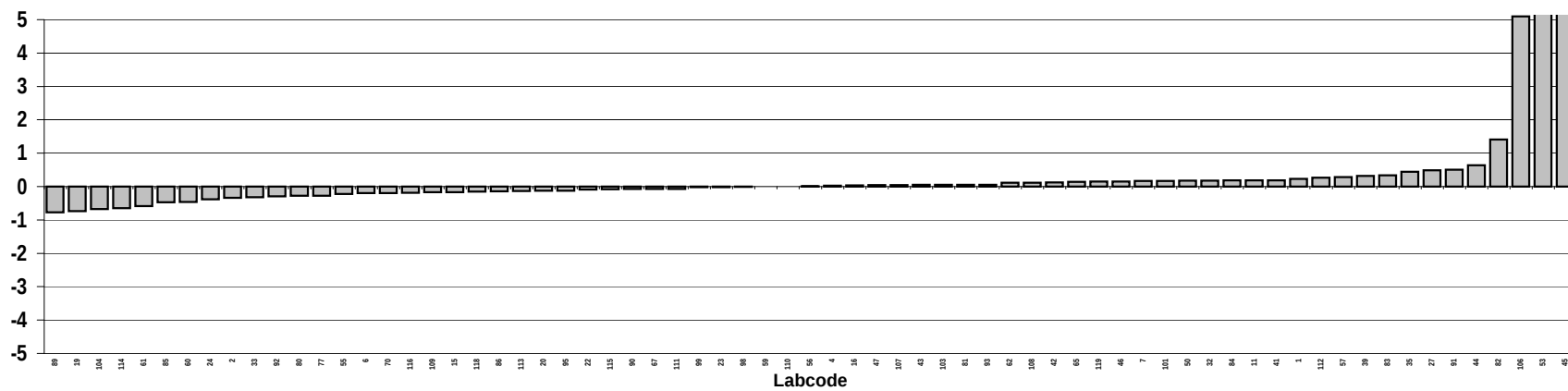
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2		89	4.2	
2	4.6		90	4.9	
4	5.0		91	5.5	
6	4.8		92	4.7	
7	5.1		93	5.0	
11	5.2		95	4.8	
15	4.8		98	5.0	
16	5.0		99	5.0	
19	4.2		101	5.1	
20	4.8		103	5.0	
22	4.9		104	4.3	
23	5.0		106	10	Outlier
24	4.6		107	5.0	
27	5.5		108	5.1	
32	5.1		109	4.8	
33	4.7		110	5.0	
35	5.4		111	4.9	
39	5.3		112	5.2	
41	5.2		113	4.8	
42	5.1		114	4.3	
43	5.0		115	4.9	
44	5.6		116	4.8	
45	105	Outlier	118	4.8	
46	5.1		119	5.1	
47	5.0				
50	5.1				
53	24	Outlier			
55	4.8				
56	5.0				
57	5.2				
59	5.0				
60	4.5				
61	4.4				
62	5.1				
65	5.1				
67	4.9				
70	4.8				
77	4.7				
80	4.7				
81	5.0				
82	6.4				
83	5.3				
84	5.1				
85	4.5				
86	4.8				

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	0.34
Relative standard deviation, %	6.8
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

1,2,3,7,8 PeCDF



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

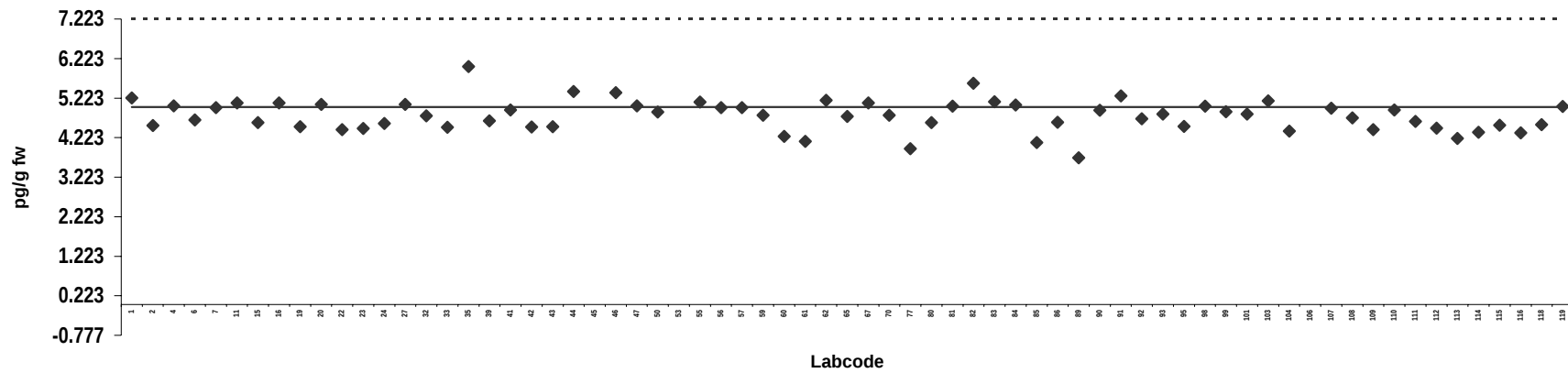


Analyte solution
Congener: 2,3,4,7,8 PeCDF

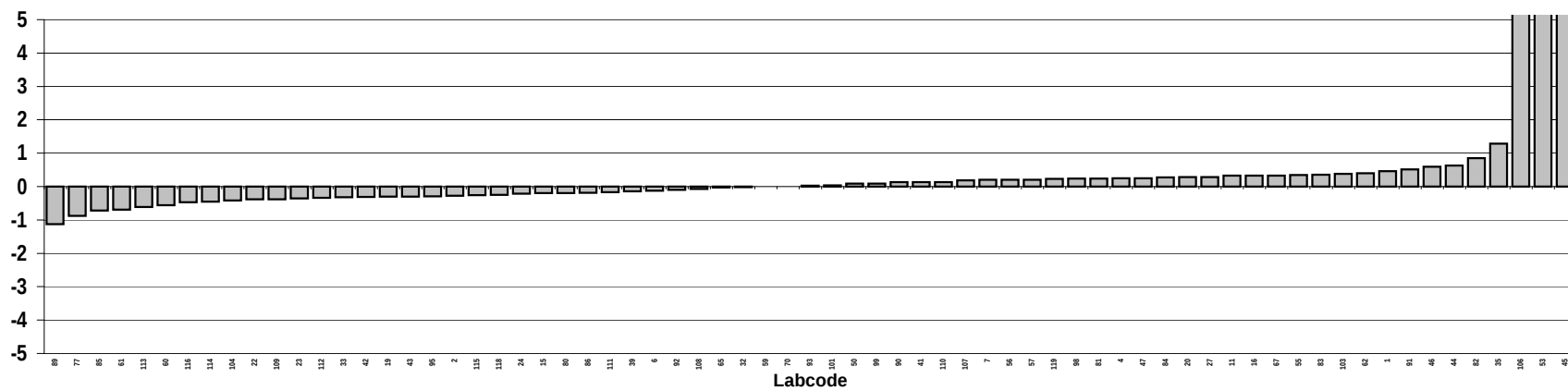
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2		89	3.7	
2	4.5		90	4.9	
4	5.0		91	5.3	
6	4.7		92	4.7	
7	5.0		93	4.8	
11	5.1		95	4.5	
15	4.6		98	5.0	
16	5.1		99	4.9	
19	4.5		101	4.8	
20	5.1		103	5.2	
22	4.4		104	4.4	
23	4.5		106	10	Outlier
24	4.6		107	5.0	
27	5.1		108	4.7	
32	4.8		109	4.4	
33	4.5		110	4.9	
35	6.0		111	4.6	
39	4.7		112	4.5	
41	4.9		113	4.2	
42	4.5		114	4.4	
43	4.5		115	4.5	
44	5.4		116	4.3	
45	113	Outlier	118	4.6	
46	5.4		119	5.0	
47	5.0				
50	4.9				
53	26	Outlier			
55	5.1				
56	5.0				
57	5.0				
59	4.8				
60	4.3				
61	4.1				
62	5.2				
65	4.8				
67	5.1				
70	4.8				
77	3.9				
80	4.6				
81	5.0				
82	5.6				
83	5.1				
84	5.1				
85	4.1				
86	4.6				

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	0.39
Relative standard deviation, %	8.2
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

2,3,4,7,8 PeCDF



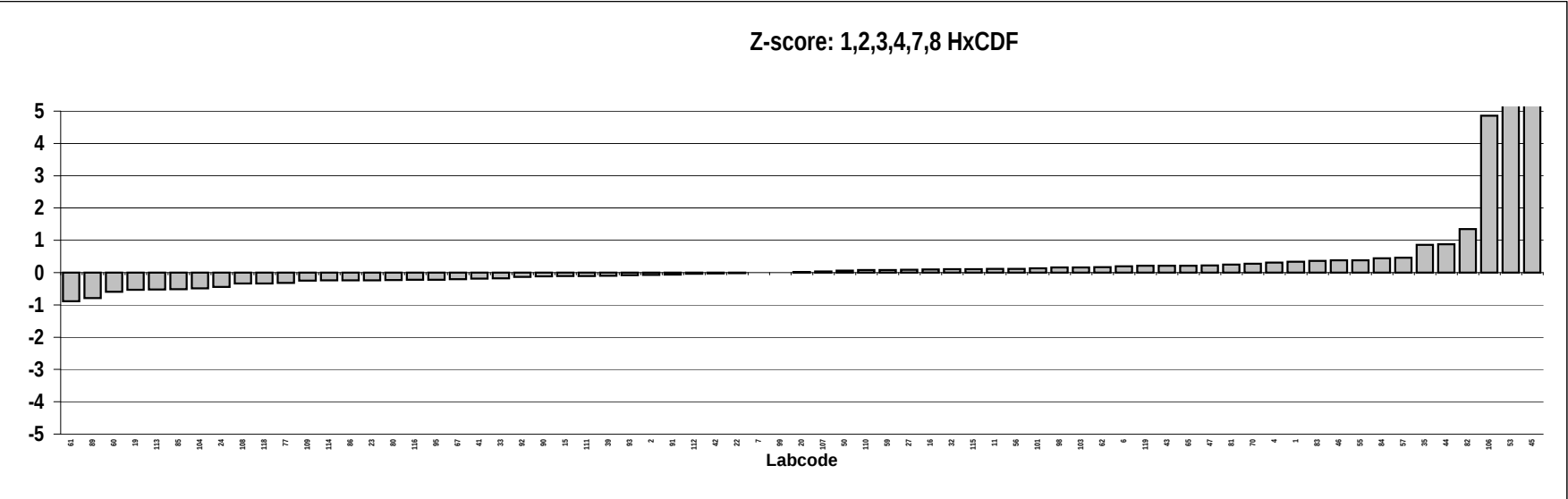
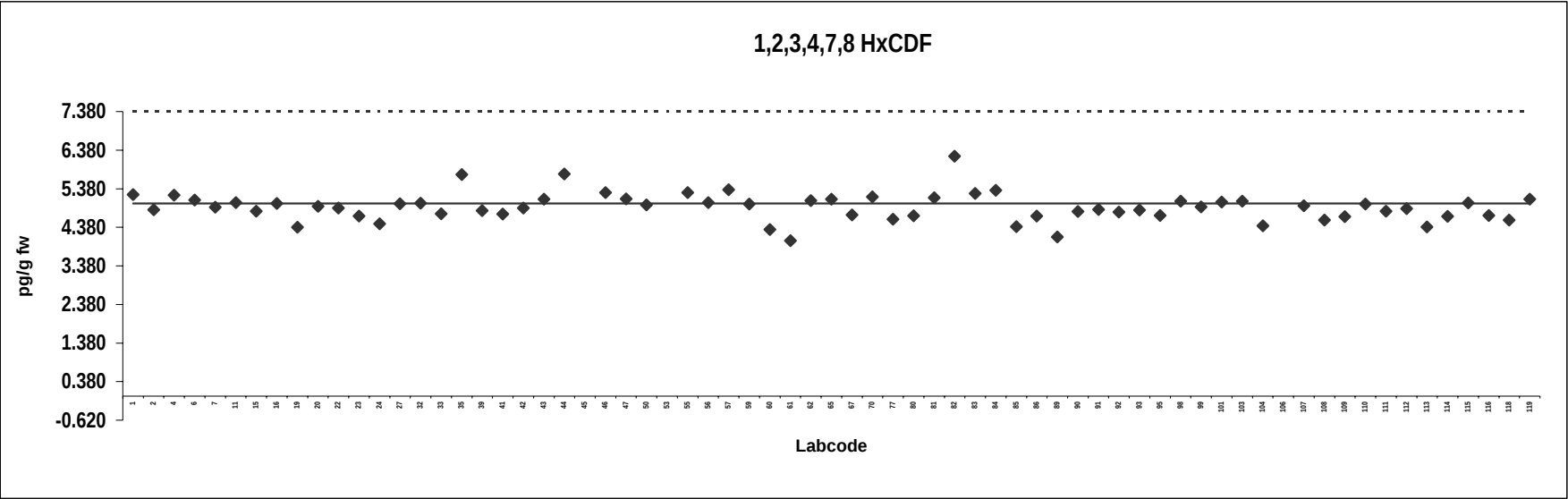
Z-score: 2,3,4,7,8 PeCDF



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2		89	4.1	
2	4.8		90	4.8	
4	5.2		91	4.8	
6	5.1		92	4.8	
7	4.9		93	4.8	
11	5.0		95	4.7	
15	4.8		98	5.1	
16	5.0		99	4.9	
19	4.4		101	5.0	
20	4.9		103	5.1	
22	4.9		104	4.4	
23	4.7		106	9.7	Outlier
24	4.5		107	4.9	
27	5.0		108	4.6	
32	5.0		109	4.7	
33	4.7		110	5.0	
35	5.8		111	4.8	
39	4.8		112	4.9	
41	4.7		113	4.4	
42	4.9		114	4.7	
43	5.1		115	5.0	
44	5.8		116	4.7	
45	116	Outlier	118	4.6	
46	5.3		119	5.1	
47	5.1				
50	5.0				
53	26	Outlier			
55	5.3				
56	5.0				
57	5.4				
59	5.0				
60	4.3				
61	4.0				
62	5.1				
65	5.1				
67	4.7				
70	5.2				
77	4.6				
80	4.7				
81	5.1				
82	6.2				
83	5.3				
84	5.3				
85	4.4				
86	4.7				

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	0.36
Relative standard deviation, %	7.4
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

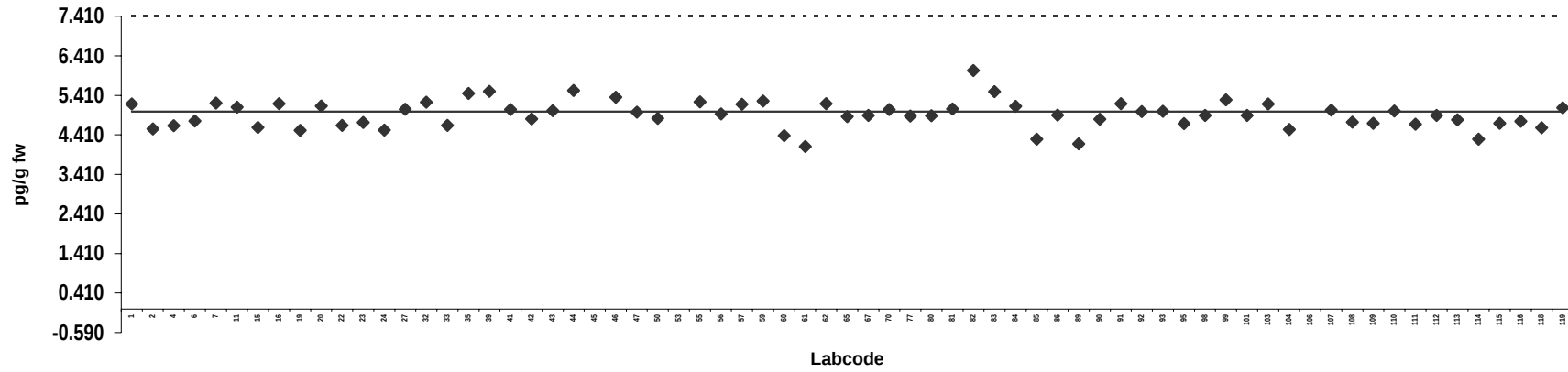


Analyte solution
Congener: 1,2,3,6,7,8 HxCDF

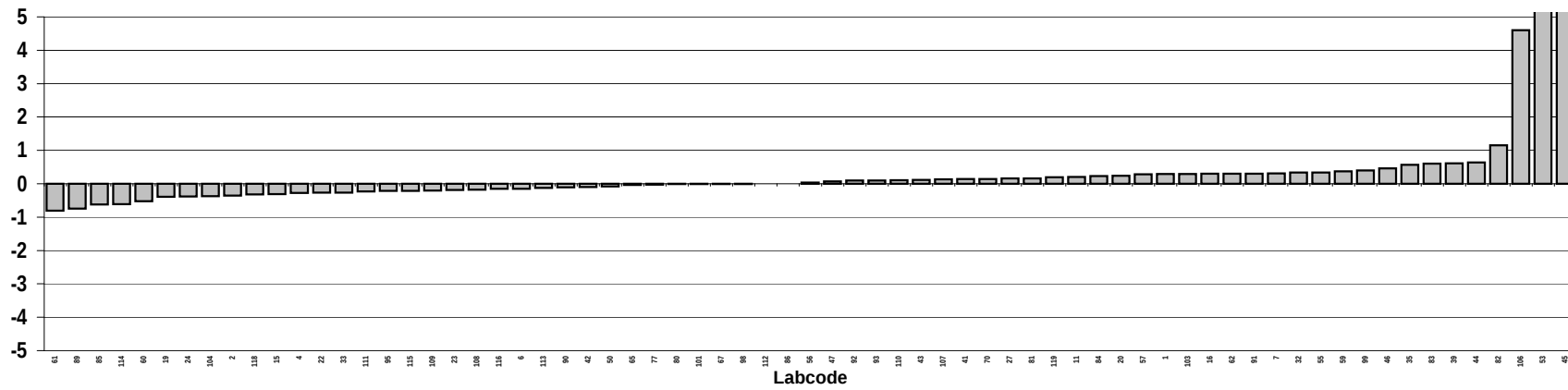
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2		89	4.2	
2	4.6		90	4.8	
4	4.6		91	5.2	
6	4.8		92	5.0	
7	5.2		93	5.0	
11	5.1		95	4.7	
15	4.6		98	4.9	
16	5.2		99	5.3	
19	4.5		101	4.9	
20	5.1		103	5.2	
22	4.6		104	4.5	
23	4.7		106	9.4	Outlier
24	4.5		107	5.0	
27	5.1		108	4.7	
32	5.2		109	4.7	
33	4.6		110	5.0	
35	5.5		111	4.7	
39	5.5		112	4.9	
41	5.1		113	4.8	
42	4.8		114	4.3	
43	5.0		115	4.7	
44	5.5		116	4.8	
45	111	Outlier	118	4.6	
46	5.4		119	5.1	
47	5.0				
50	4.8				
53	27	Outlier			
55	5.2				
56	4.9				
57	5.2				
59	5.3				
60	4.4				
61	4.1				
62	5.2				
65	4.9				
67	4.9				
70	5.1				
77	4.9				
80	4.9				
81	5.1				
82	6.0				
83	5.5				
84	5.1				
85	4.3				
86	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	0.34
Relative standard deviation, %	7.0
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

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



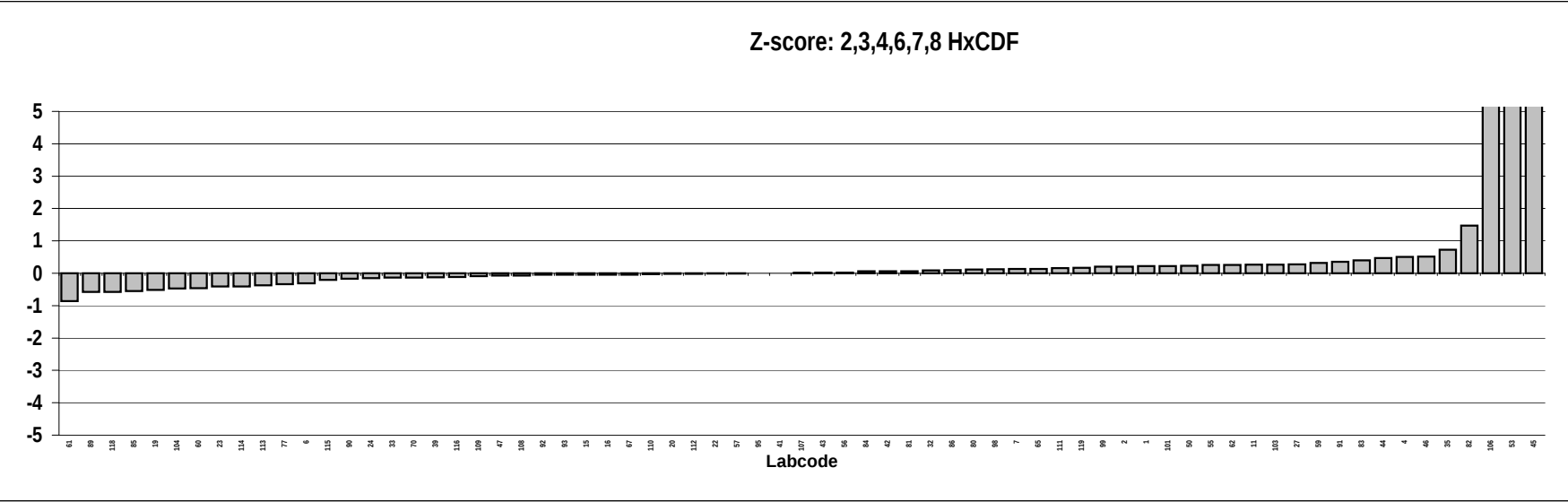
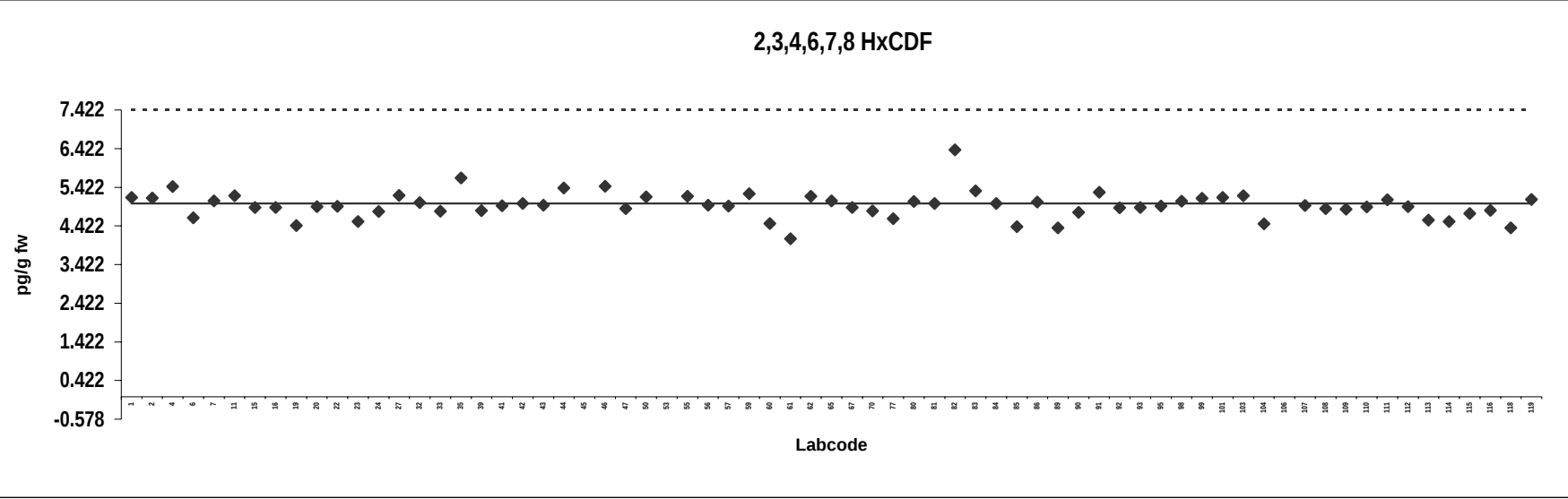
Z-score: 1,2,3,6,7,8 HxCDF



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2		89	4.4	
2	5.1		90	4.8	
4	5.4		91	5.3	
6	4.6		92	4.9	
7	5.1		93	4.9	
11	5.2		95	4.9	
15	4.9		98	5.1	
16	4.9		99	5.1	
19	4.4		101	5.2	
20	4.9		103	5.2	
22	4.9		104	4.5	
23	4.5		106	11	Outlier
24	4.8		107	4.9	
27	5.2		108	4.9	
32	5.0		109	4.9	
33	4.8		110	4.9	
35	5.7		111	5.1	
39	4.8		112	4.9	
41	4.9		113	4.6	
42	5.0		114	4.5	
43	5.0		115	4.7	
44	5.4		116	4.8	
45	118	Outlier	118	4.4	
46	5.5		119	5.1	
47	4.9				
50	5.2				
53	27	Outlier			
55	5.2				
56	5.0				
57	4.9				
59	5.3				
60	4.5				
61	4.1				
62	5.2				
65	5.1				
67	4.9				
70	4.8				
77	4.6				
80	5.1				
81	5.0				
82	6.4				
83	5.3				
84	5.0				
85	4.4				
86	5.0				

Consensus statistics	
Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.34
Relative standard deviation, %	6.9
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

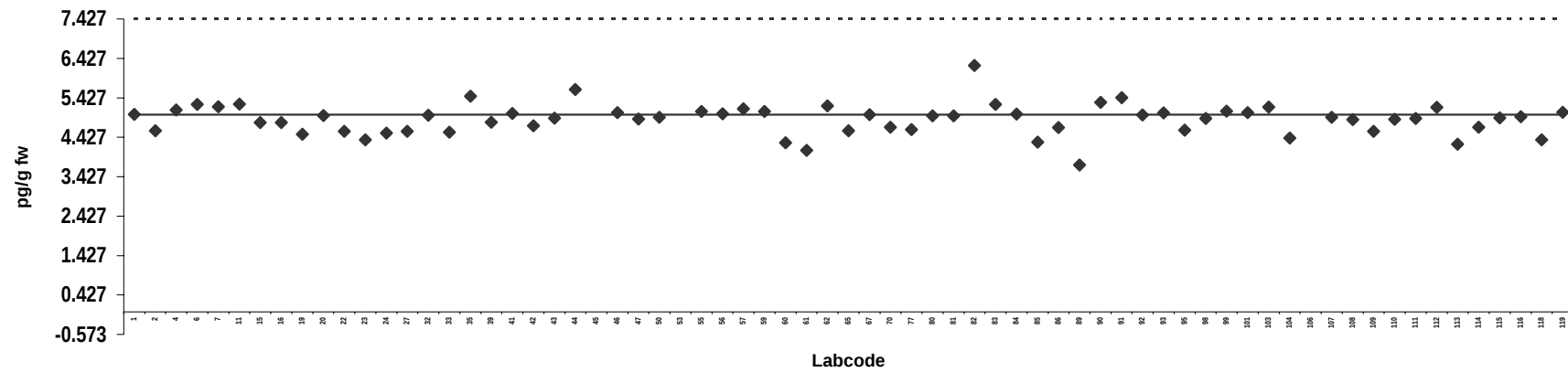


Analyte solution
Congener: 1,2,3,7,8,9 HxCDF

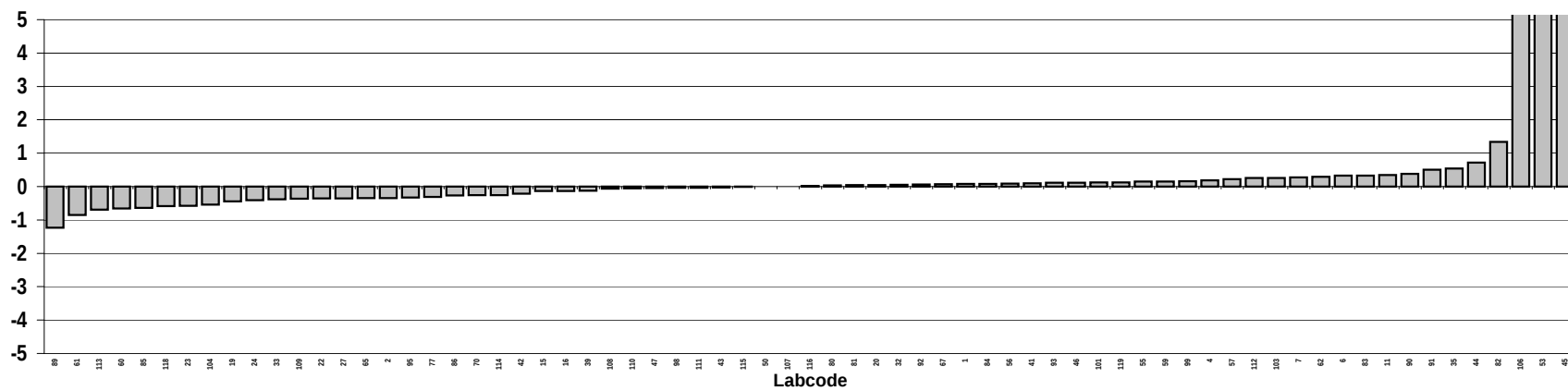
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.0		89	3.7	
2	4.6		90	5.3	
4	5.1		91	5.4	
6	5.3		92	5.0	
7	5.2		93	5.0	
11	5.3		95	4.6	
15	4.8		98	4.9	
16	4.8		99	5.1	
19	4.5		101	5.1	
20	5.0		103	5.2	
22	4.6		104	4.4	
23	4.4		106	11	Outlier
24	4.5		107	4.9	
27	4.6		108	4.9	
32	5.0		109	4.6	
33	4.6		110	4.9	
35	5.5		111	4.9	
39	4.8		112	5.2	
41	5.0		113	4.3	
42	4.7		114	4.7	
43	4.9		115	4.9	
44	5.6		116	5.0	
45	107	Outlier	118	4.4	
46	5.1		119	5.1	
47	4.9				
50	4.9				
53	23	Outlier			
55	5.1				
56	5.0				
57	5.2				
59	5.1				
60	4.3				
61	4.1				
62	5.2				
65	4.6				
67	5.0				
70	4.7				
77	4.6				
80	5.0				
81	5.0				
82	6.3				
83	5.3				
84	5.0				
85	4.3				
86	4.7				

Consensus statistics	
Consensus median, pg/g	4.9
Median all values pg/g	5.0
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.38
Relative standard deviation, %	7.9
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

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



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

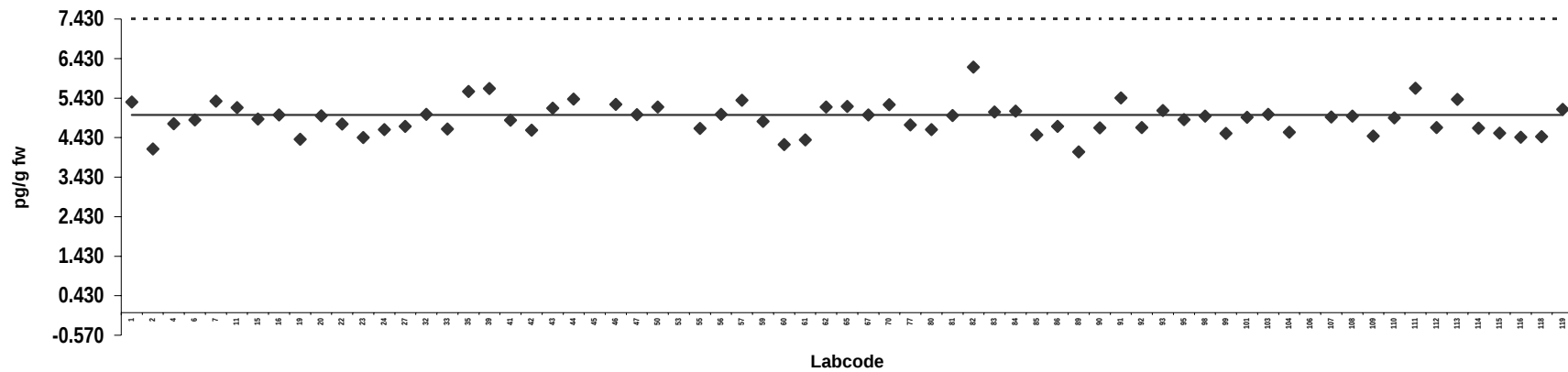


Analyte solution
Congener: 1,2,3,4,6,7,8 HpCDF

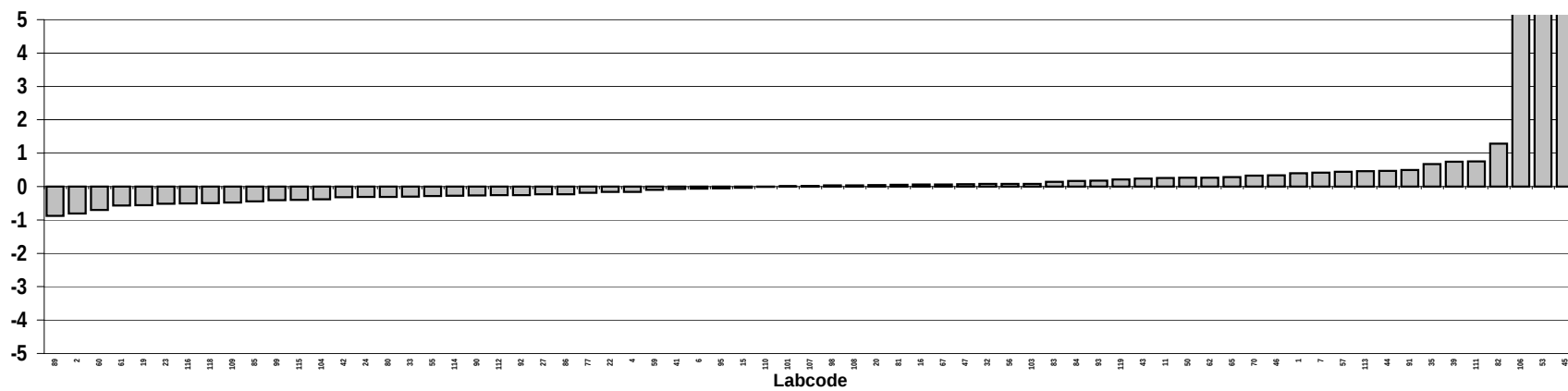
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.3		89	4.1	
2	4.1		90	4.7	
4	4.8		91	5.4	
6	4.9		92	4.7	
7	5.4		93	5.1	
11	5.2		95	4.9	
15	4.9		98	5.0	
16	5.0		99	4.5	
19	4.4		101	4.9	
20	5.0		103	5.0	
22	4.8		104	4.6	
23	4.4		106	12	Outlier
24	4.6		107	5.0	
27	4.7		108	5.0	
32	5.0		109	4.5	
33	4.6		110	4.9	
35	5.6		111	5.7	
39	5.7		112	4.7	
41	4.9		113	5.4	
42	4.6		114	4.7	
43	5.2		115	4.5	
44	5.4		116	4.4	
45	111	Outlier	118	4.5	
46	5.3		119	5.1	
47	5.0				
50	5.2				
53	25	Outlier			
55	4.7				
56	5.0				
57	5.4				
59	4.8				
60	4.3				
61	4.4				
62	5.2				
65	5.2				
67	5.0				
70	5.3				
77	4.8				
80	4.6				
81	5.0				
82	6.2				
83	5.1				
84	5.1				
85	4.5				
86	4.7				

Consensus statistics	
Consensus median, pg/g	4.9
Median all values pg/g	5.0
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.39
Relative standard deviation, %	8.0
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

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



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

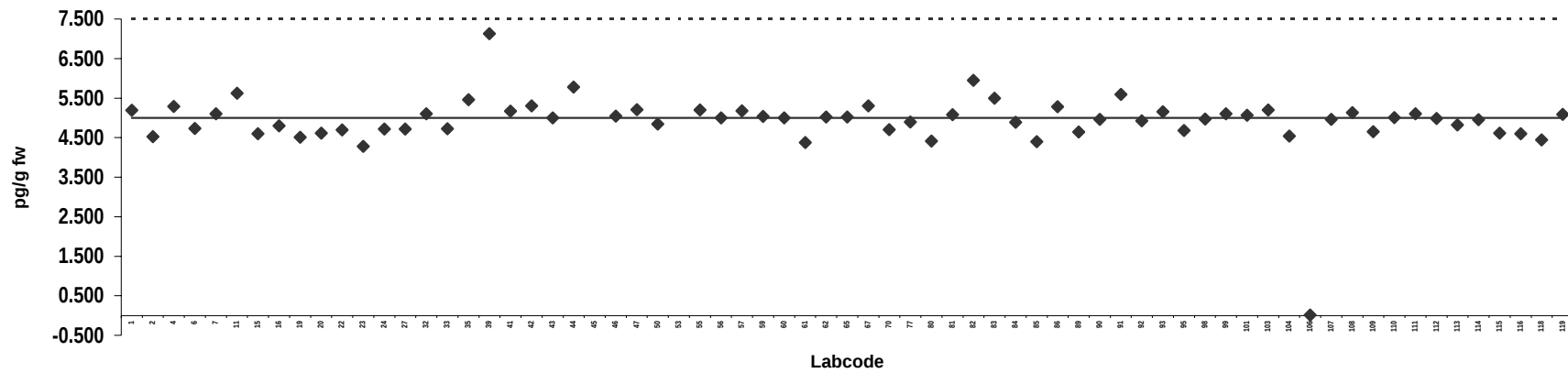


Analyte solution
Congener: 1,2,3,4,7,8,9 HpCDF

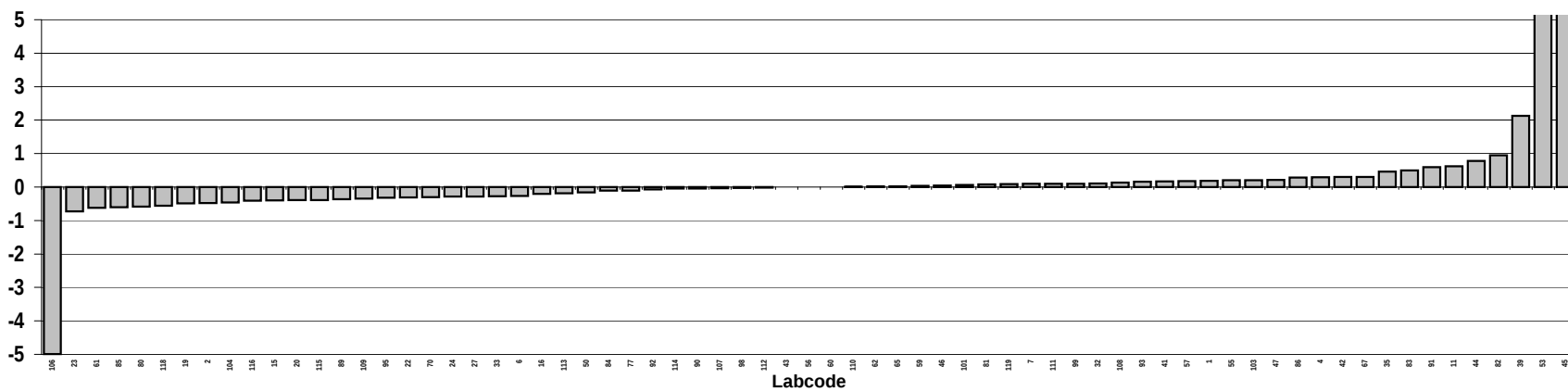
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2		89	4.6	
2	4.5		90	5.0	
4	5.3		91	5.6	
6	4.7		92	4.9	
7	5.1		93	5.2	
11	5.6		95	4.7	
15	4.6		98	5.0	
16	4.8		99	5.1	
19	4.5		101	5.1	
20	4.6		103	5.2	
22	4.7		104	4.5	
23	4.3		106	0.010	Outlier
24	4.7		107	5.0	
27	4.7		108	5.1	
32	5.1		109	4.7	
33	4.7		110	5.0	
35	5.5		111	5.1	
39	7.1		112	5.0	
41	5.2		113	4.8	
42	5.3		114	5.0	
43	5.0		115	4.6	
44	5.8		116	4.6	
45	108	Outlier	118	4.4	
46	5.0		119	5.1	
47	5.2				
50	4.8				
53	27	Outlier			
55	5.2				
56	5.0				
57	5.2				
59	5.0				
60	5.0				
61	4.4				
62	5.0				
65	5.0				
67	5.3				
70	4.7				
77	4.9				
80	4.4				
81	5.1				
82	6.0				
83	5.5				
84	4.9				
85	4.4				
86	5.3				

Consensus statistics	
Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.43
Relative standard deviation, %	8.6
No. of values reported	69
No. of values removed	3
No. of reported non-detects	0

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



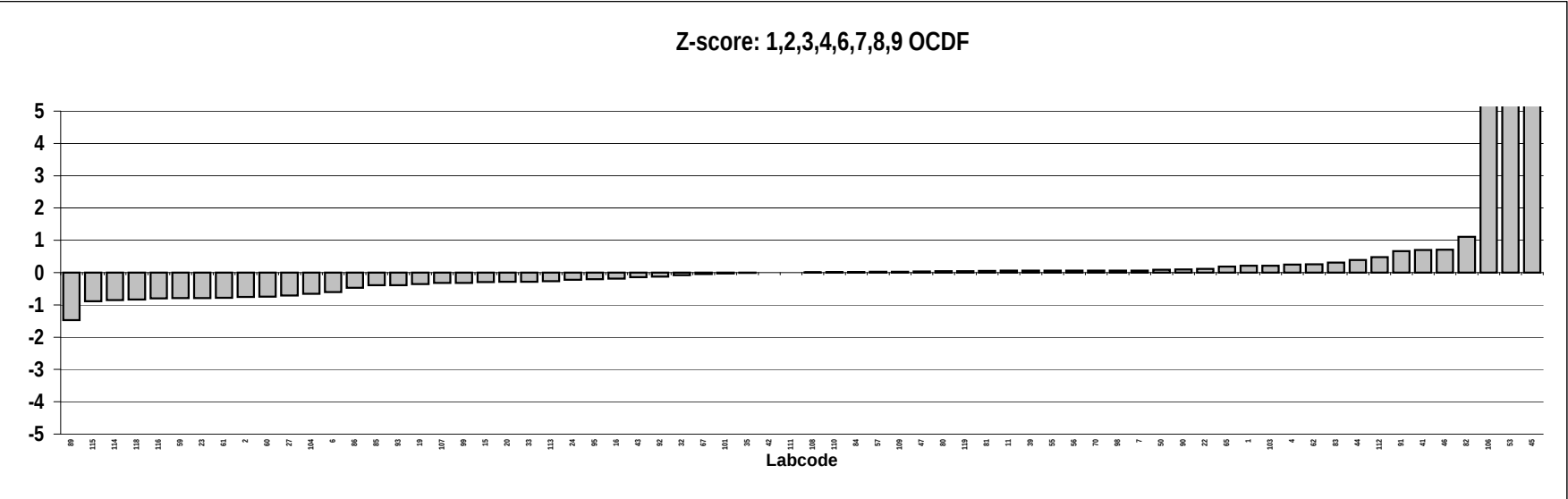
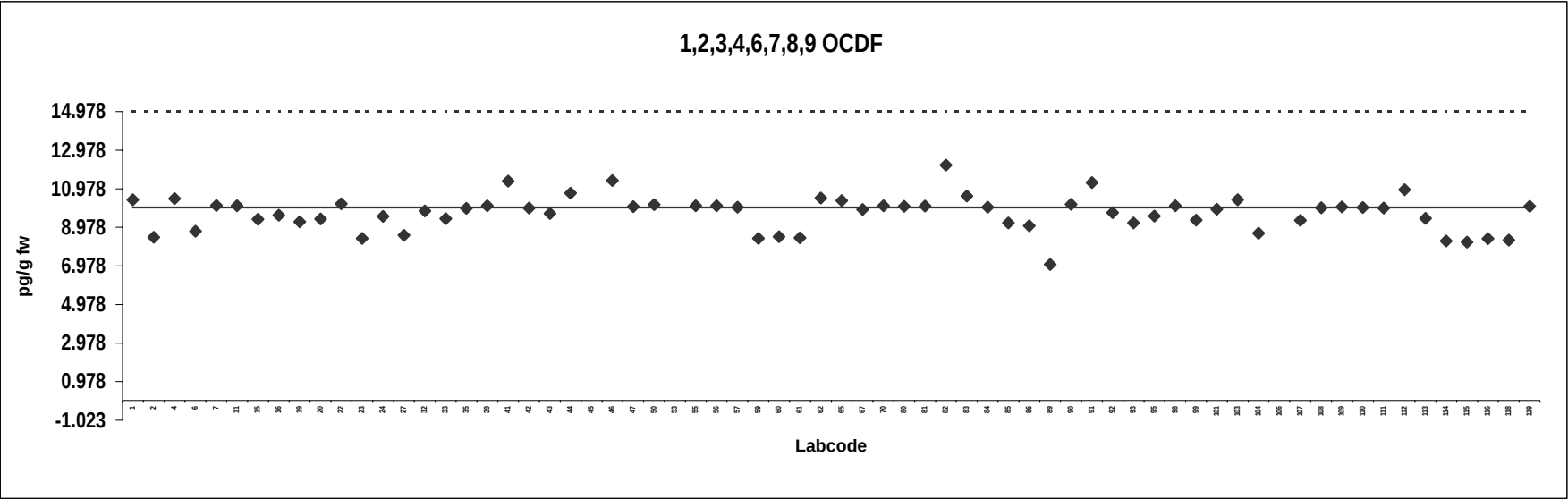
Z-score: 1,2,3,4,7,8,9 HpCDF



Analyte solution
Congener: 1,2,3,4,6,7,8,9 OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	10		90	10	
2	8.5		91	11	
4	10		92	9.7	
6	8.8		93	9.2	
7	10		95	9.6	
11	10		98	10	
15	9.4		99	9.3	
16	9.6		101	9.9	
19	9.3		103	10	
20	9.4		104	8.7	
22	10		106	24	Outlier
23	8.4		107	9.3	
24	9.5		108	10	
27	8.6		109	10	
32	9.8		110	10	
33	9.4		111	10	
35	10		112	11	
39	10		113	9.4	
41	11		114	8.3	
42	10		115	8.2	
43	9.7		116	8.4	
44	11		118	8.3	
45	198	Outlier	119	10	
46	11				
47	10				
50	10				
53	47	Outlier			
55	10				
56	10				
57	10				
59	8.4				
60	8.5				
61	8.4				
62	11				
65	10				
67	9.9				
70	10				
80	10				
81	10				
82	12				
83	11				
84	10				
85	9.2				
86	9.1				
89	7.1				

Consensus statistics	
Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	9.7
Standard deviation, pg/g	0.90
Relative standard deviation, %	9.2
No. of values reported	68
No. of values removed	3
No. of reported non-detects	0



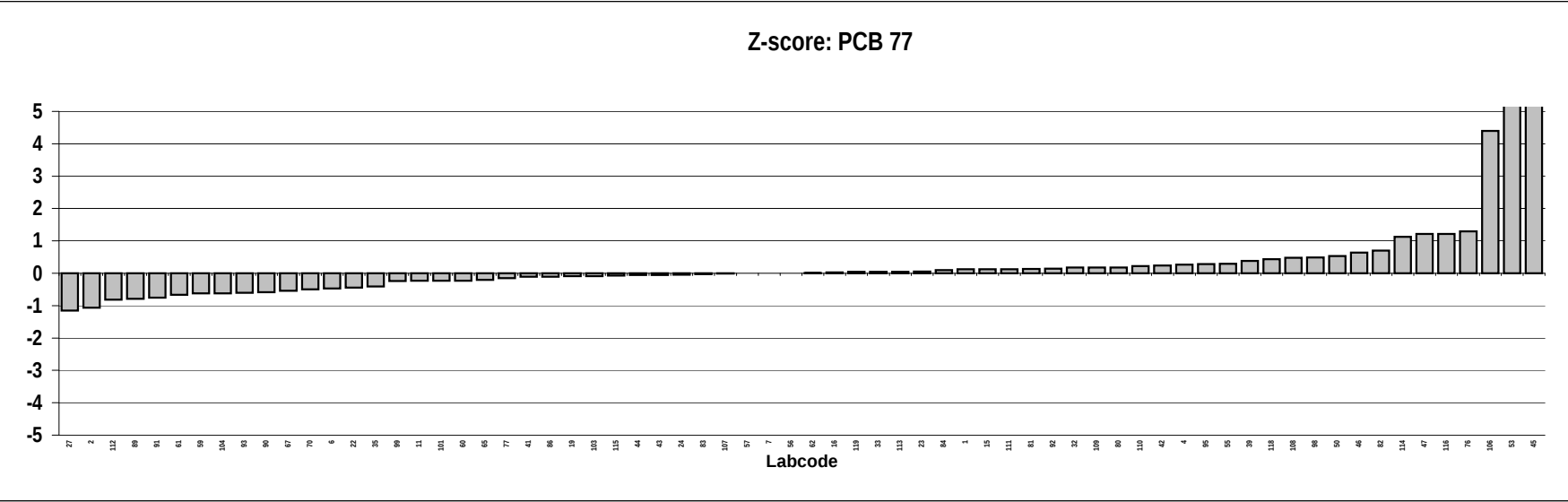
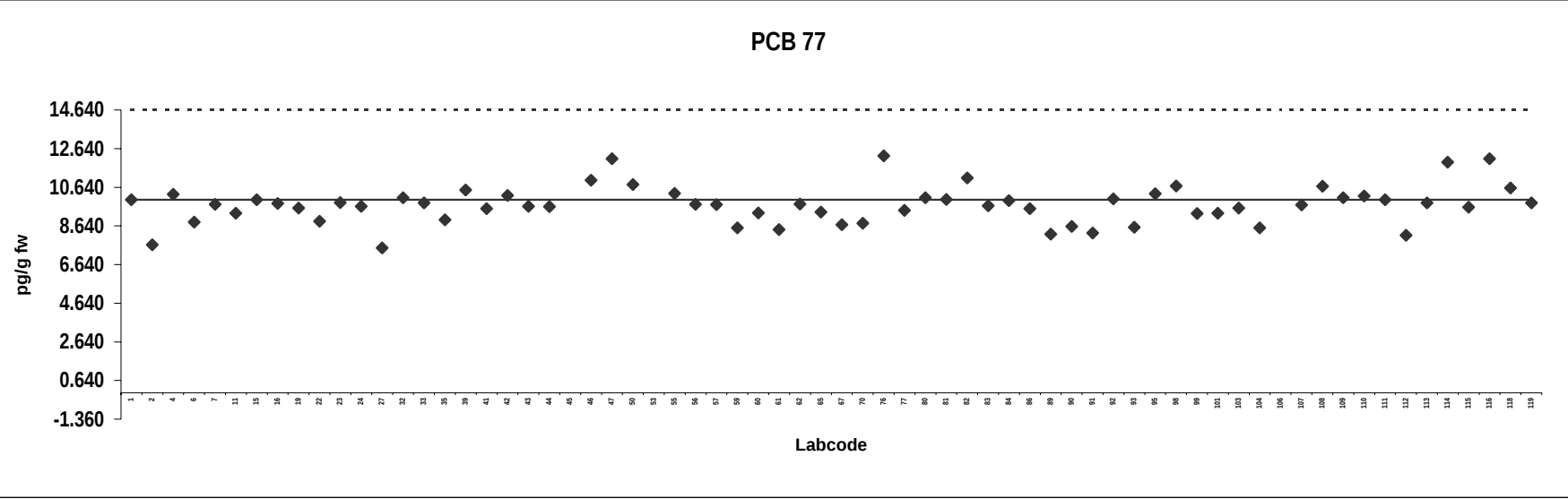
Analyte solution

Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	10		90	8.6	
2	7.7		91	8.3	
4	10		92	10	
6	8.8		93	8.6	
7	9.8		95	10	
11	9.3		98	11	
15	10		99	9.3	
16	9.8		101	9.3	
19	9.6		103	9.6	
22	8.9		104	8.5	
23	9.9		106	18	Outlier
24	9.7		107	9.7	
27	7.5		108	11	
32	10		109	10	
33	9.8		110	10	
35	9.0		111	10	
39	11		112	8.2	
41	9.5		113	9.8	
42	10		114	12	
43	9.7		115	9.6	
44	9.6		116	12	
45	195	Outlier	118	11	
46	11		119	9.8	
47	12				
50	11				
53	59	Outlier			
55	10				
56	9.8				
57	9.7				
59	8.5				
60	9.3				
61	8.4				
62	9.8				
65	9.4				
67	8.7				
70	8.8				
76	12				
77	9.5				
80	10				
81	10				
82	11				
83	9.7				
84	9.9				
86	9.5				
89	8.2				

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	0.98
Relative standard deviation, %	10
No. of values reported	68
No. of values removed	3
No. of reported non-detects	0

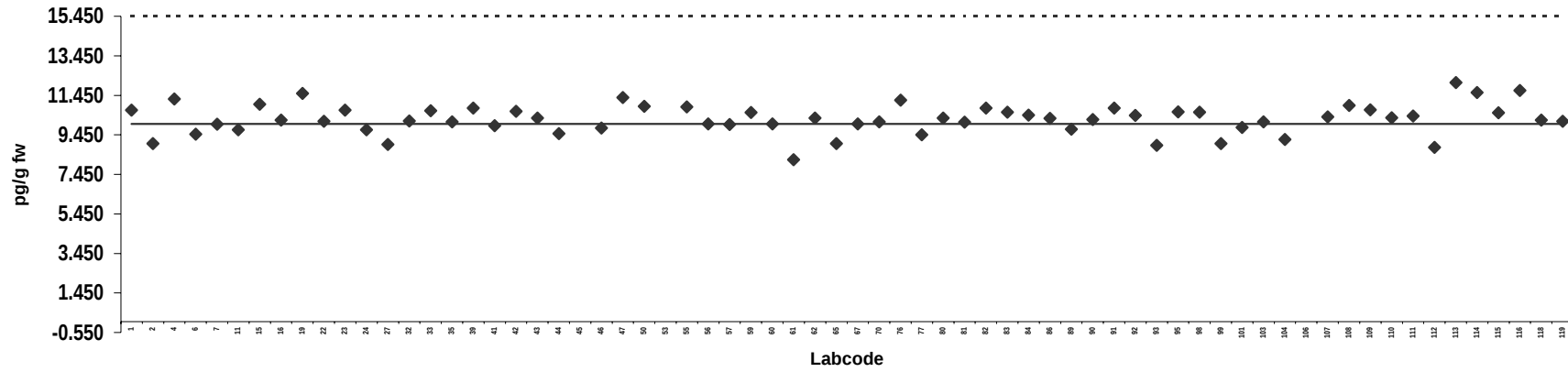


Analyte solution
Congener: PCB 126

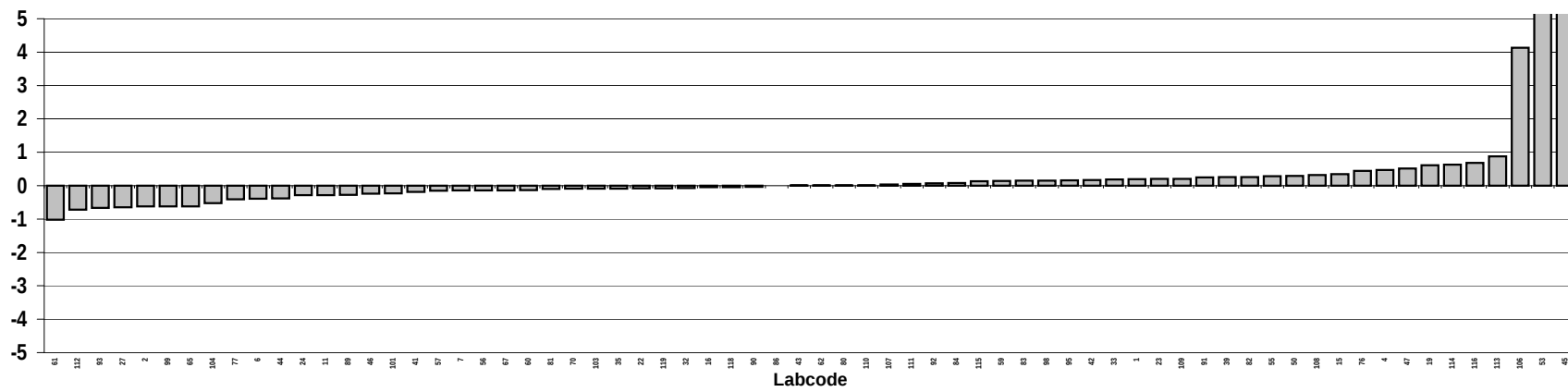
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		90	10	
2	9.0		91	11	
4	11		92	10	
6	9.5		93	8.9	
7	10		95	11	
11	9.7		98	11	
15	11		99	9.0	
16	10		101	9.8	
19	12		103	10	
22	10		104	9.2	
23	11		106	19	Outlier
24	9.7		107	10	
27	9.0		108	11	
32	10		109	11	
33	11		110	10	
35	10		111	10	
39	11		112	8.8	
41	9.9		113	12	
42	11		114	12	
43	10		115	11	
44	9.5		116	12	
45	253	Outlier	118	10	
46	9.8		119	10	
47	11				
50	11				
53	50	Outlier			
55	11				
56	10				
57	10				
59	11				
60	10				
61	8.2				
62	10				
65	9.0				
67	10				
70	10				
76	11				
77	9.5				
80	10				
81	10				
82	11				
83	11				
84	10				
86	10				
89	9.7				

Consensus statistics	
Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.75
Relative standard deviation, %	7.3
No. of values reported	68
No. of values removed	3
No. of reported non-detects	0

PCB 126



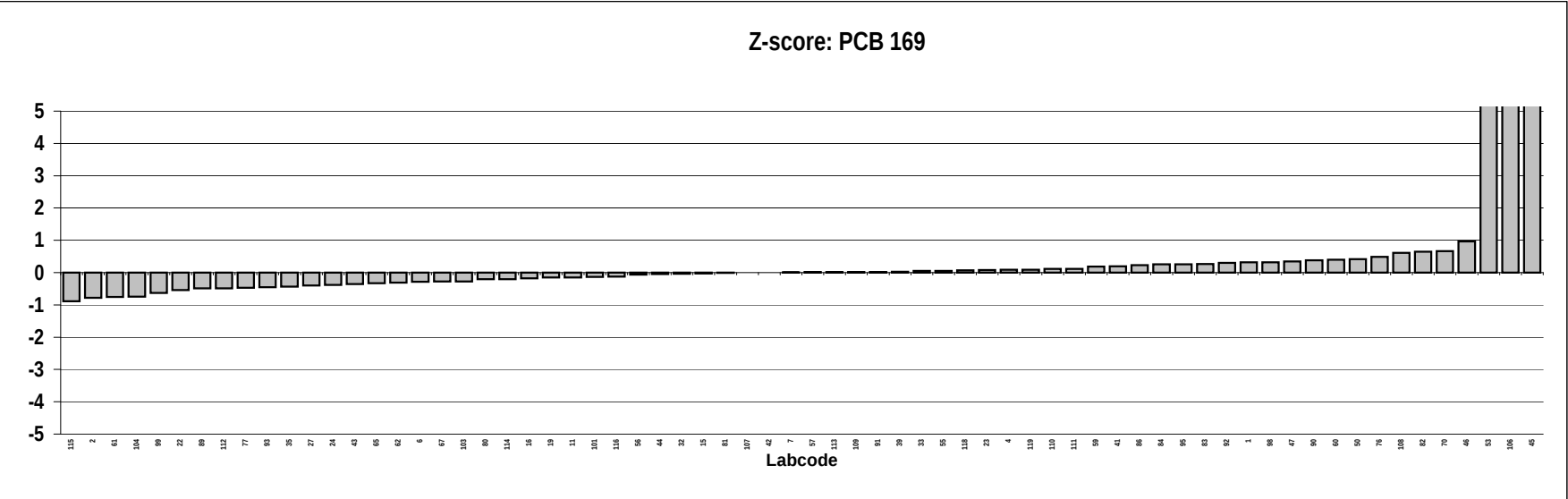
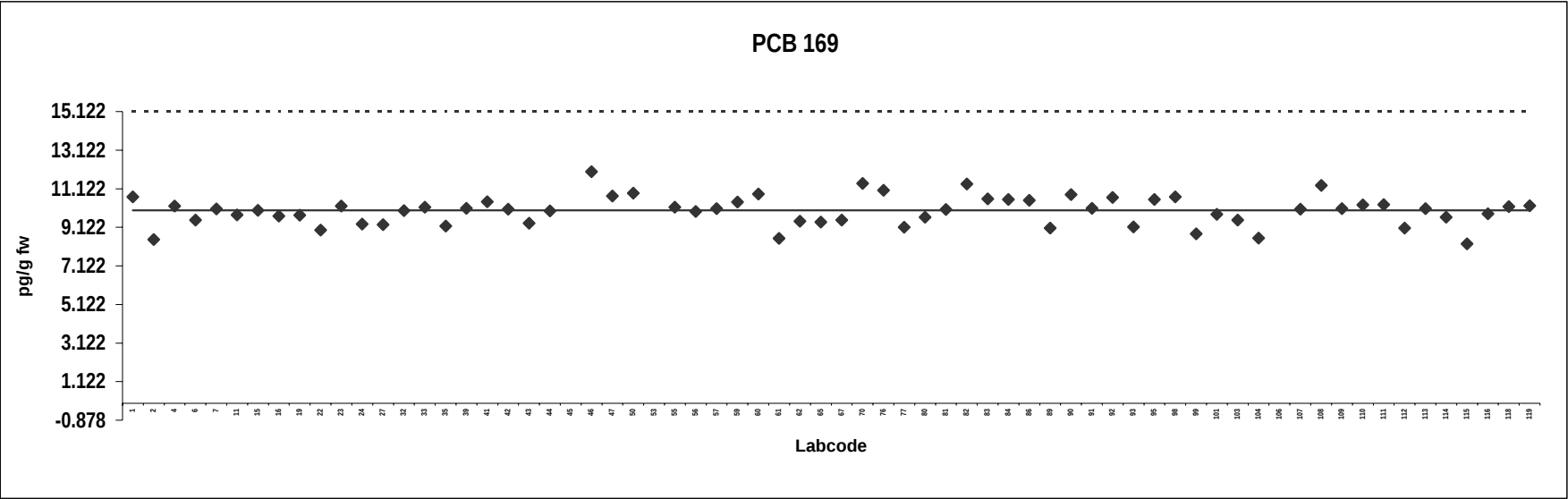
Z-score: PCB 126



Analyte solution
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		90	11	
2	8.5		91	10	
4	10		92	11	
6	9.5		93	9.1	
7	10		95	11	
11	9.8		98	11	
15	10		99	8.8	
16	9.7		101	9.8	
19	9.8		103	9.5	
22	9.0		104	8.6	
23	10		106	111	Outlier
24	9.3		107	10	
27	9.3		108	11	
32	10		109	10	
33	10		110	10	
35	9.2		111	10	
39	10		112	9.1	
41	10		113	10	
42	10		114	9.6	
43	9.3		115	8.3	
44	10		116	9.8	
45	228	Outlier	118	10	
46	12		119	10	
47	11				
50	11				
53	51	Outlier			
55	10				
56	9.9				
57	10				
59	10				
60	11				
61	8.5				
62	9.4				
65	9.4				
67	9.5				
70	11				
76	11				
77	9.1				
80	9.6				
81	10				
82	11				
83	11				
84	11				
86	11				
89	9.1				

Consensus statistics	
Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.75
Relative standard deviation, %	7.5
No. of values reported	68
No. of values removed	3
No. of reported non-detects	0



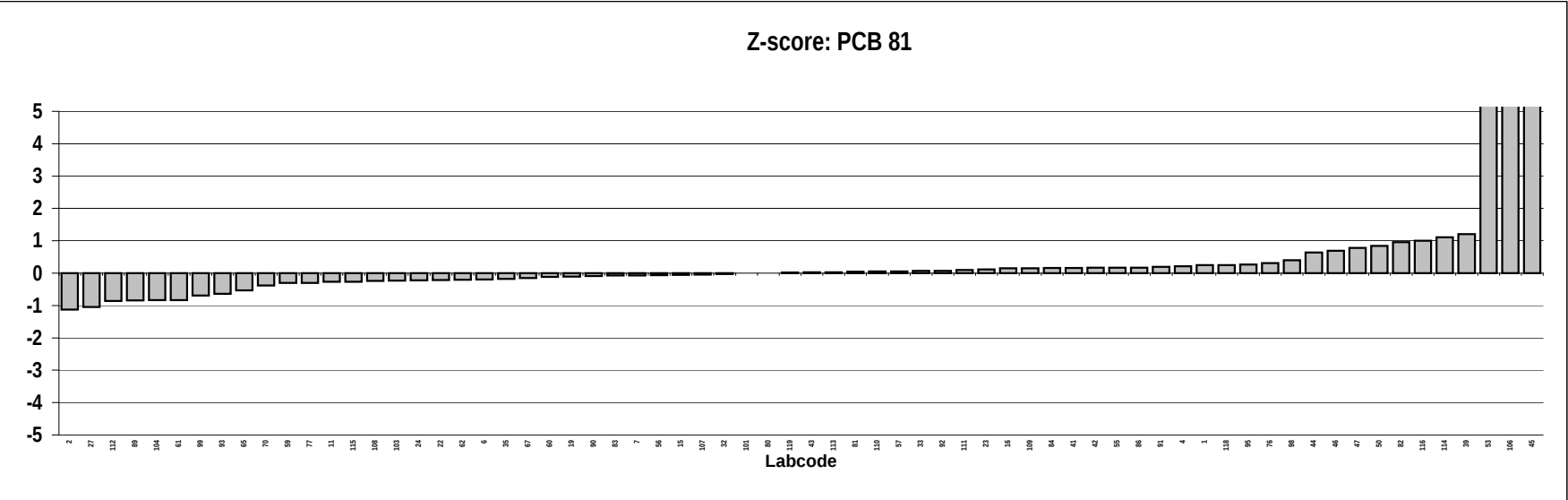
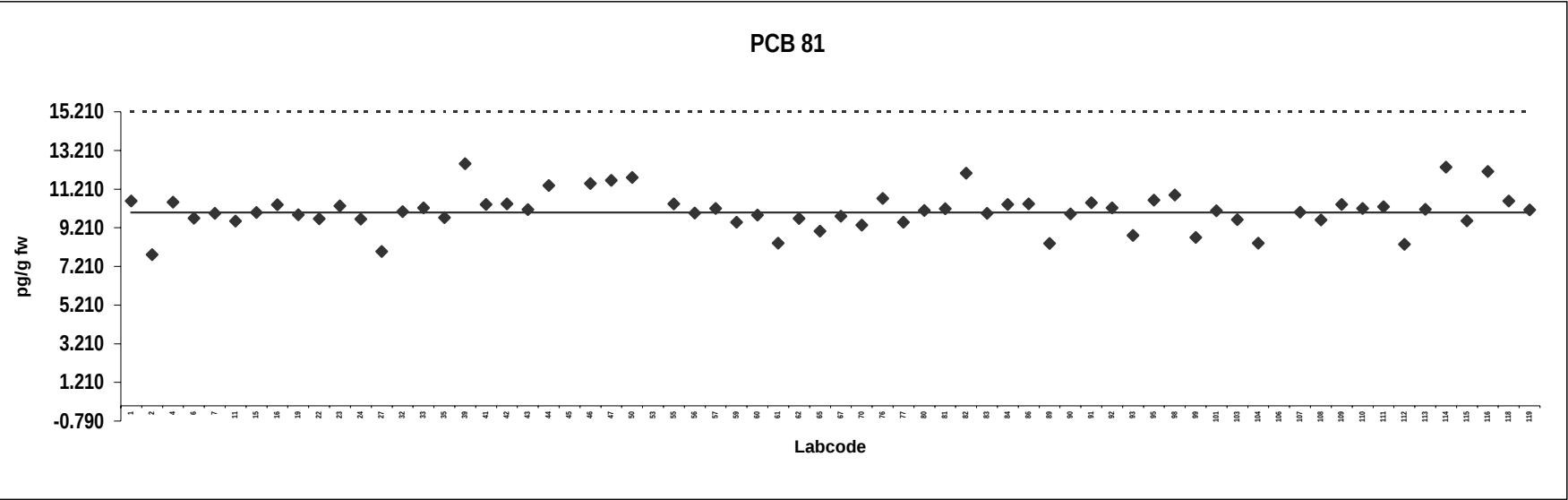
Analyte solution

Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		90	9.9	
2	7.8		91	11	
4	11		92	10	
6	9.7		93	8.8	
7	10		95	11	
11	9.6		98	11	
15	10		99	8.7	
16	10		101	10	
19	9.9		103	9.6	
22	9.7		104	8.4	
23	10		106	119	Outlier
24	9.7		107	10	
27	8.0		108	9.6	
32	10		109	10	
33	10		110	10	
35	9.7		111	10	
39	13		112	8.4	
41	10		113	10	
42	10		114	12	
43	10		115	9.6	
44	11		116	12	
45	210	Outlier	118	11	
46	12		119	10	
47	12				
50	12				
53	53	Outlier			
55	10				
56	10				
57	10				
59	9.5				
60	9.9				
61	8.4				
62	9.7				
65	9.0				
67	9.8				
70	9.3				
76	11				
77	9.5				
80	10				
81	10				
82	12				
83	10				
84	10				
86	10				
89	8.4				

Consensus statistics

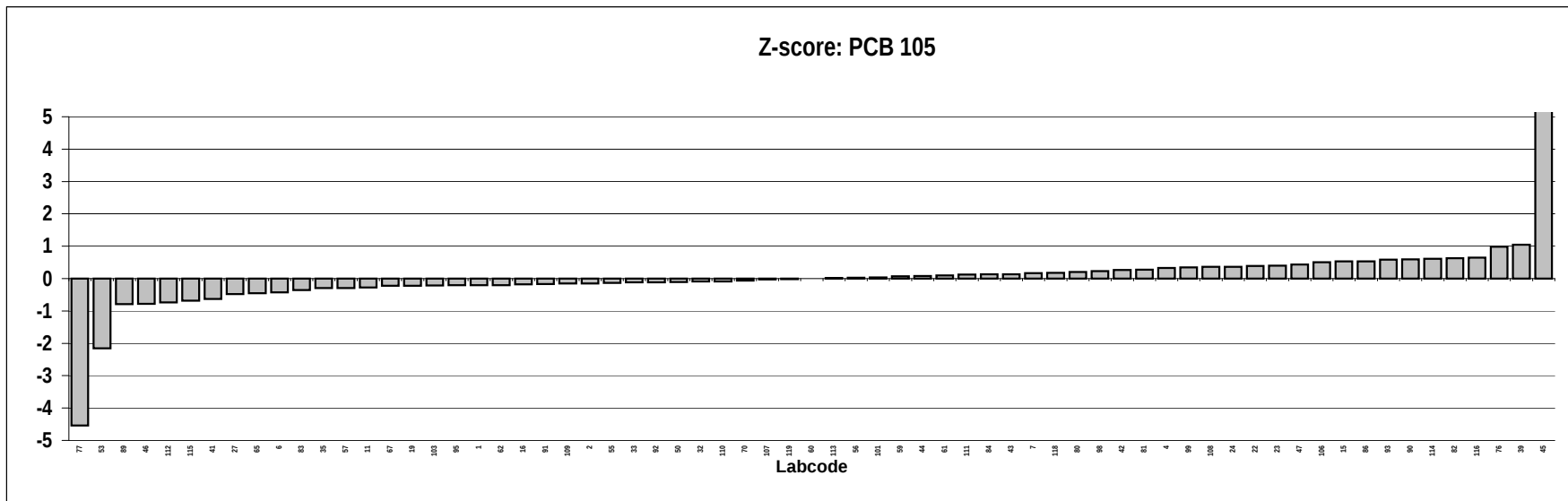
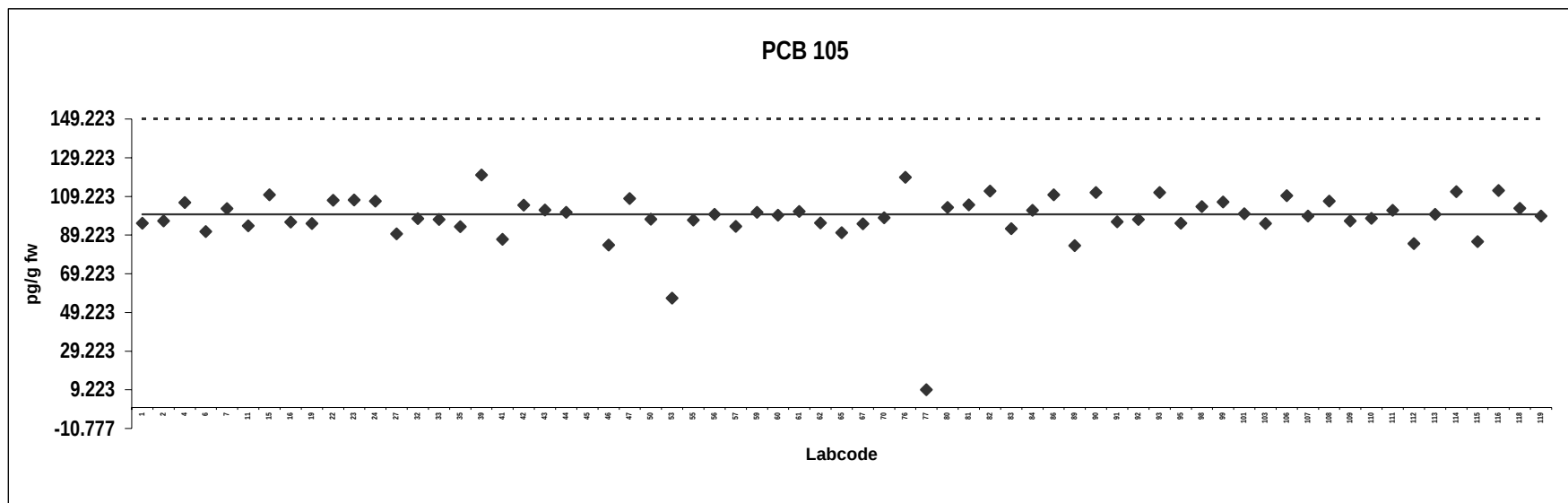
Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.97
Relative standard deviation, %	10
No. of values reported	68
No. of values removed	3
No. of reported non-detects	0



Analyte solution
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	95		90	111	
2	97		91	96	
4	106		92	97	
6	91		93	111	
7	103		95	95	
11	94		98	104	
15	110		99	106	
16	96		101	100	
19	95		103	95	
22	107		106	110	
23	107		107	99	
24	107		108	107	
27	90		109	97	
32	98		110	98	
33	97		111	102	
35	94		112	85	
39	120		113	100	
41	87		114	112	
42	105		115	86	
43	102		116	112	
44	101		118	103	
45	2478	Outlier	119	99	
46	84				
47	108				
50	97				
53	57				
55	97				
56	100				
57	94				
59	101				
60	99				
61	101				
62	96				
65	90				
67	95				
70	98				
76	119				
77	9.2	Outlier			
80	104				
81	105				
82	112				
83	93				
84	102				
86	110				
89	84				

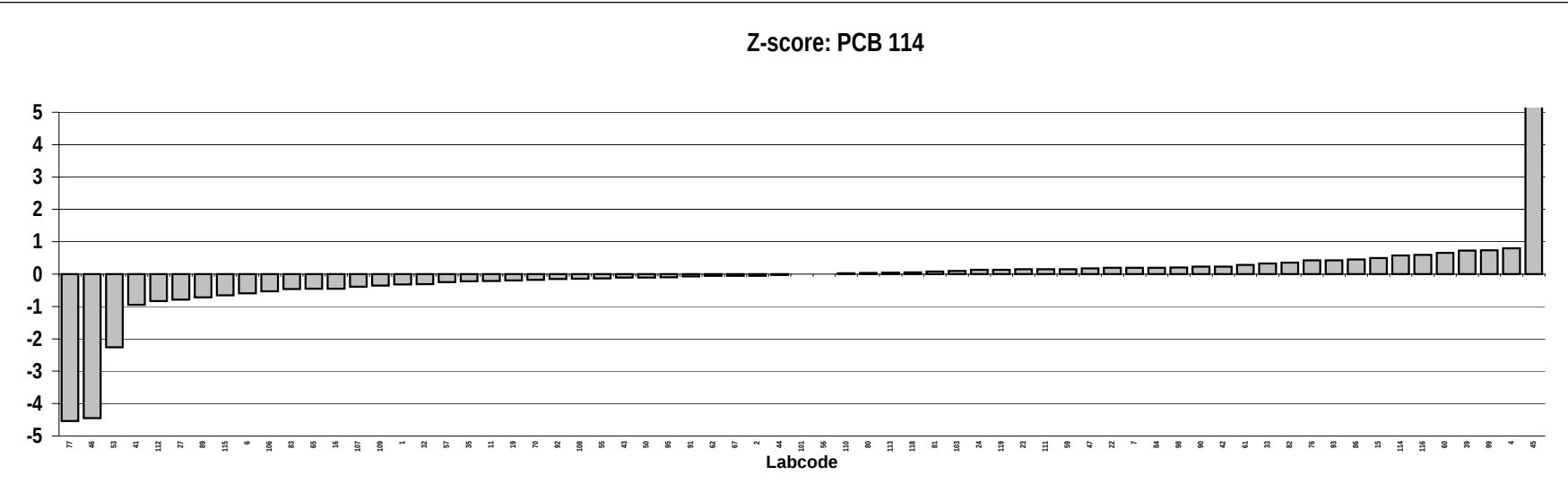
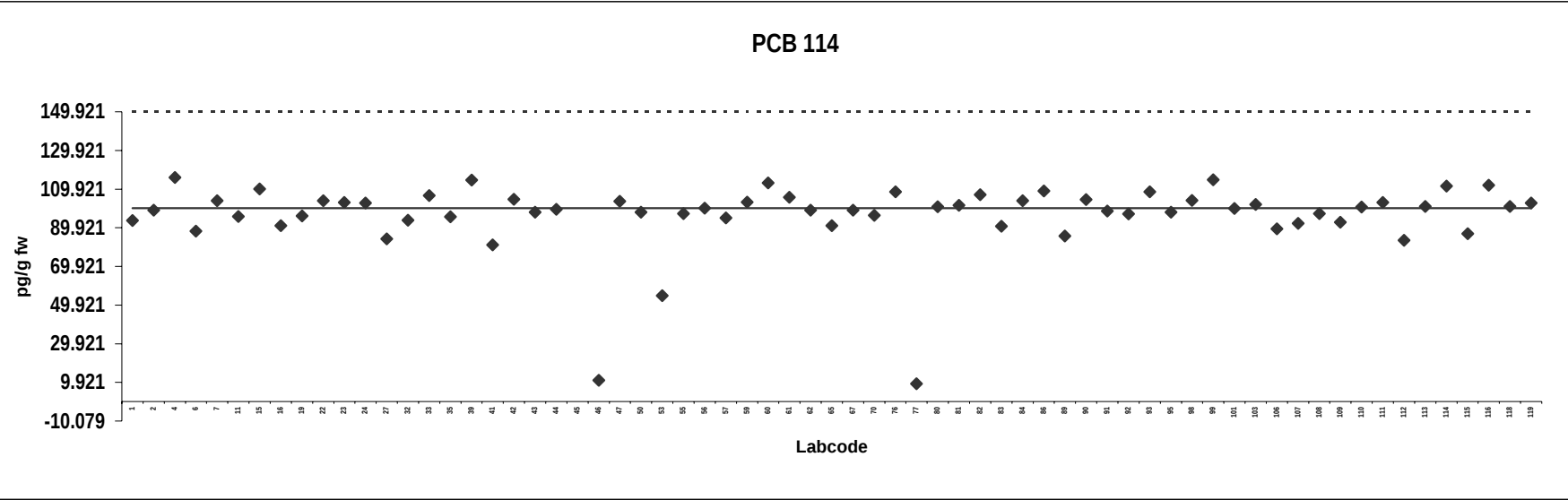
Consensus statistics	
Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	100
Standard deviation, pg/g	9.6
Relative standard deviation, %	10
No. of values reported	67
No. of values removed	2
No. of reported non-detects	0



Analyte solution
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	94		90	105	
2	99		91	99	
4	116		92	97	
6	88		93	109	
7	104		95	98	
11	96		98	104	
15	110		99	115	
16	91		101	100	
19	96		103	102	
22	104		106	89	
23	103		107	92	
24	103		108	97	
27	84		109	93	
32	94		110	101	
33	107		111	103	
35	96		112	83	
39	115		113	101	
41	81		114	112	
42	105		115	87	
43	98		116	112	
44	99		118	101	
45	2320	Outlier	119	103	
46	11	Outlier			
47	104				
50	98				
53	55				
55	97				
56	100				
57	95				
59	103				
60	113				
61	106				
62	99				
65	91				
67	99				
70	96				
76	109				
77	9.2	Outlier			
80	101				
81	102				
82	107				
83	91				
84	104				
86	109				
89	86				

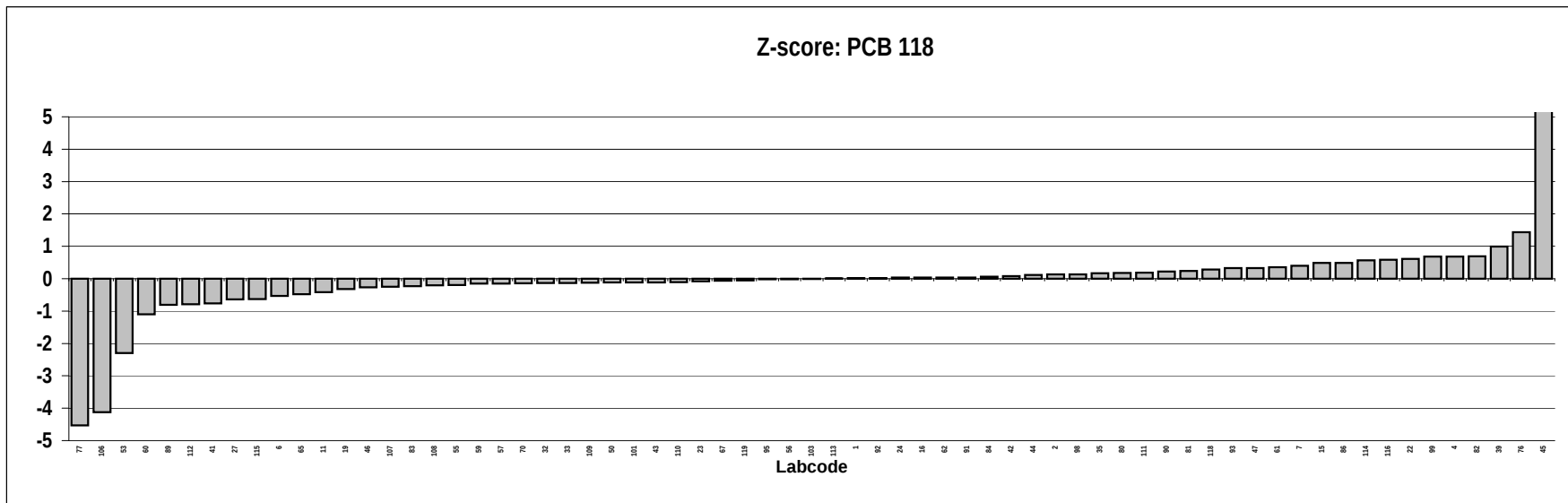
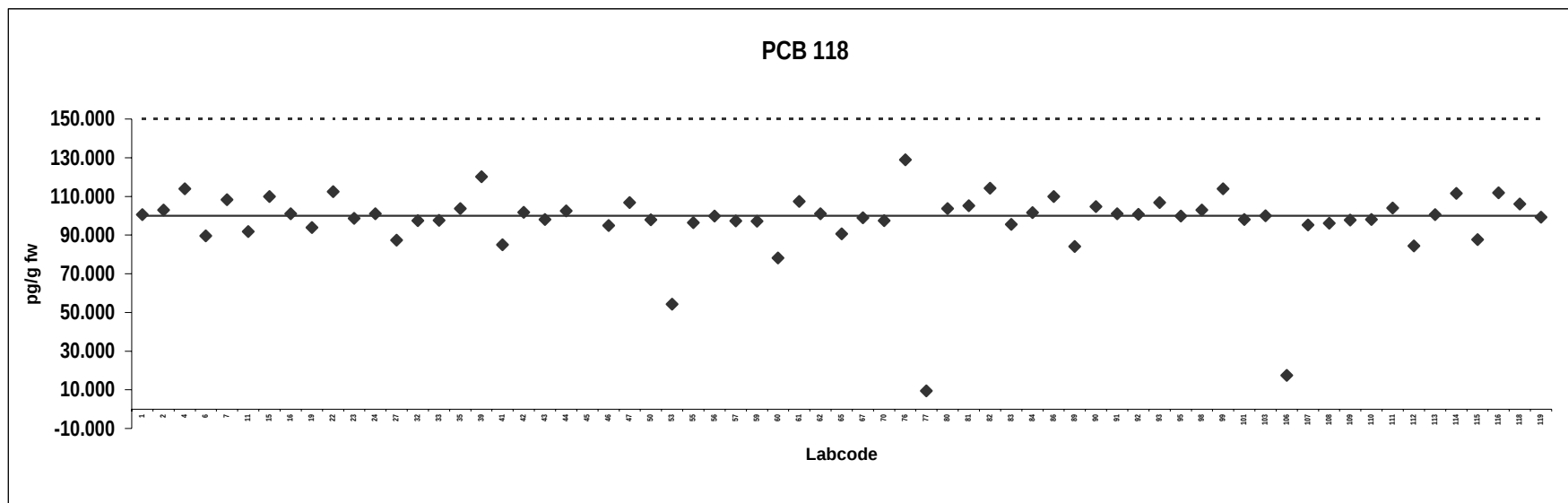
Consensus statistics	
Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	99
Standard deviation, pg/g	9.6
Relative standard deviation, %	10
No. of values reported	67
No. of values removed	3
No. of reported non-detects	0



Analyte solution
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	101		90	105	
2	103		91	101	
4	114		92	101	
6	90		93	107	
7	108		95	100	
11	92		98	103	
15	110		99	114	
16	101		101	98	
19	94		103	100	
22	112		106	18	Outlier
23	99		107	95	
24	101		108	96	
27	87		109	98	
32	98		110	98	
33	98		111	104	
35	104		112	84	
39	120		113	101	
41	85		114	112	
42	102		115	88	
43	98		116	112	
44	102		118	106	
45	2319	Outlier	119	99	
46	95				
47	107				
50	98				
53	54				
55	96				
56	100				
57	97				
59	97				
60	78				
61	107				
62	101				
65	91				
67	99				
70	98				
76	129				
77	9.4	Outlier			
80	104				
81	105				
82	114				
83	96				
84	102				
86	110				
89	84				

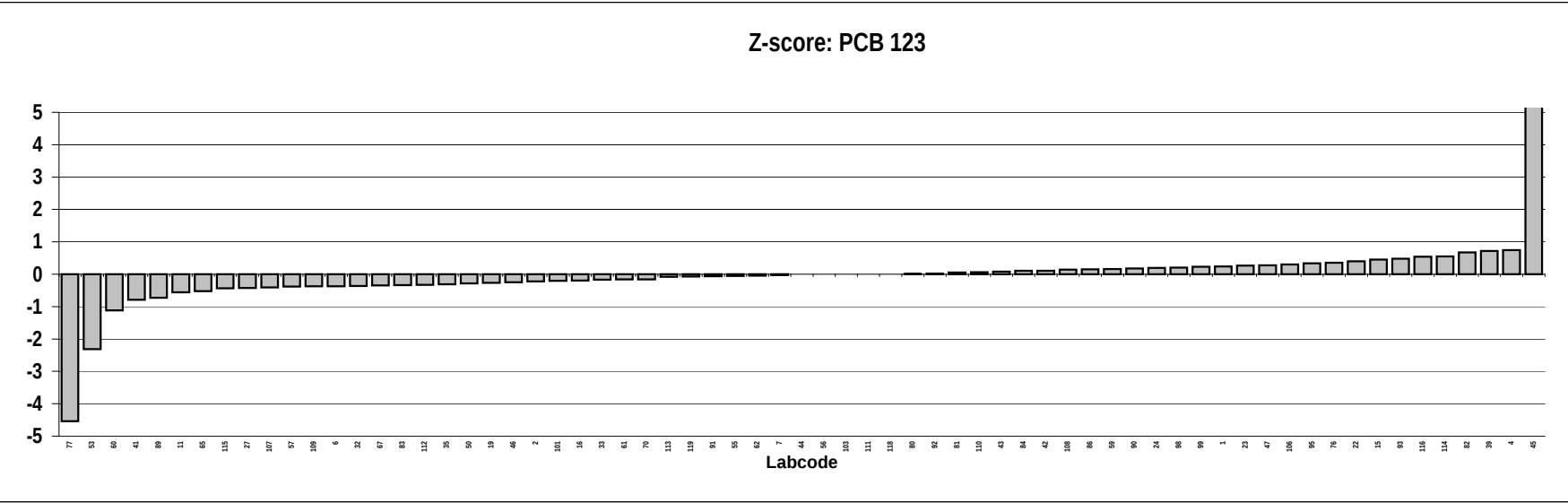
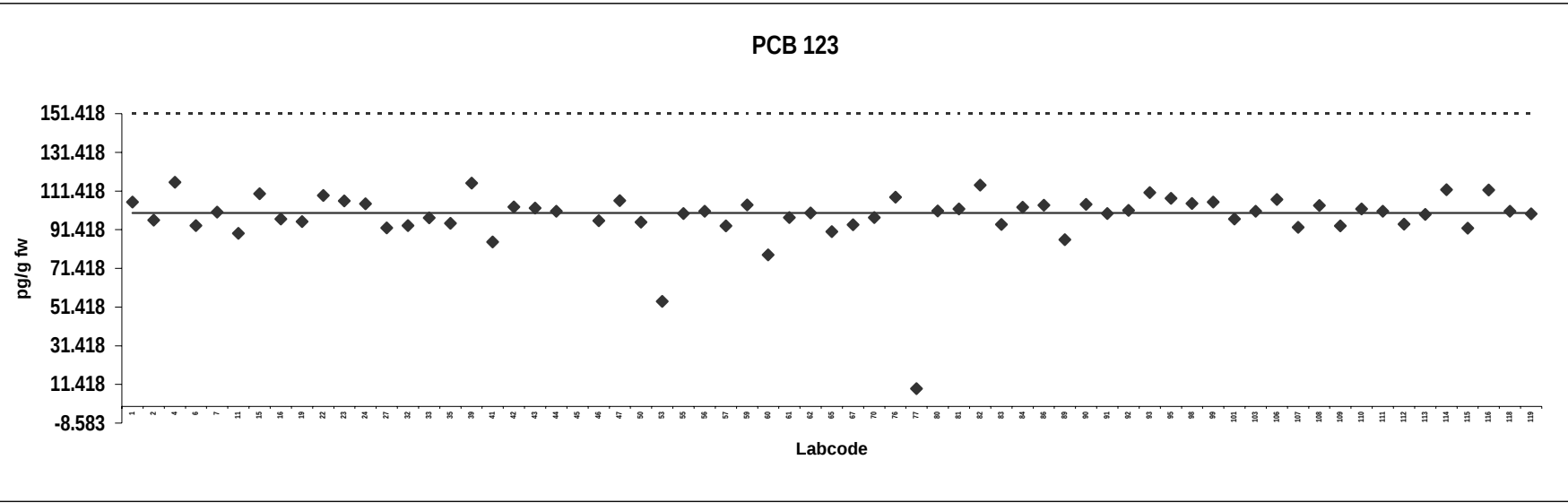
Consensus statistics	
Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	10
Relative standard deviation, %	10
No. of values reported	67
No. of values removed	3
No. of reported non-detects	0



Analyte solution
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	106	Outlier	90	105	
2	96		91	100	
4	116		92	101	
6	94		93	111	
7	100		95	108	
11	90		98	105	
15	110		99	106	
16	97		101	97	
19	96		103	101	
22	109		106	107	
23	106		107	93	
24	105		108	104	
27	92		109	93	
32	94		110	102	
33	98		111	101	
35	95		112	94	
39	116		113	99	
41	85		114	112	
42	103		115	92	
43	103		116	112	
44	101		118	101	
45	2164		119	100	
46	96				
47	107				
50	95				
53	54				
55	100				
56	101				
57	93				
59	104				
60	78				
61	98				
62	100				
65	90				
67	94				
70	98				
76	108				
77	9.3	Outlier			
80	101				
81	102				
82	114				
83	94				
84	103				
86	104				
89	86				

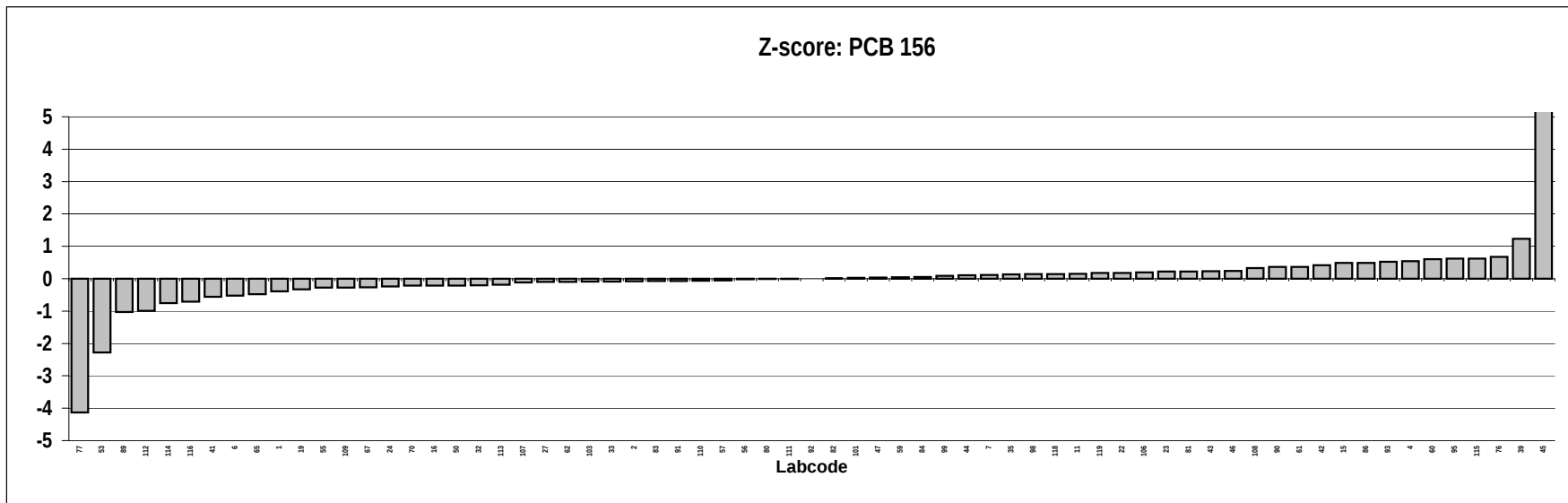
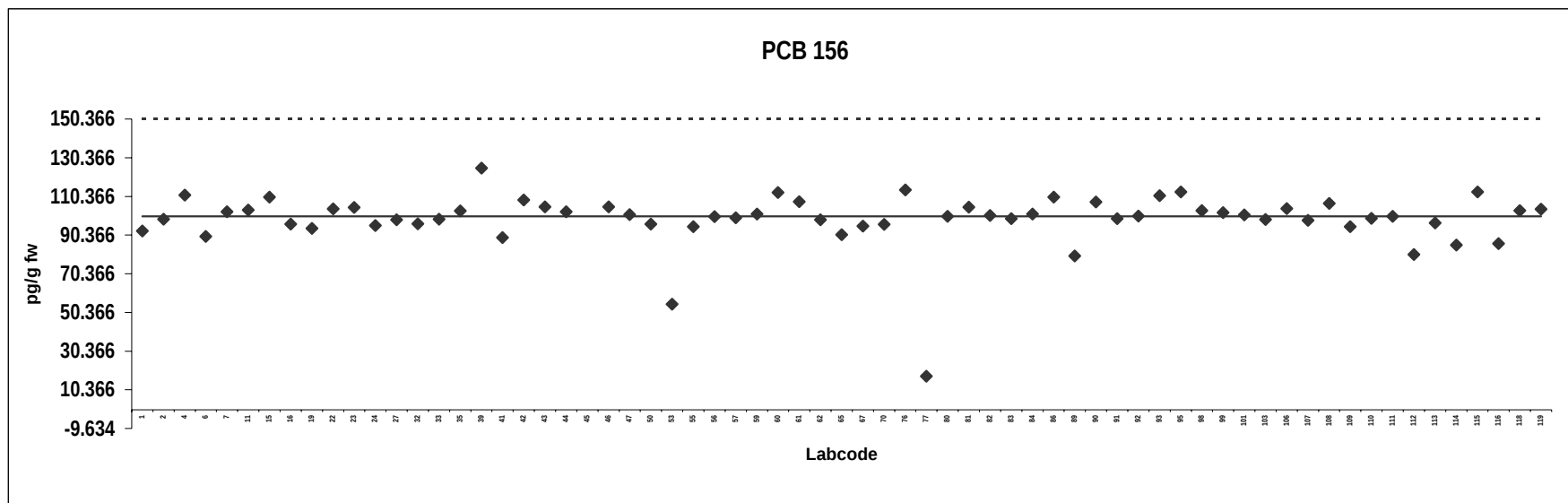
Consensus statistics	
Consensus median, pg/g	101
Median all values pg/g	101
Consensus mean, pg/g	100
Standard deviation, pg/g	9.3
Relative standard deviation, %	9.3
No. of values reported	67
No. of values removed	2
No. of reported non-detects	0



Analyte solution
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	93	Outlier	90	107	
2	99		91	99	
4	111		92	100	
6	90		93	111	
7	102		95	113	
11	103		98	103	
15	110		99	102	
16	96		101	101	
19	94		103	98	
22	104		106	104	
23	105		107	98	
24	95		108	107	
27	98		109	95	
32	96		110	99	
33	98		111	100	
35	103		112	80	
39	125		113	97	
41	89		114	85	
42	109		115	113	
43	105		116	86	
44	102		118	103	
45	2392		119	104	
46	105				
47	101				
50	96				
53	55				
55	95				
56	100				
57	99				
59	101				
60	112				
61	108				
62	98				
65	91				
67	95				
70	96				
76	114				
77	17	Outlier			
80	100				
81	105				
82	100				
83	99				
84	101				
86	110				
89	80				

Consensus statistics	
Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	9.7
Relative standard deviation, %	10
No. of values reported	67
No. of values removed	2
No. of reported non-detects	0



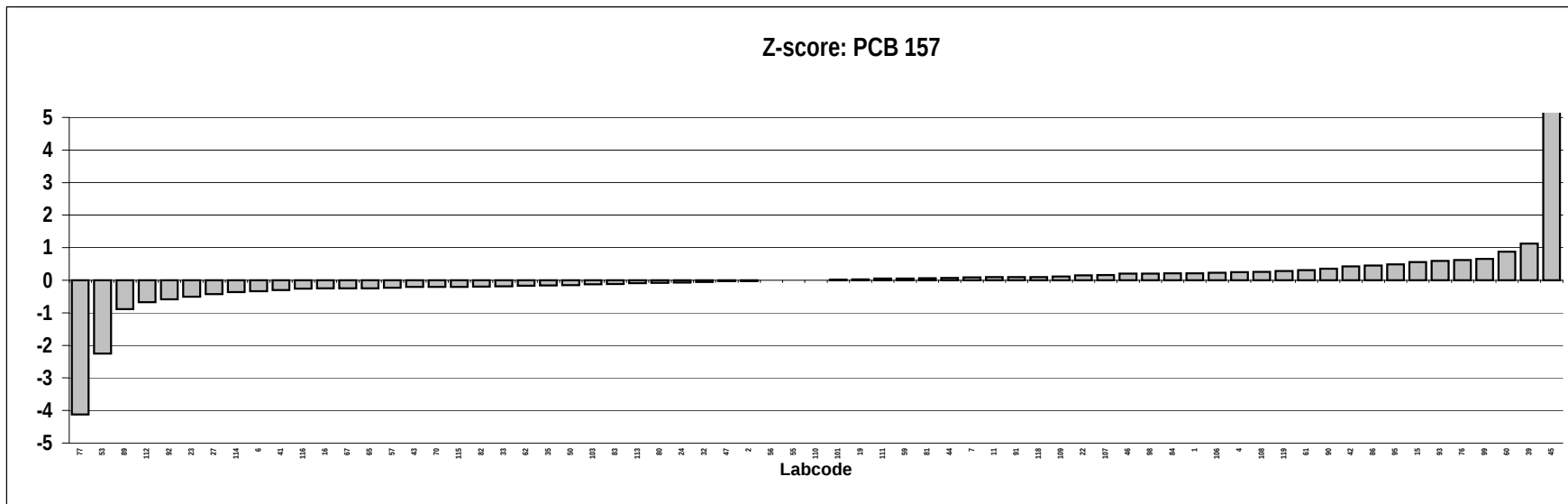
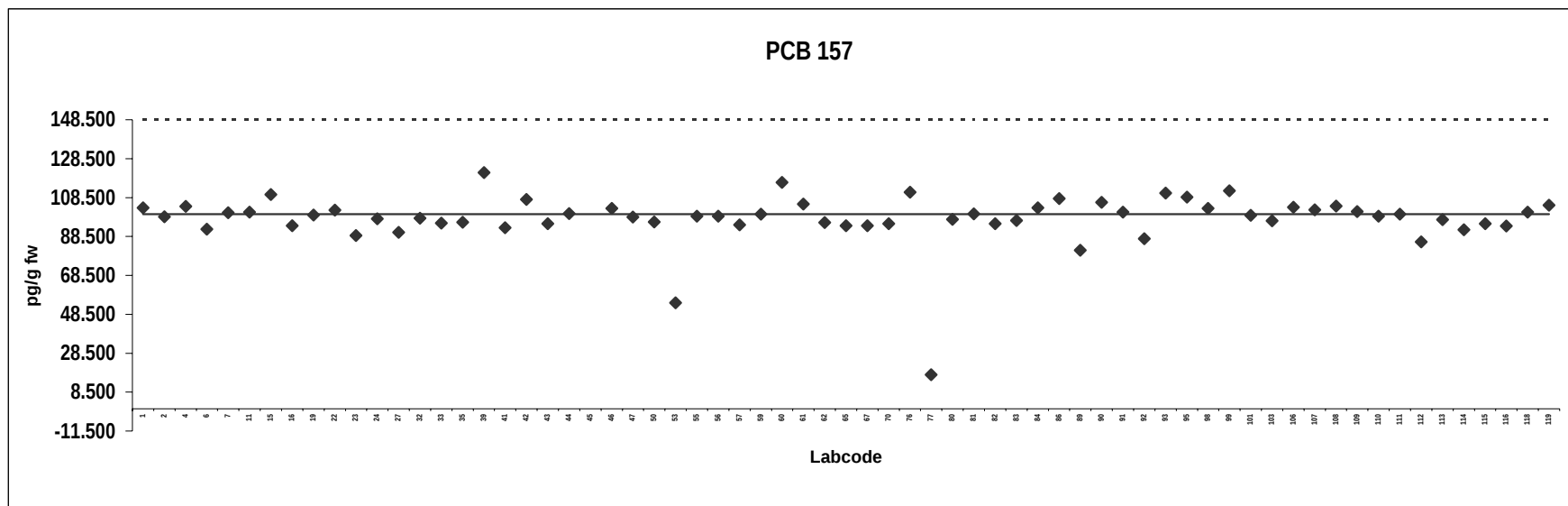
Analyte solution

Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	103		90	106	
2	99		91	101	
4	104		92	87	
6	92		93	111	
7	101		95	109	
11	101		98	103	
15	110		99	112	
16	94		101	99	
19	100		103	97	
22	102		106	103	
23	89		107	102	
24	98		108	104	
27	91		109	101	
32	98		110	99	
33	95		111	100	
35	96		112	86	
39	121		113	97	
41	93		114	92	
42	107		115	95	
43	95		116	94	
44	100		118	101	
45	2195	Outlier	119	105	
46	103				
47	98				
50	96				
53	54				
55	99				
56	99				
57	95				
59	100				
60	116				
61	105				
62	96				
65	94				
67	94				
70	95				
76	111				
77	17	Outlier			
80	97				
81	100				
82	95				
83	97				
84	103				
86	108				
89	81				

Consensus statistics

Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	99
Standard deviation, pg/g	8.9
Relative standard deviation, %	9.0
No. of values reported	67
No. of values removed	2
No. of reported non-detects	0



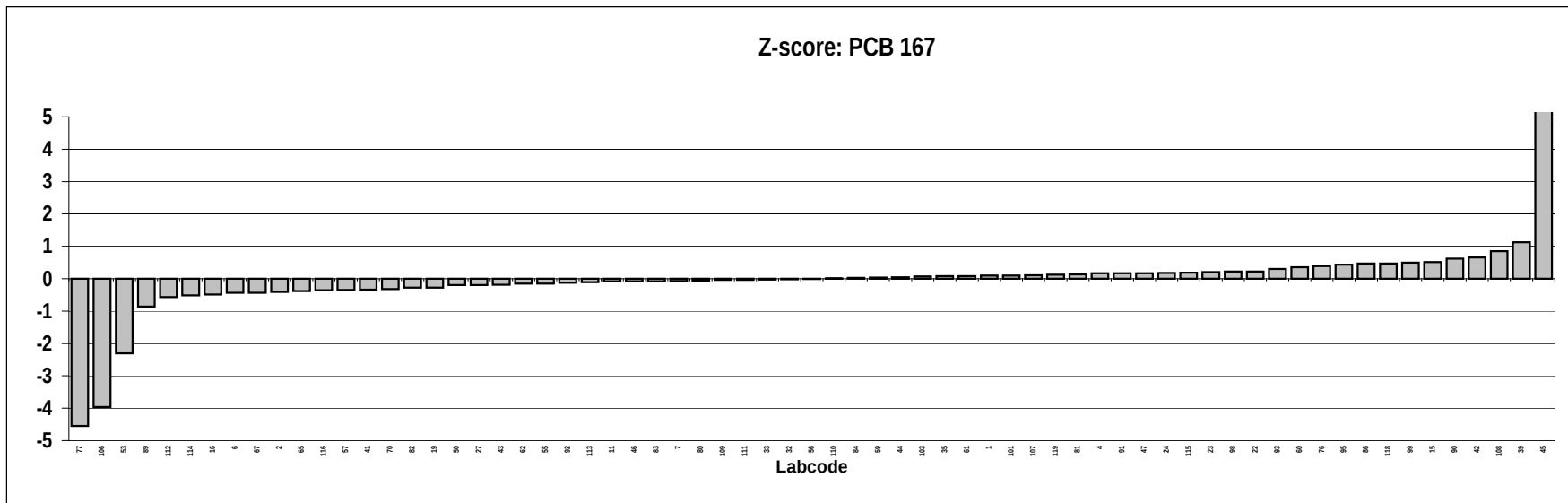
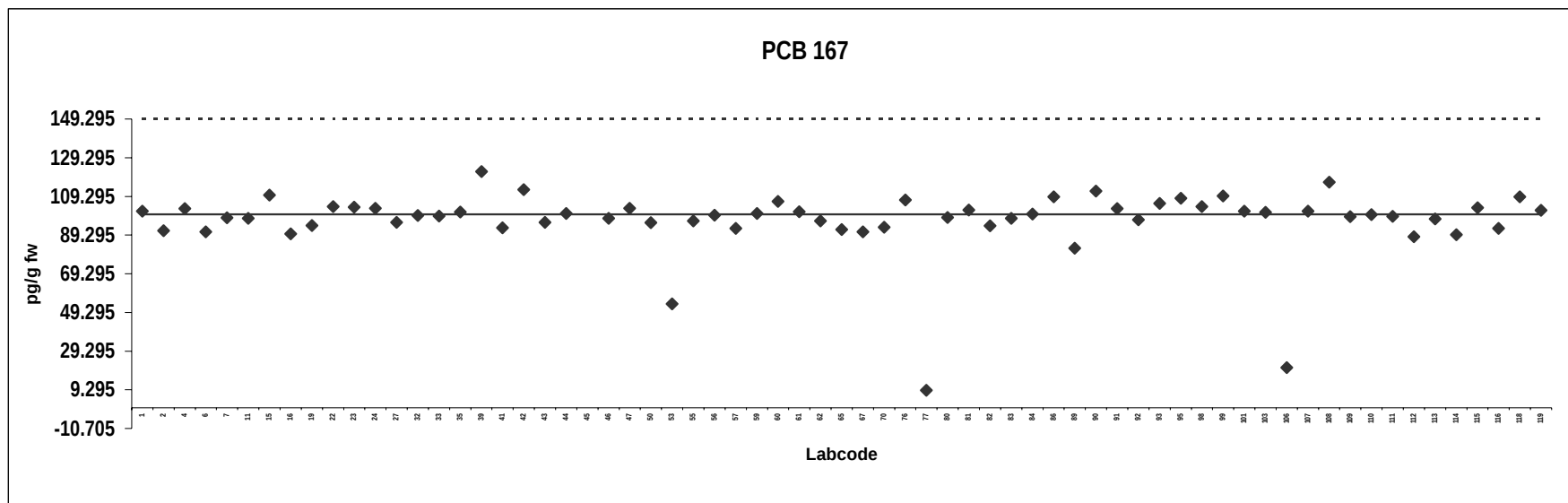
Analyte solution

Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	102		90	112	
2	92		91	103	
4	103		92	97	
6	91		93	106	
7	98		95	108	
11	98		98	104	
15	110		99	109	
16	90		101	102	
19	94		103	101	
22	104		106	21	Outlier
23	104		107	102	
24	103		108	117	
27	96		109	99	
32	99		110	100	
33	99		111	99	
35	101		112	88	
39	122		113	98	
41	93		114	89	
42	113		115	103	
43	96		116	93	
44	100		118	109	
45	2303	Outlier	119	102	
46	98				
47	103				
50	96				
53	54				
55	97				
56	100				
57	93				
59	100				
60	107				
61	101				
62	97				
65	92				
67	91				
70	93				
76	107				
77	9.0	Outlier			
80	98				
81	102				
82	94				
83	98				
84	100				
86	109				
89	83				

Consensus statistics

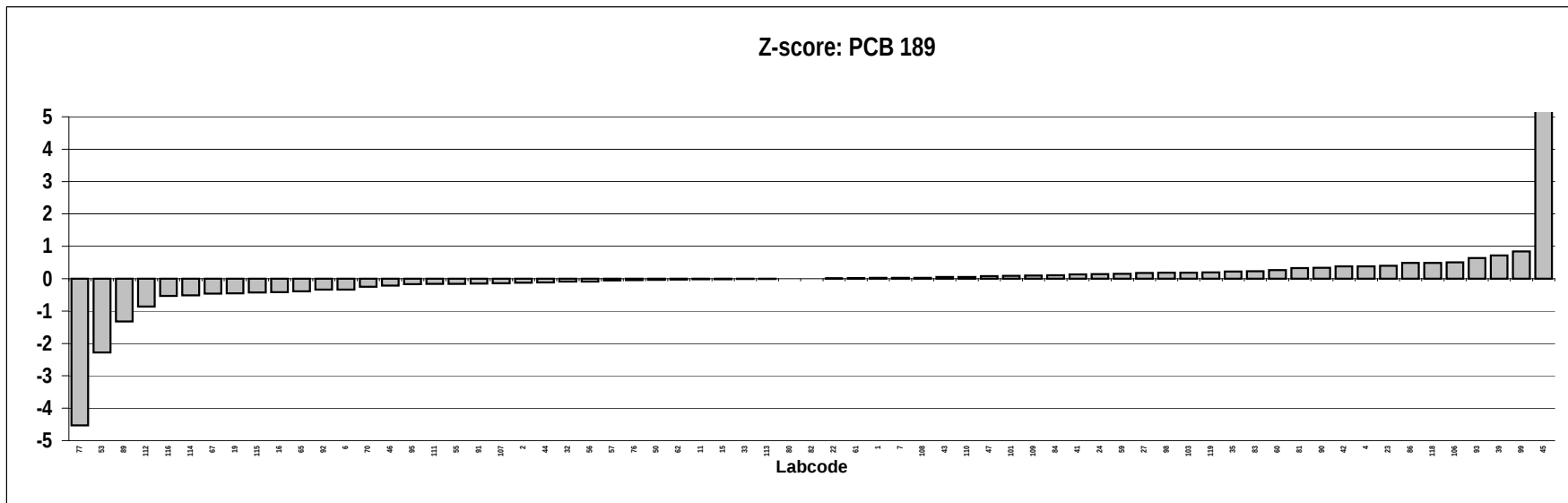
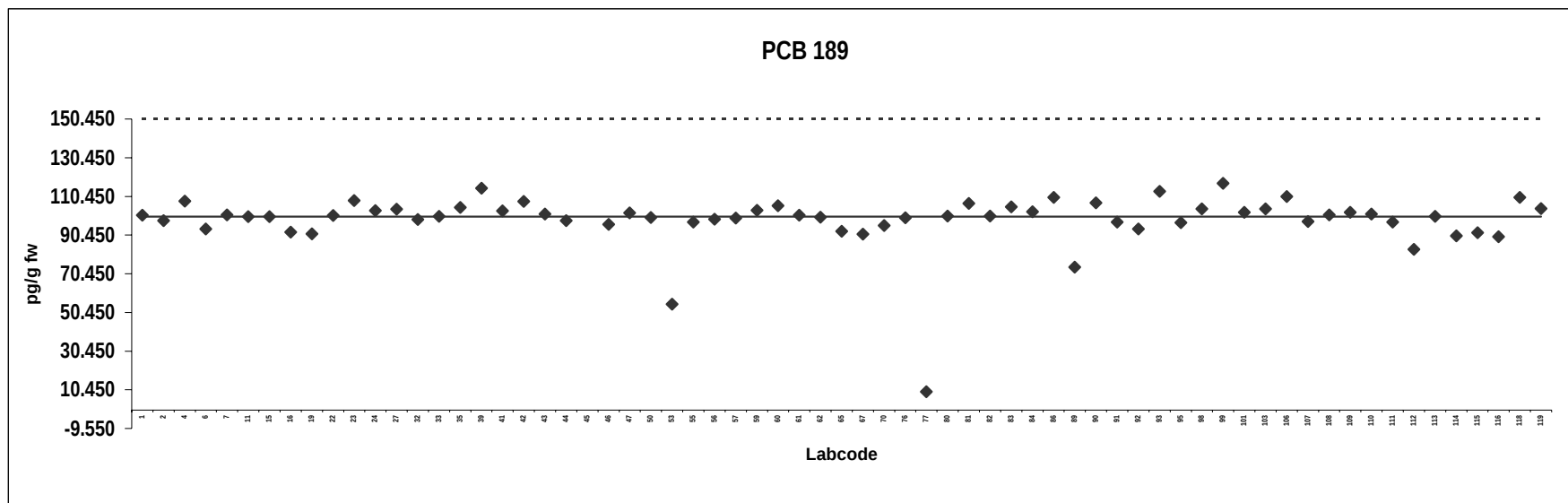
Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	99
Standard deviation, pg/g	9.1
Relative standard deviation, %	9.1
No. of values reported	67
No. of values removed	3
No. of reported non-detects	0



Analyte solution
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	101	Outlier	90	107	
2	98		91	97	
4	108		92	94	
6	94		93	113	
7	101		95	97	
11	100		98	104	
15	100		99	117	
16	92		101	102	
19	91		103	104	
22	101		106	110	
23	108		107	97	
24	103		108	101	
27	104		109	102	
32	98		110	101	
33	100		111	97	
35	105		112	83	
39	115		113	100	
41	103		114	90	
42	108		115	92	
43	101		116	90	
44	98		118	110	
45	2473		119	104	
46	96				
47	102				
50	100				
53	55				
55	97				
56	99				
57	99				
59	103				
60	106				
61	101				
62	100				
65	92				
67	91				
70	95				
76	99				
77	9.5	Outlier			
80	100				
81	107				
82	100				
83	105				
84	102				
86	110				
89	74				

Consensus statistics	
Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	9.0
Relative standard deviation, %	9.1
No. of values reported	67
No. of values removed	2
No. of reported non-detects	0



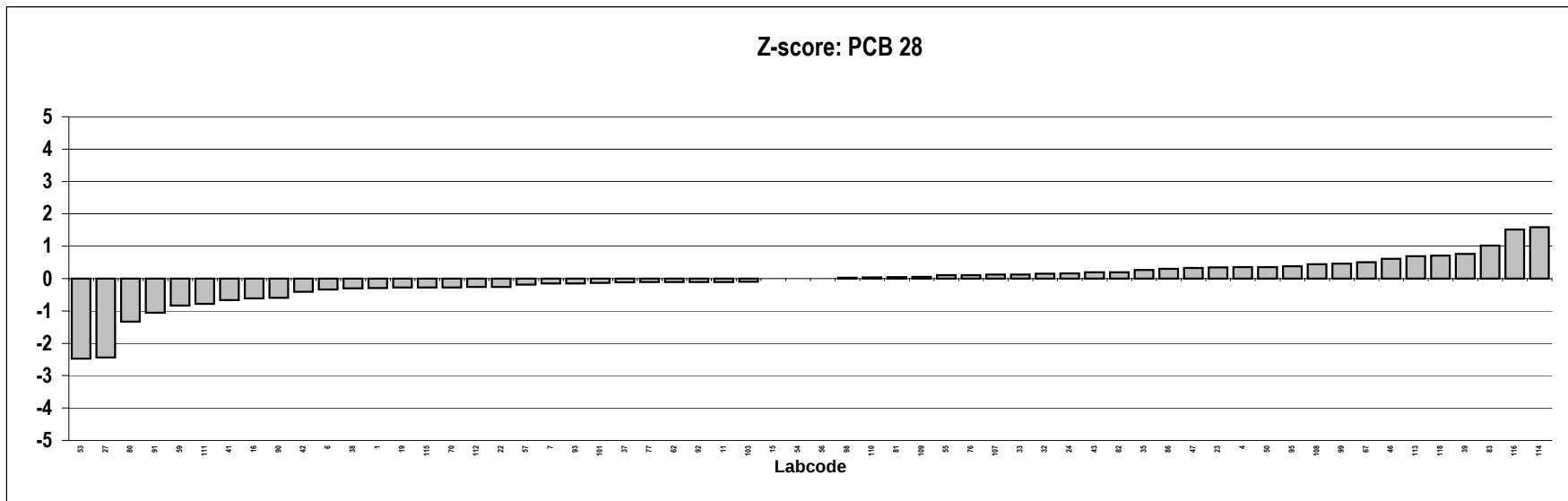
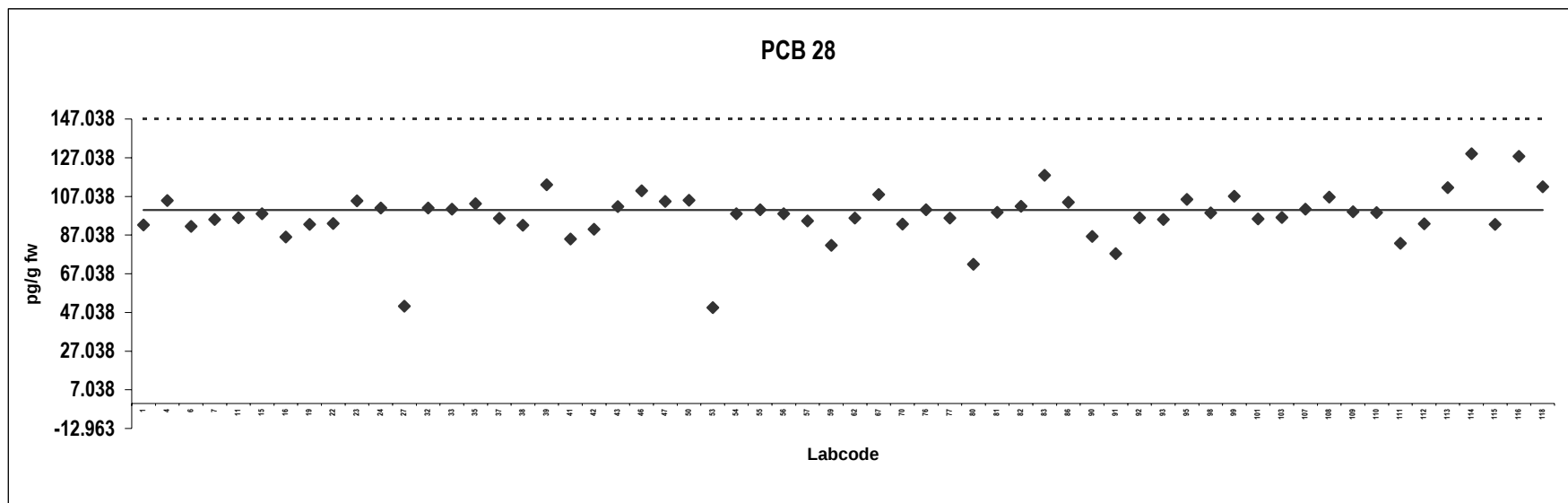
Analyte solution

Congener: PCB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	92		98	99	
4	105		99	107	
6	92		101	95	
7	95		103	96	
11	96		107	100	
15	98		108	107	
16	86		109	99	
19	93		110	99	
22	93		111	83	
23	105		112	93	
24	101		113	112	
27	50		114	129	
32	101		115	93	
33	101		116	128	
35	103		118	112	
37	96				
38	92				
39	113				
41	85				
42	90				
43	102				
46	110				
47	104				
50	105				
53	50				
54	98				
55	100				
56	98				
57	94				
59	82				
62	96				
67	108				
70	93				
76	100				
77	96				
80	72				
81	99				
82	102				
83	118				
86	104				
90	86				
91	77				
92	96				
93	95				
95	105				

Consensus statistics

Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	97
Standard deviation, pg/g	13
Relative standard deviation, %	14
No. of values reported	60
No. of values removed	0
No. of reported non-detects	0



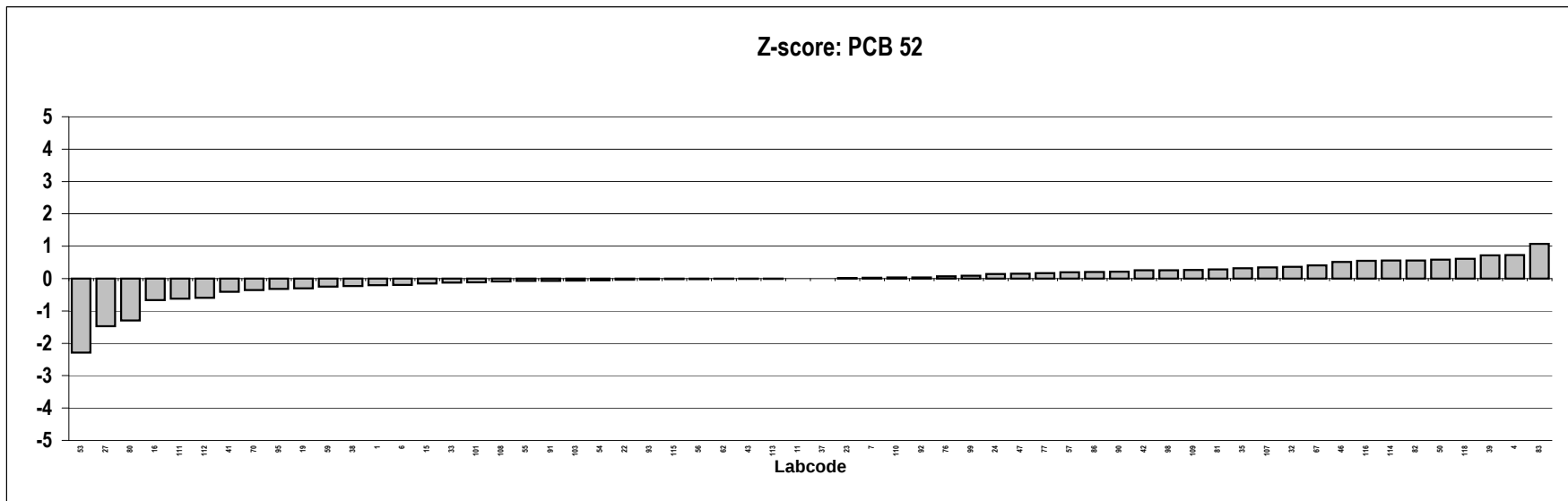
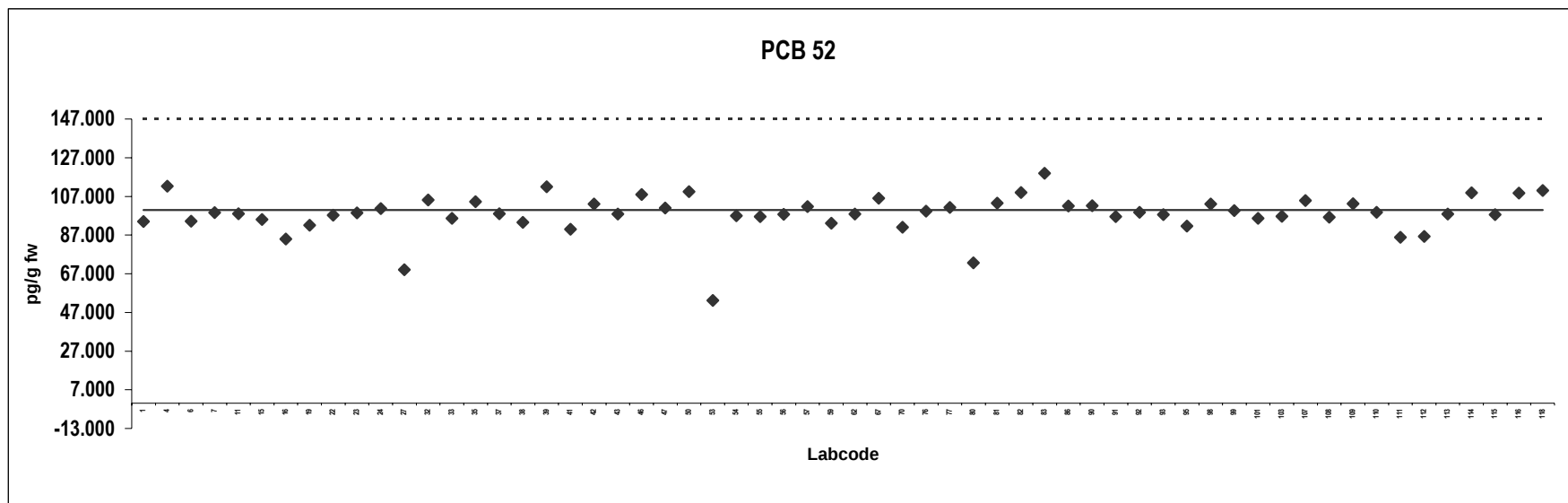
Analyte solution

Congener: PCB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	94		98	103	
4	112		99	100	
6	94		101	96	
7	99		103	97	
11	98		107	105	
15	95		108	96	
16	85		109	103	
19	92		110	99	
22	97		111	86	
23	98		112	86	
24	101		113	98	
27	69		114	109	
32	105		115	98	
33	96		116	109	
35	104		118	110	
37	98				
38	94				
39	112				
41	90				
42	103				
43	98				
46	108				
47	101				
50	110				
53	53				
54	97				
55	97				
56	98				
57	102				
59	93				
62	98				
67	106				
70	91				
76	99				
77	101				
80	73				
81	104				
82	109				
83	119				
86	102				
90	102				
91	97				
92	99				
93	98				
95	92				

Consensus statistics

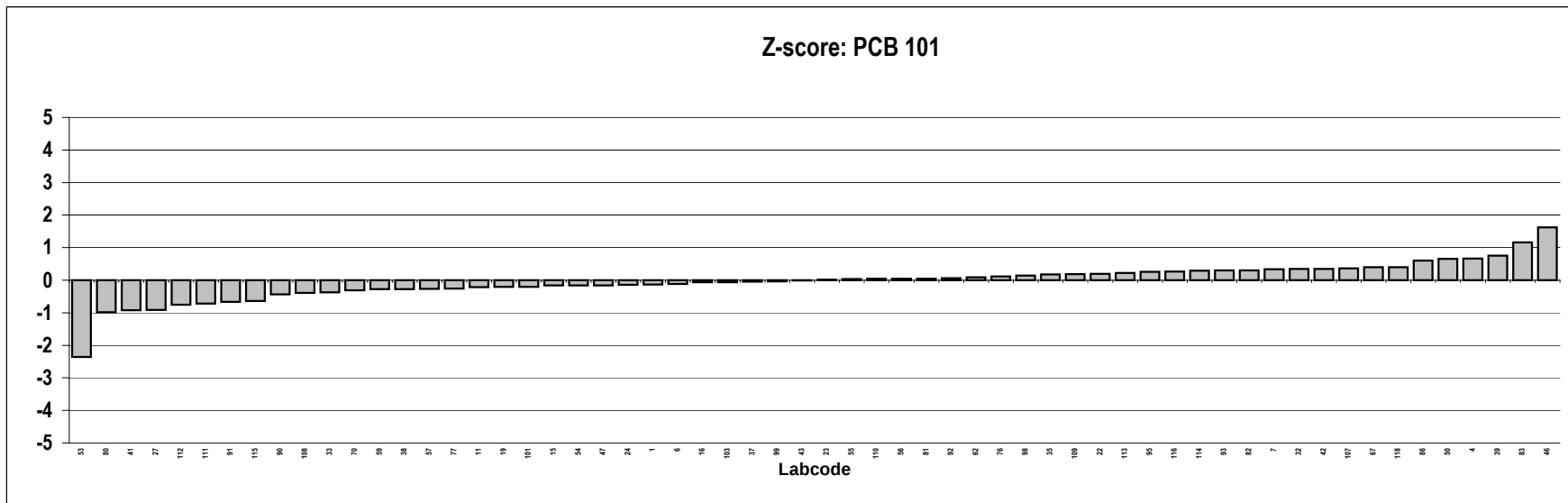
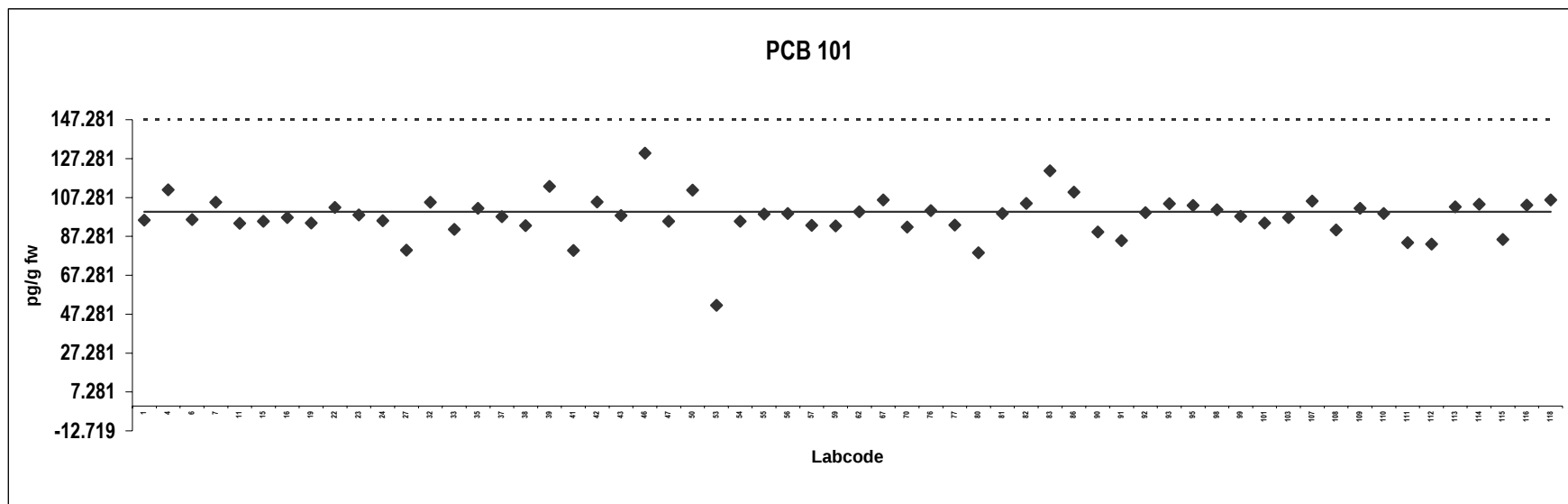
Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	98
Standard deviation, pg/g	10
Relative standard deviation, %	10
No. of values reported	60
No. of values removed	0
No. of reported non-detects	0



Analyte solution
Congener: PCB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	96		98	101	
4	111		99	98	
6	96		101	94	
7	105		103	97	
11	94		107	105	
15	95		108	91	
16	97		109	102	
19	94		110	99	
22	102		111	84	
23	98		112	83	
24	95		113	102	
27	80		114	104	
32	105		115	86	
33	91		116	103	
35	102		118	106	
37	97				
38	93				
39	113				
41	80				
42	105				
43	98				
46	130				
47	95				
50	111				
53	52				
54	95				
55	99				
56	99				
57	93				
59	93				
62	100				
67	106				
70	92				
76	101				
77	93				
80	79				
81	99				
82	104				
83	121				
86	110				
90	90				
91	85				
92	99				
93	104				
95	103				

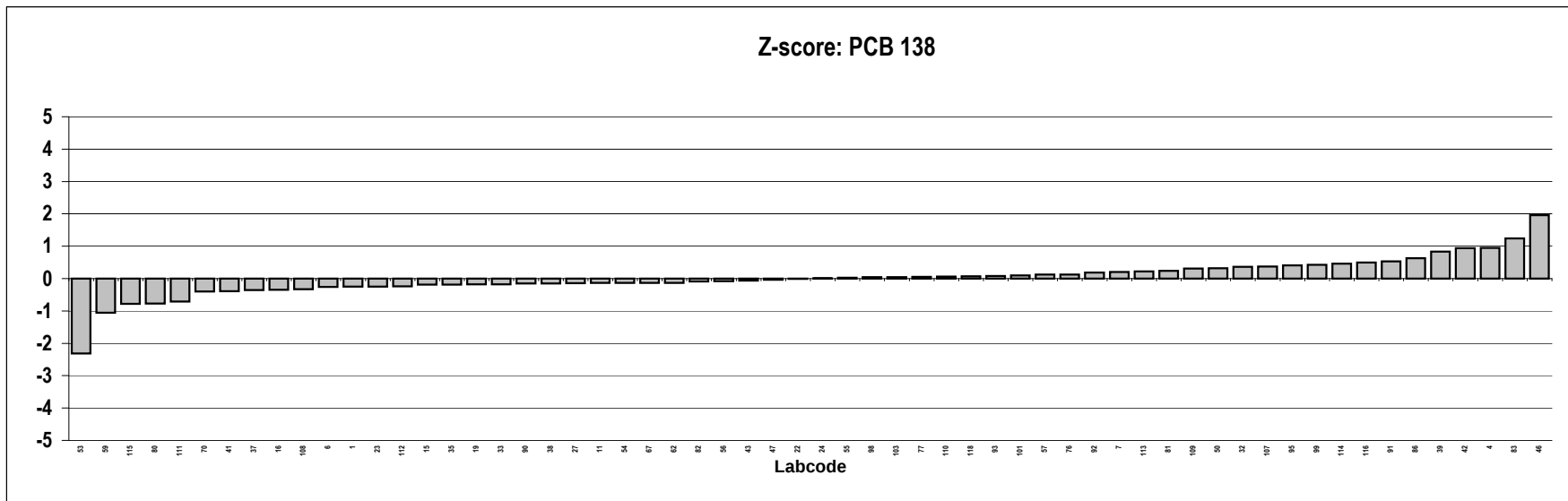
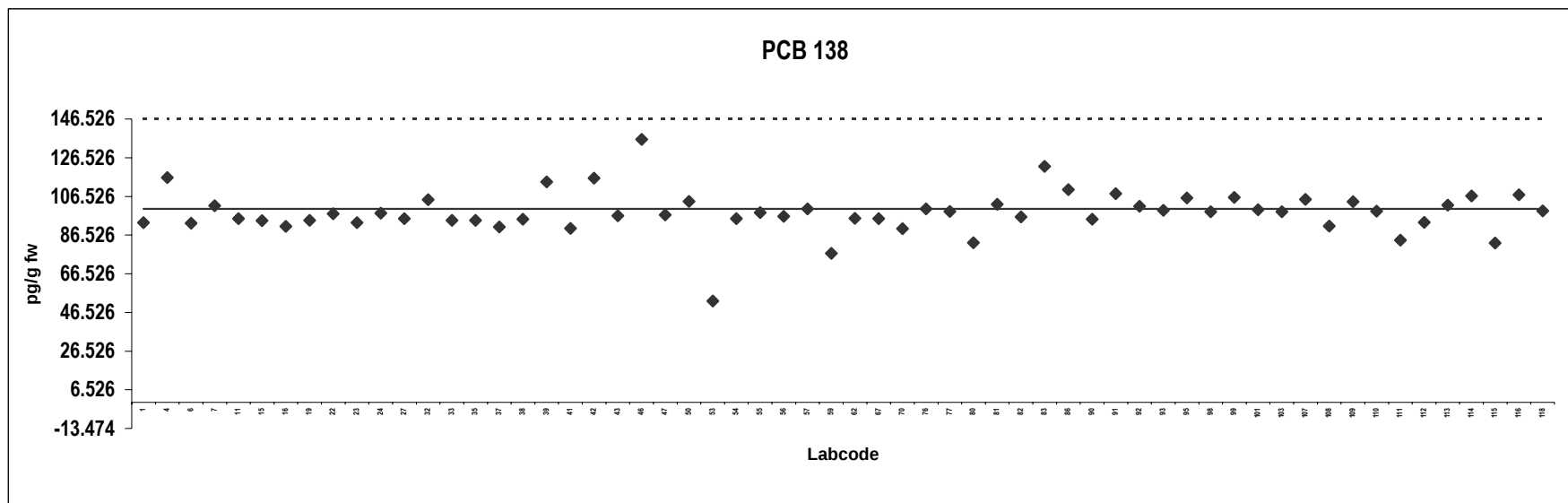
Consensus statistics	
Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	98
Standard deviation, pg/g	11
Relative standard deviation, %	11
No. of values reported	60
No. of values removed	0
No. of reported non-detects	0



Analyte solution
Congener: PCB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	93		98	99	
4	116		99	106	
6	93		101	100	
7	102		103	99	
11	95		107	105	
15	94		108	91	
16	91		109	104	
19	94		110	99	
22	98		111	84	
23	93		112	93	
24	98		113	102	
27	95		114	107	
32	105		115	82	
33	94		116	107	
35	94		118	99	
37	91				
38	95				
39	114				
41	90				
42	116				
43	97				
46	136				
47	97				
50	104				
53	52				
54	95				
55	98				
56	96				
57	100				
59	77				
62	95				
67	95				
70	90				
76	100				
77	99				
80	83				
81	102				
82	96				
83	122				
86	110				
90	95				
91	108				
92	101				
93	99				
95	106				

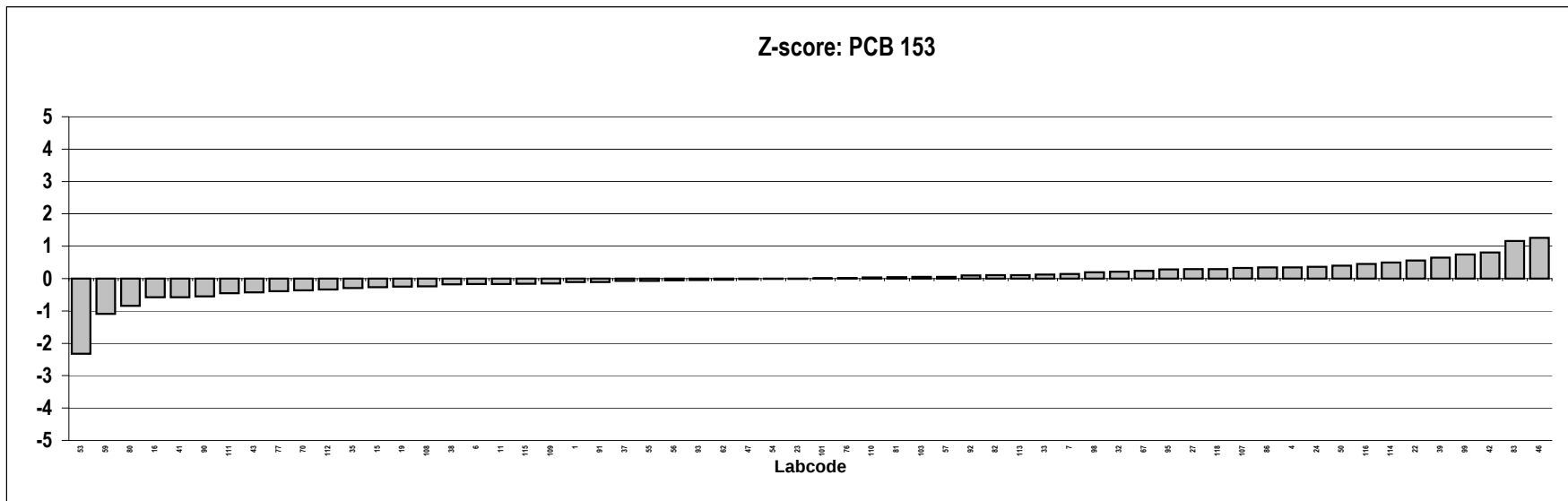
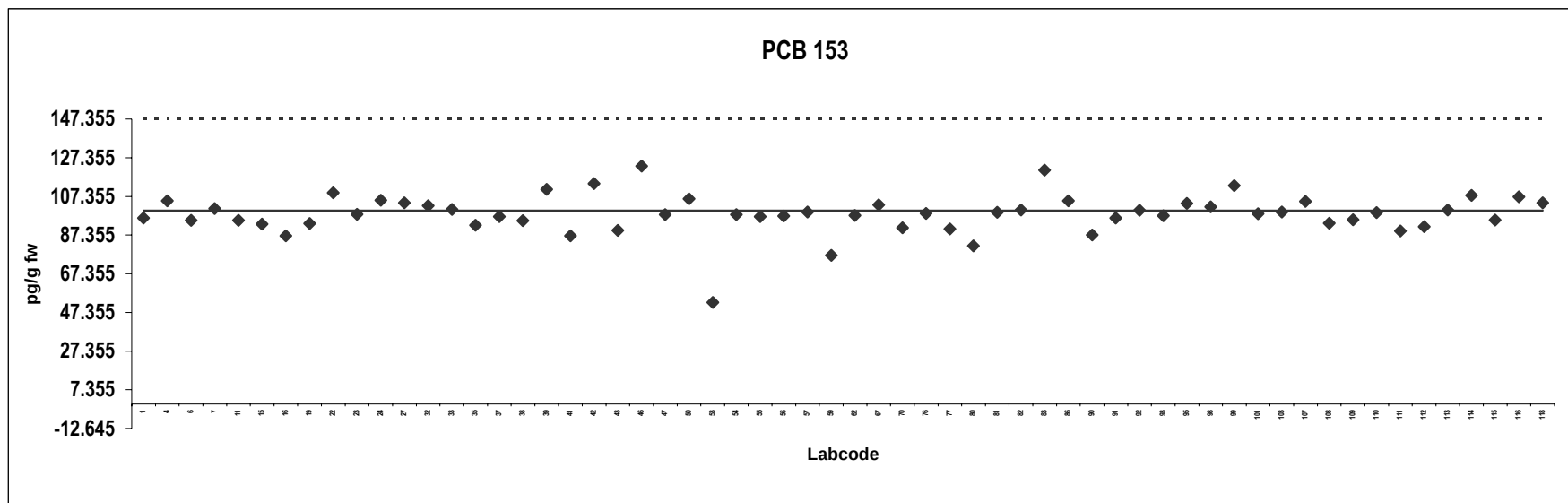
Consensus statistics	
Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	98
Standard deviation, pg/g	11
Relative standard deviation, %	11
No. of values reported	60
No. of values removed	0
No. of reported non-detects	0



Analyte solution
Congener: PCB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	96		98	102	
4	105		99	113	
6	95		101	98	
7	101		103	99	
11	95		107	105	
15	93		108	93	
16	87		109	95	
19	93		110	99	
22	109		111	89	
23	98		112	92	
24	105		113	100	
27	104		114	108	
32	102		115	95	
33	101		116	107	
35	92		118	104	
37	97				
38	95				
39	111				
41	87				
42	114				
43	90				
46	123				
47	98				
50	106				
53	53				
54	98				
55	97				
56	97				
57	99				
59	77				
62	98				
67	103				
70	91				
76	99				
77	90				
80	82				
81	99				
82	100				
83	121				
86	105				
90	87				
91	96				
92	100				
93	97				
95	104				

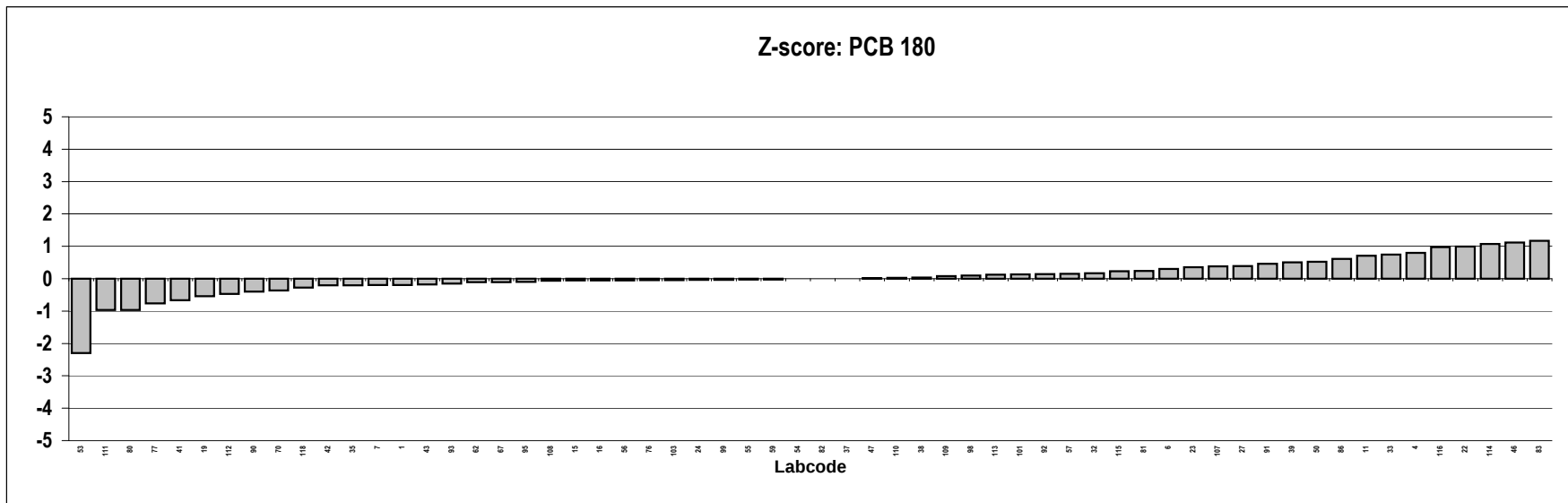
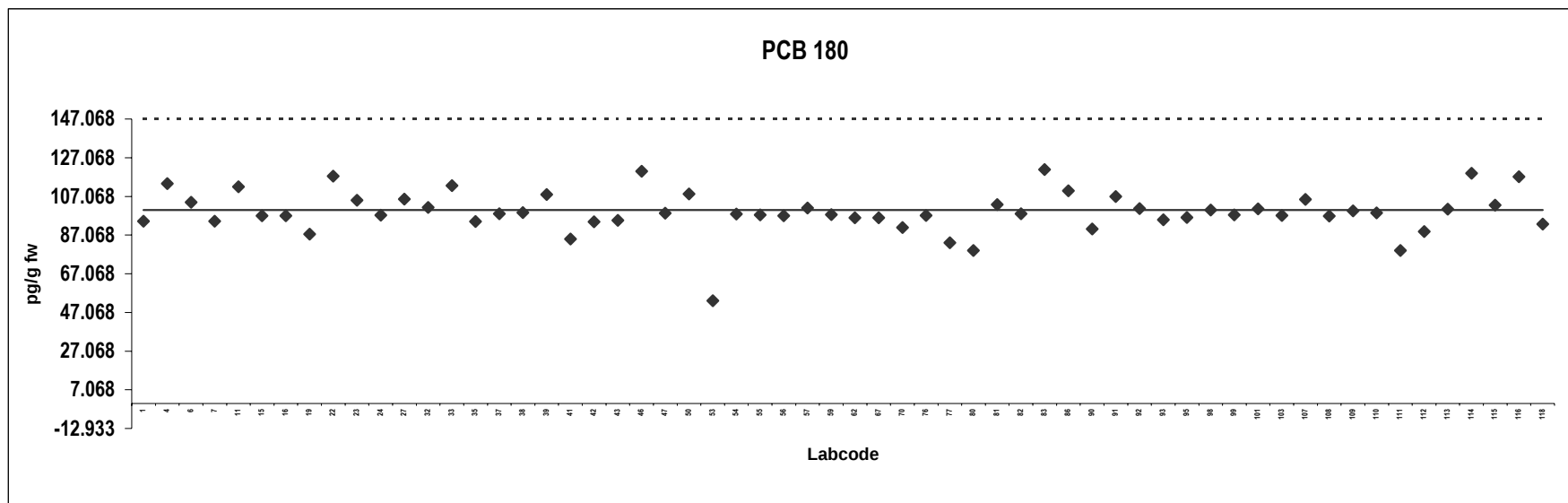
Consensus statistics	
Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	98
Standard deviation, pg/g	10
Relative standard deviation, %	10
No. of values reported	60
No. of values removed	0
No. of reported non-detects	0



Analyte solution
Congener: PCB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	94		98	100	
4	114		99	97	
6	104		101	101	
7	94		103	97	
11	112		107	105	
15	97		108	97	
16	97		109	100	
19	88		110	99	
22	118		111	79	
23	105		112	89	
24	97		113	100	
27	106		114	119	
32	101		115	103	
33	113		116	117	
35	94		118	93	
37	98				
38	99				
39	108				
41	85				
42	94				
43	95				
46	120				
47	98				
50	108				
53	53				
54	98				
55	98				
56	97				
57	101				
59	98				
62	96				
67	96				
70	91				
76	97				
77	83				
80	79				
81	103				
82	98				
83	121				
86	110				
90	90				
91	107				
92	101				
93	95				
95	96				

Consensus statistics	
Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	99
Standard deviation, pg/g	11
Relative standard deviation, %	11
No. of values reported	60
No. of values removed	0
No. of reported non-detects	0



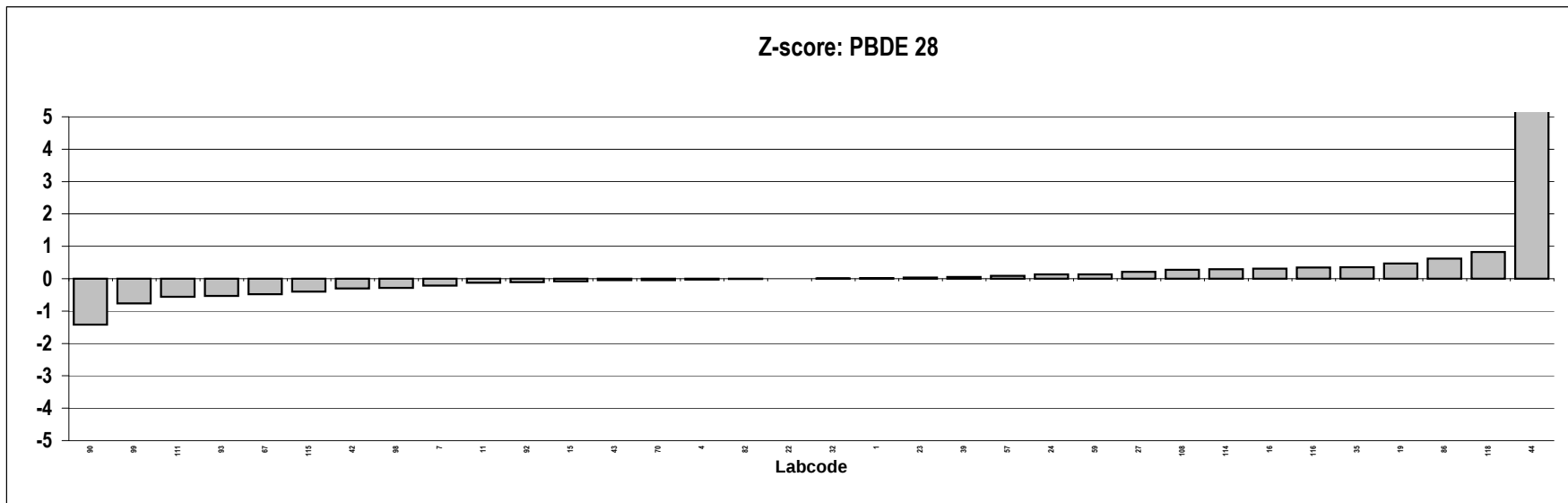
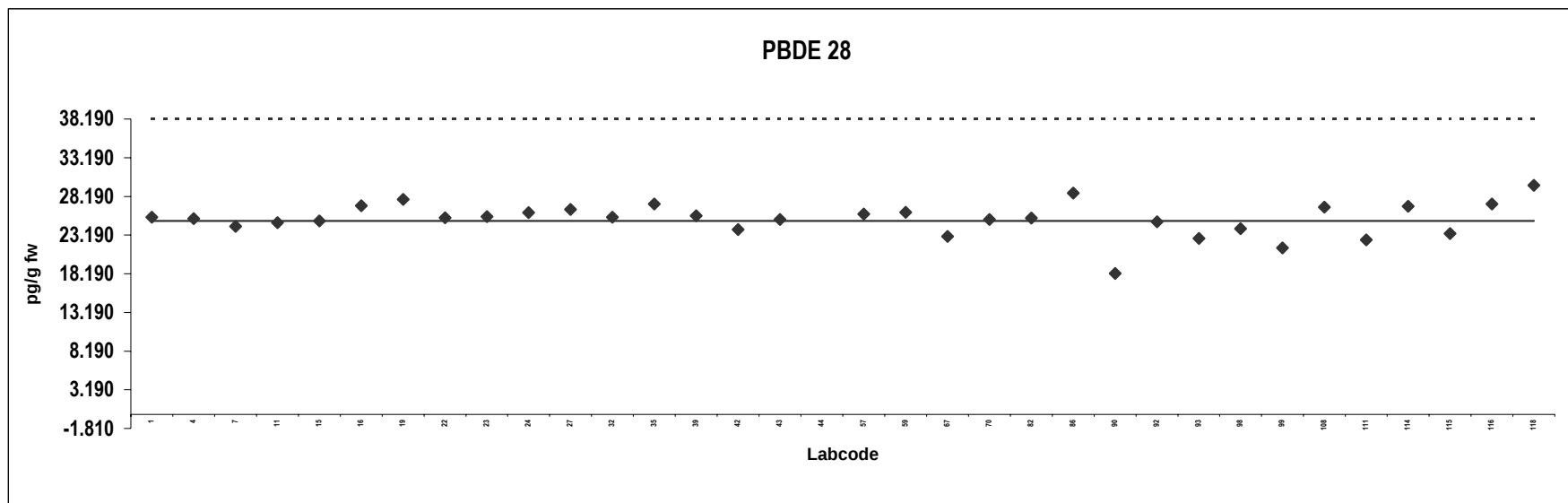
Analyte solution

Congener: PBDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	26	Outlier			
4	25				
7	24				
11	25				
15	25				
16	27				
19	28				
22	25				
23	26				
24	26				
27	27				
32	25				
35	27				
39	26				
42	24				
43	25				
44	24928				
57	26				
59	26				
67	23				
70	25				
82	25				
86	29				
90	18				
92	25				
93	23				
98	24				
99	22				
108	27				
111	23				
114	27				
115	23				
116	27				
118	30				

Consensus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.1
Relative standard deviation, %	8.5
No. of values reported	34
No. of values removed	1
No. of reported non-detects	0

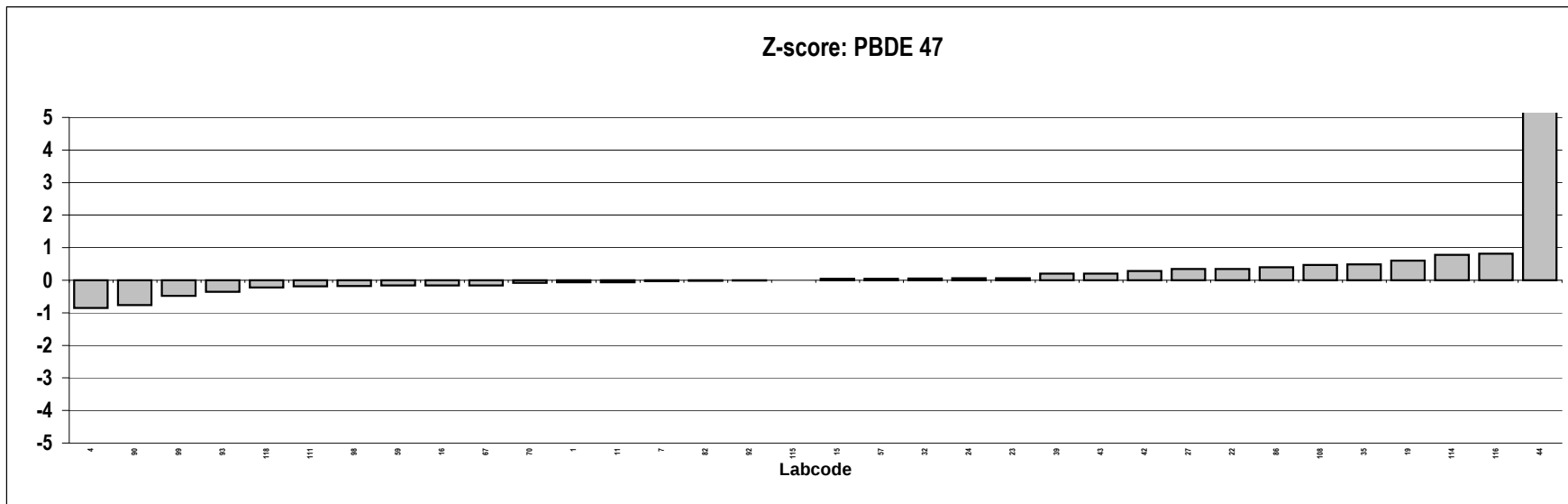
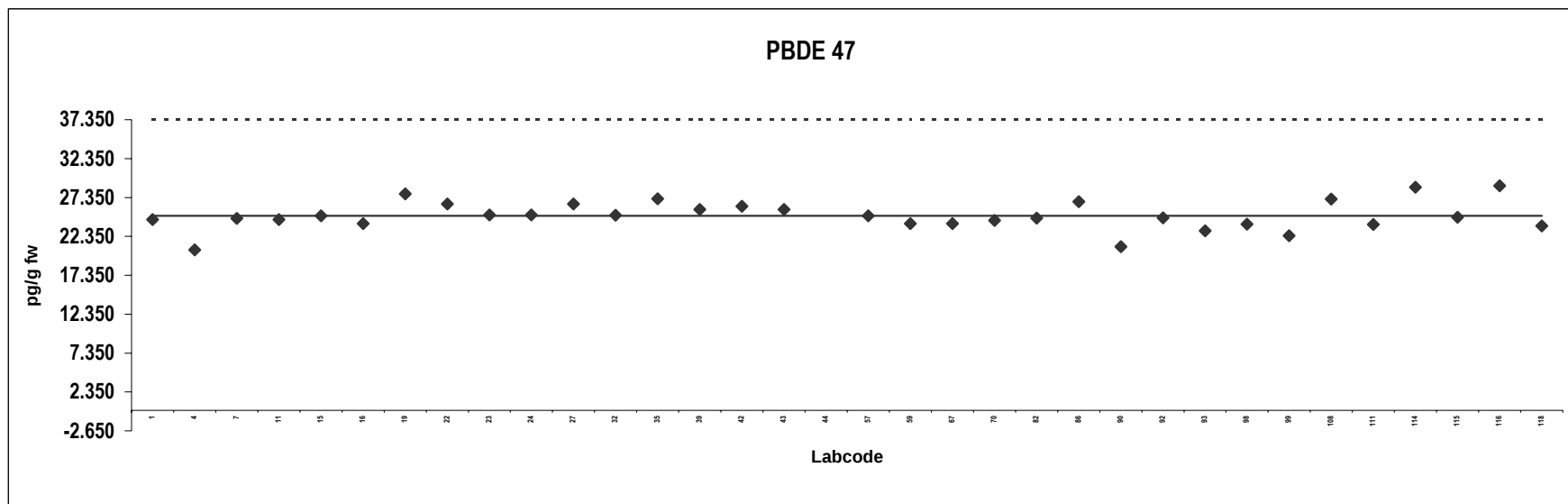


Analyte solution

Congener: PBDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	25	Outlier			
4	21				
7	25				
11	25				
15	25				
16	24				
19	28				
22	27				
23	25				
24	25				
27	27				
32	25				
35	27				
39	26				
42	26				
43	26				
44	24505				
57	25				
59	24				
67	24				
70	24				
82	25				
86	27				
90	21				
92	25				
93	23				
98	24				
99	22				
108	27				
111	24				
114	29				
115	25				
116	29				
118	24				

Consensus statistics	
Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	1.9
Relative standard deviation, %	7.4
No. of values reported	34
No. of values removed	1
No. of reported non-detects	0

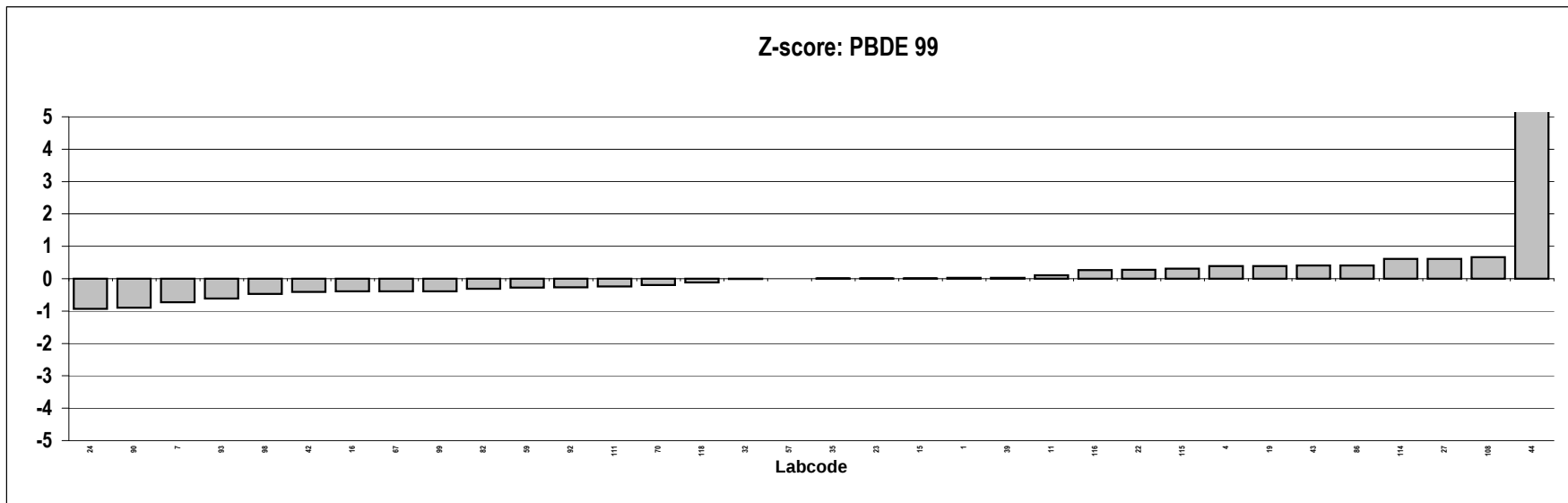
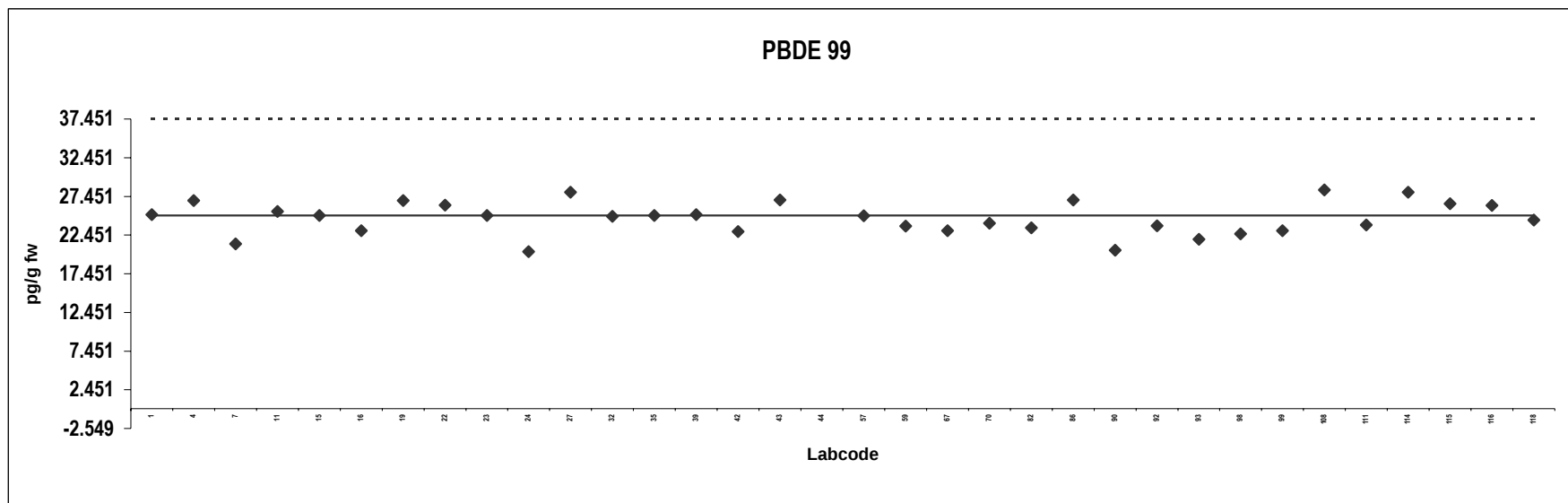


Analyte solution

Congener: PBDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	25	Outlier			
4	27				
7	21				
11	26				
15	25				
16	23				
19	27				
22	26				
23	25				
24	20				
27	28				
32	25				
35	25				
39	25				
42	23				
43	27				
44	23103				
57	25				
59	24				
67	23				
70	24				
82	23				
86	27				
90	20				
92	24				
93	22				
98	23				
99	23				
108	28				
111	24				
114	28				
115	27				
116	26				
118	24				

Consensus statistics	
Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.1
Relative standard deviation, %	8.6
No. of values reported	34
No. of values removed	1
No. of reported non-detects	0



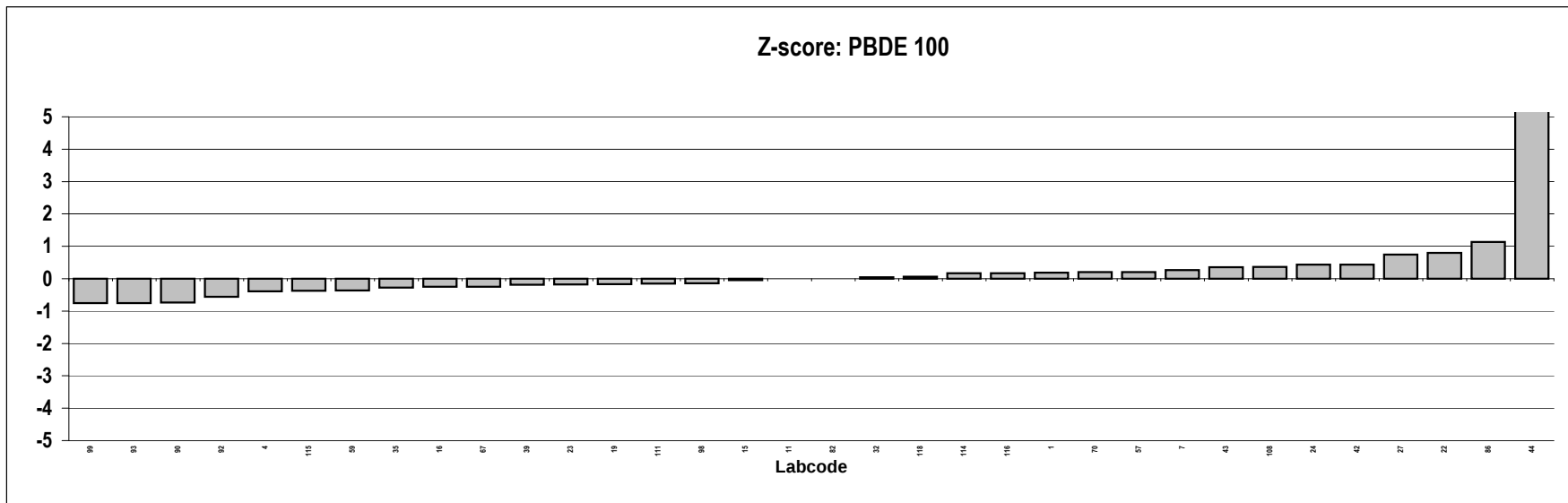
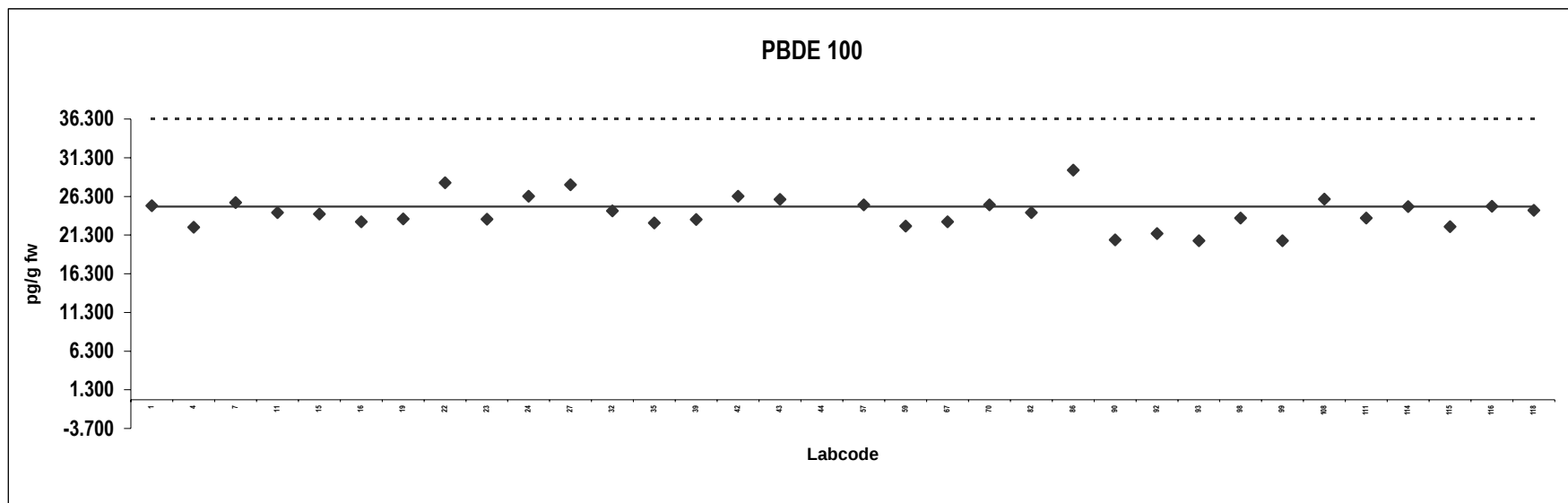
Analyte solution

Congener: PBDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	25	Outlier			
4	22				
7	26				
11	24				
15	24				
16	23				
19	23				
22	28				
23	23				
24	26				
27	28				
32	24				
35	23				
39	23				
42	26				
43	26				
44	23832				
57	25				
59	22				
67	23				
70	25				
82	24				
86	30				
90	21				
92	21				
93	21				
98	24				
99	21				
108	26				
111	23				
114	25				
115	22				
116	25				
118	25				

Consensus statistics

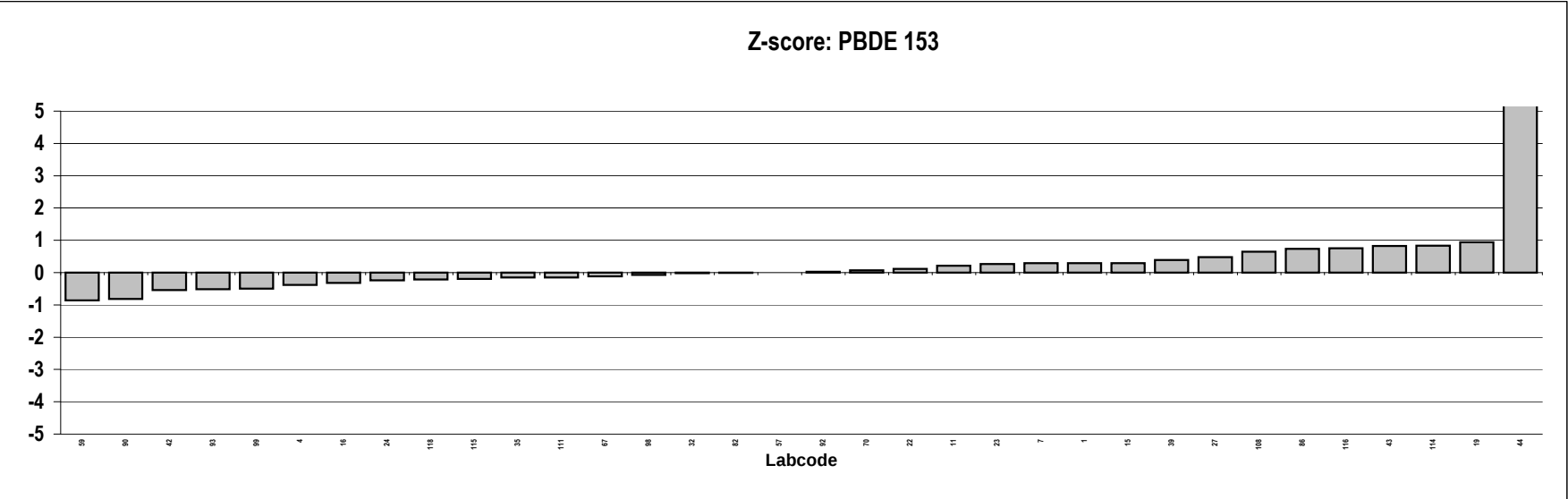
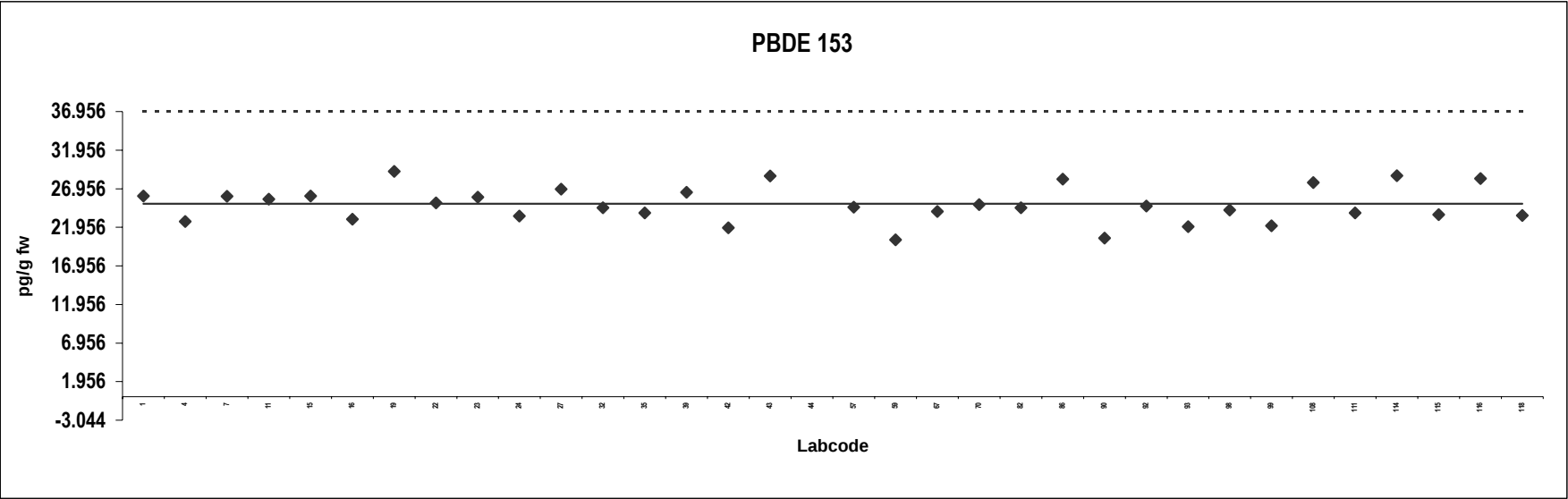
Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.1
Relative standard deviation, %	8.7
No. of values reported	34
No. of values removed	1
No. of reported non-detects	0



Analyte solution
Congener: PBDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	26	Outlier			
4	23				
7	26				
11	26				
15	26				
16	23				
19	29				
22	25				
23	26				
24	23				
27	27				
32	24				
35	24				
39	27				
42	22				
43	29				
44	23818				
57	25				
59	20				
67	24				
70	25				
82	25				
86	28				
90	21				
92	25				
93	22				
98	24				
99	22				
108	28				
111	24				
114	29				
115	24				
116	28				
118	24				

Consensus statistics	
Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.3
Relative standard deviation, %	9.3
No. of values reported	34
No. of values removed	1
No. of reported non-detects	0



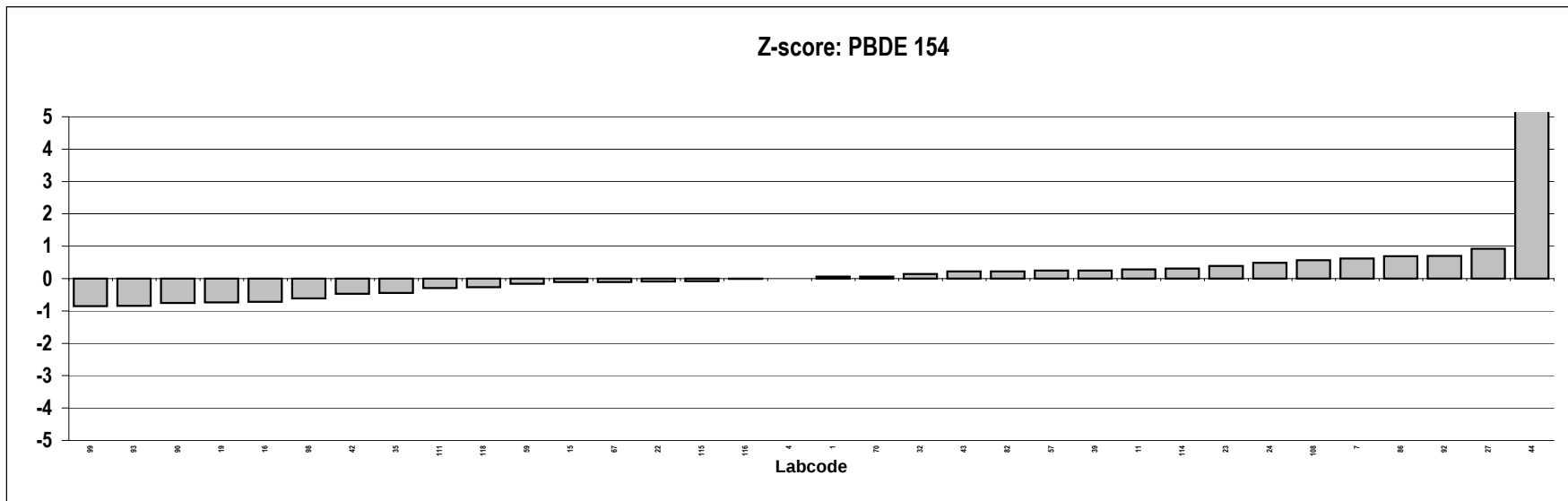
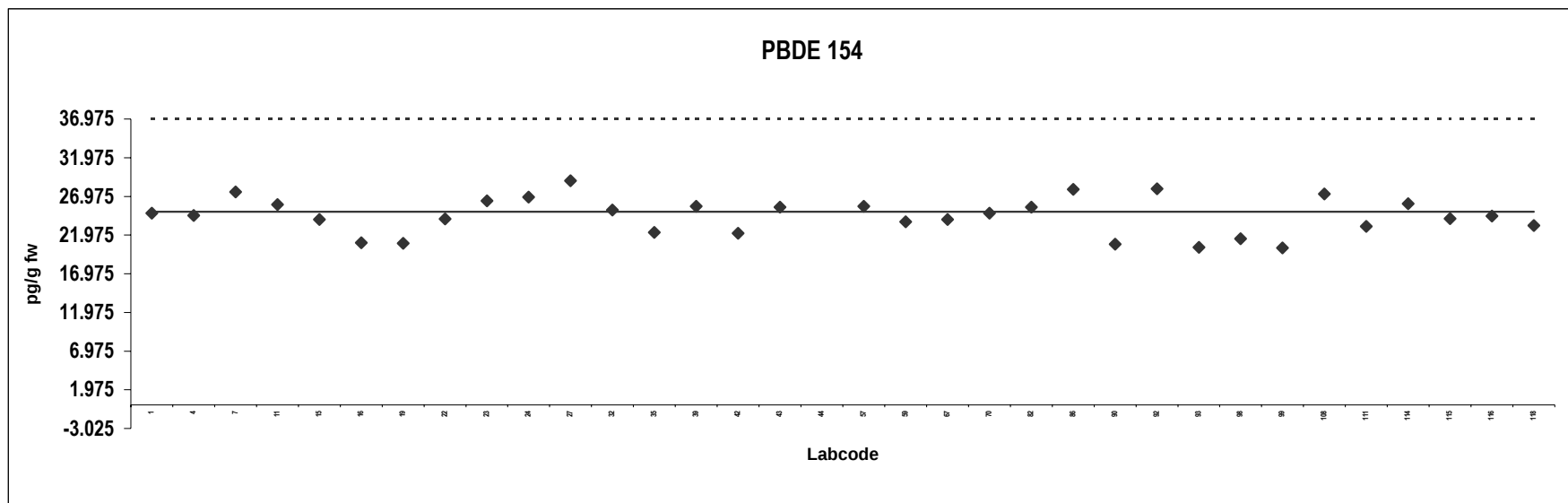
Analyte solution

Congener: PBDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	25	Outlier			
4	25				
7	28				
11	26				
15	24				
16	21				
19	21				
22	24				
23	26				
24	27				
27	29				
32	25				
35	22				
39	26				
42	22				
43	26				
44	23497				
57	26				
59	24				
67	24				
70	25				
82	26				
86	28				
90	21				
92	28				
93	20				
98	22				
99	20				
108	27				
111	23				
114	26				
115	24				
116	24				
118	23				

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, %	10
No. of values reported	34
No. of values removed	1
No. of reported non-detects	0

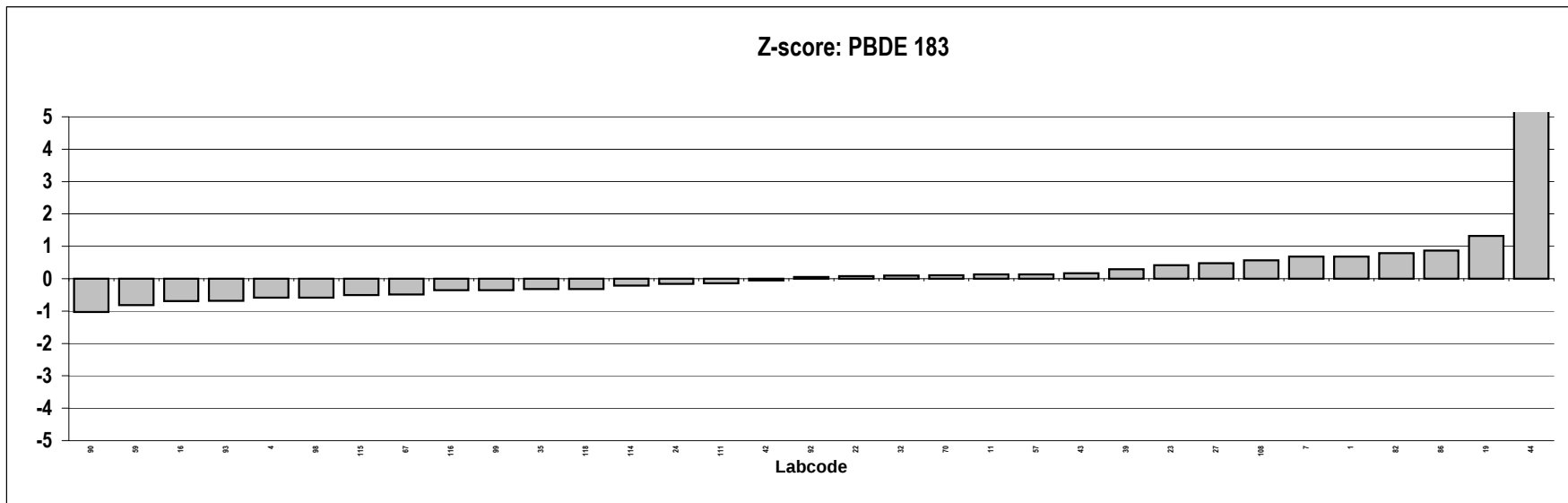
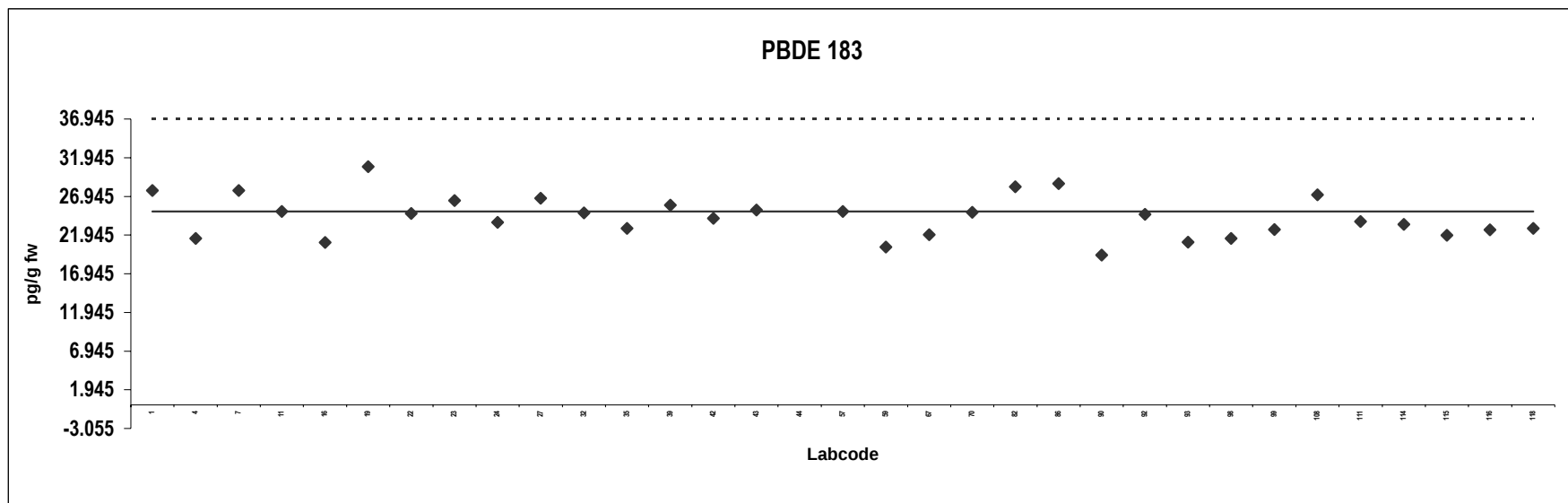


Analyte solution

Congener: PBDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	28	Outlier			
4	22				
7	28				
11	25				
16	21				
19	31				
22	25				
23	26				
24	24				
27	27				
32	25				
35	23				
39	26				
42	24				
43	25				
44	20992				
57	25				
59	20				
67	22				
70	25				
82	28				
86	29				
90	19				
92	25				
93	21				
98	22				
99	23				
108	27				
111	24				
114	23				
115	22				
116	23				
118	23				

Consensus statistics	
Consensus median, pg/g	24
Median all values pg/g	25
Consensus mean, pg/g	24
Standard deviation, pg/g	2.7
Relative standard deviation, %	11
No. of values reported	33
No. of values removed	1
No. of reported non-detects	0



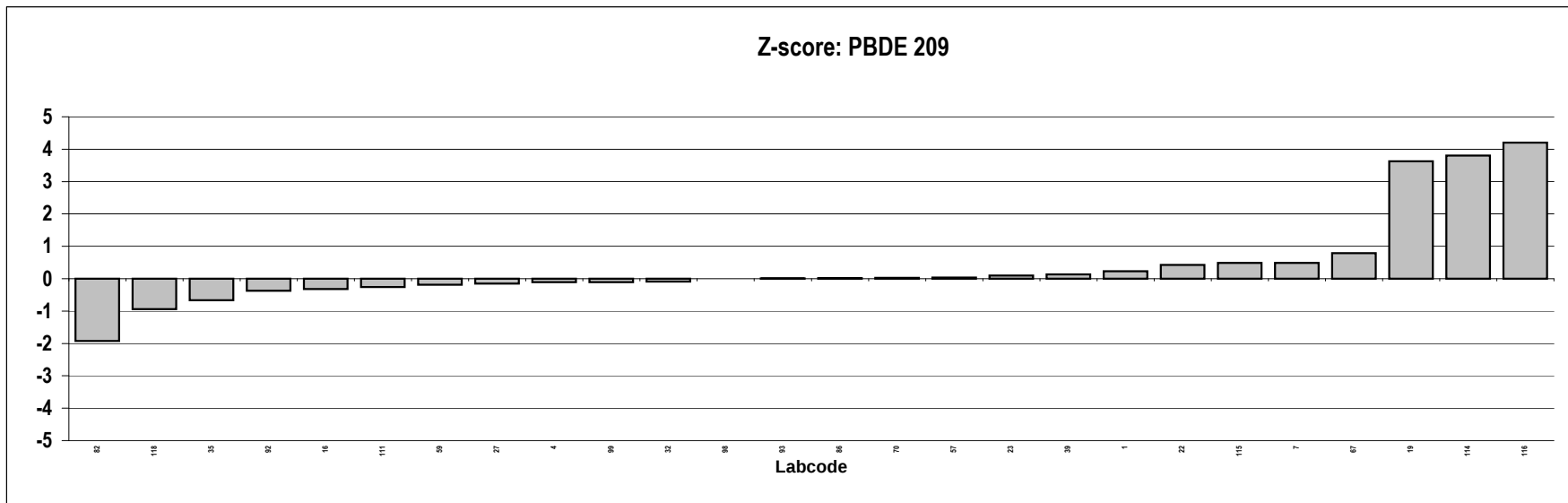
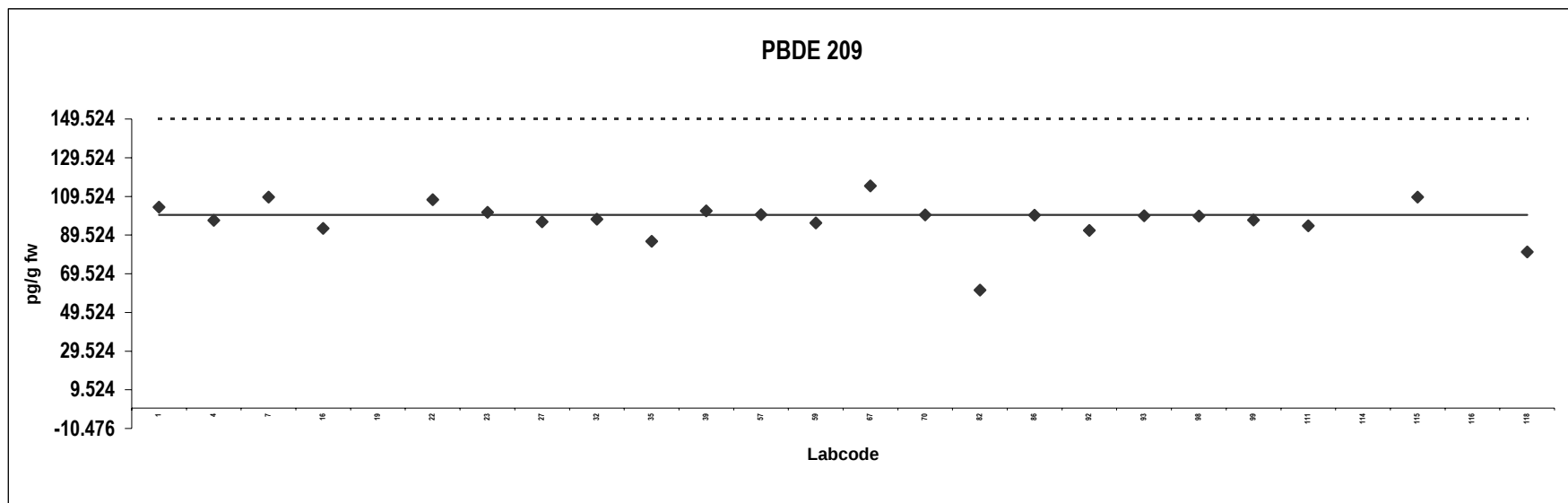
Analyte solution

Congener: PBDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	104	Outlier			
4	97				
7	109				
16	93				
19	171				
22	108				
23	101				
27	96				
32	98				
35	86				
39	102				
57	100				
59	96				
67	115				
70	100				
82	61				
86	100				
92	92				
93	100	Outlier			
98	99				
99	97				
111	94				
114	175				
115	109				
116	183	Outlier			
118	81				

Consensus statistics

Consensus median, pg/g	99
Median all values pg/g	100
Consensus mean, pg/g	97
Standard deviation, pg/g	11
Relative standard deviation, %	11
No. of values reported	26
No. of values removed	3
No. of reported non-detects	0



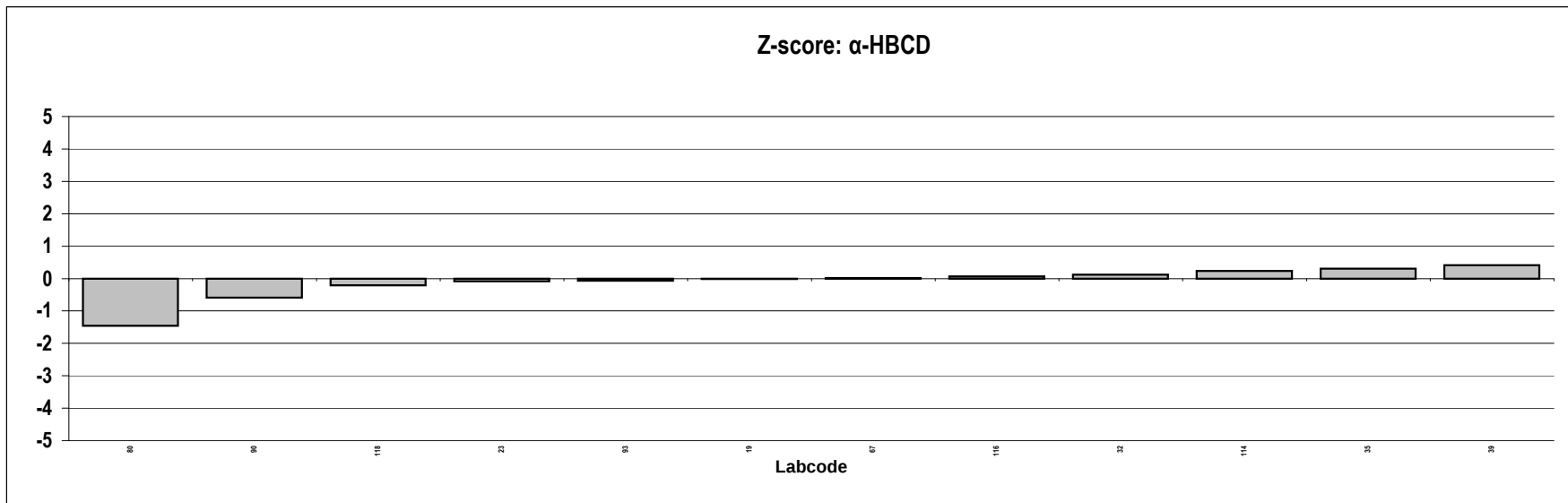
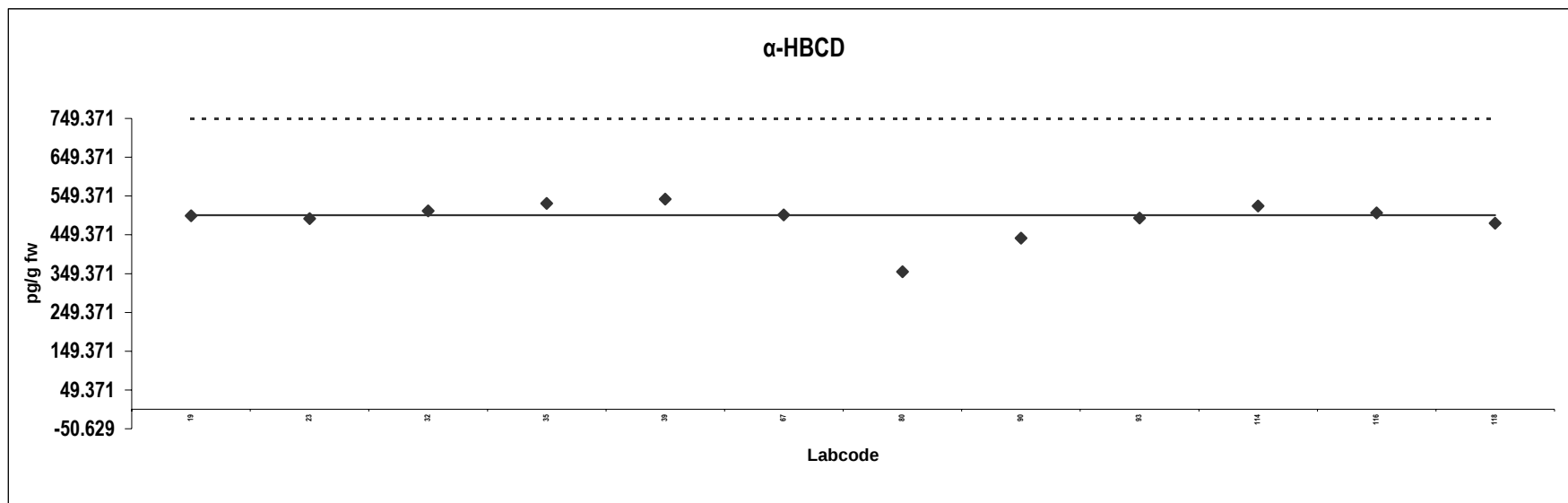
Analyte solution

Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
19	498				
23	491				
32	511				
35	530				
39	541				
67	501				
80	354				
90	441				
93	493				
114	523				
116	506				
118	479				

Consensus statistics

Consensus median, pg/g	500
Median all values pg/g	500
Consensus mean, pg/g	489
Standard deviation, pg/g	50
Relative standard deviation, %	10
No. of values reported	12
No. of values removed	0
No. of reported non-detects	0



Appendix 2:

Presentation of results
for beef-2015

Appendix 2: Presentation of results: Beef-2015

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:

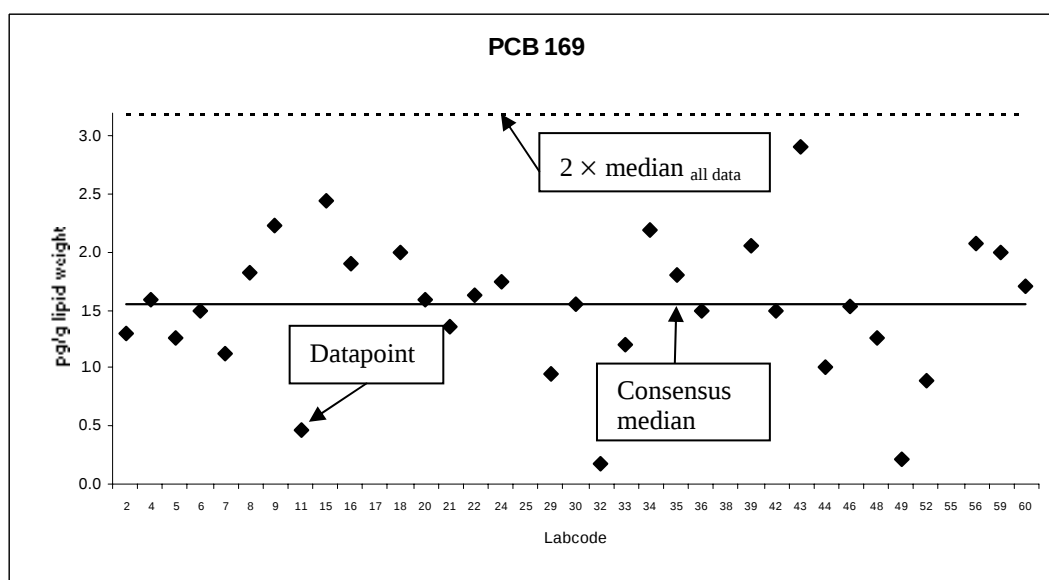
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding $2 \times$ this median were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

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

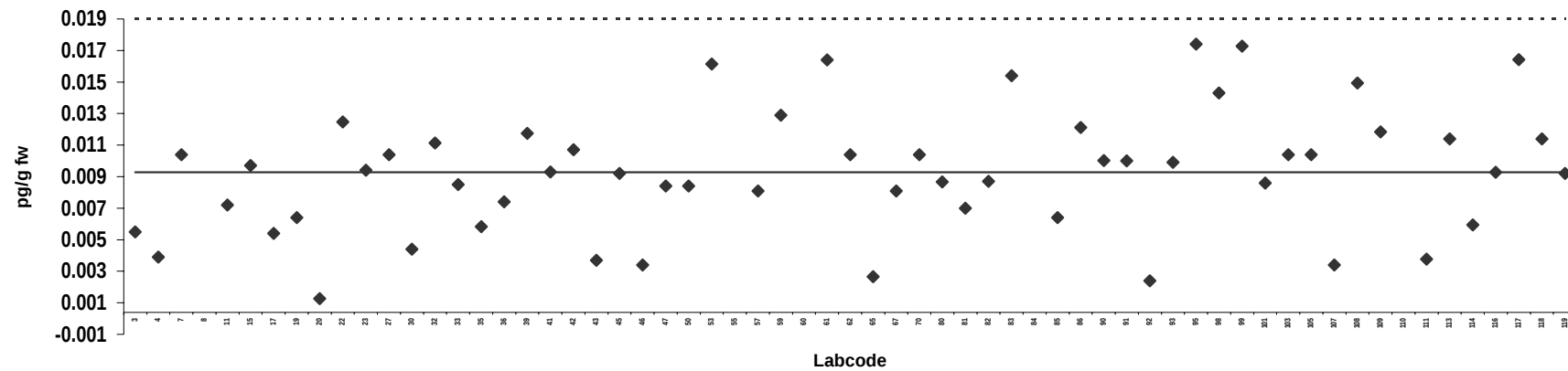
where x = reported value; X = assigned value (consensus); σ = target value for standard deviation. A σ of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of $\pm 20\%$ from the consensus value.

Beef
Congener: 2,3,7,8 TCDD

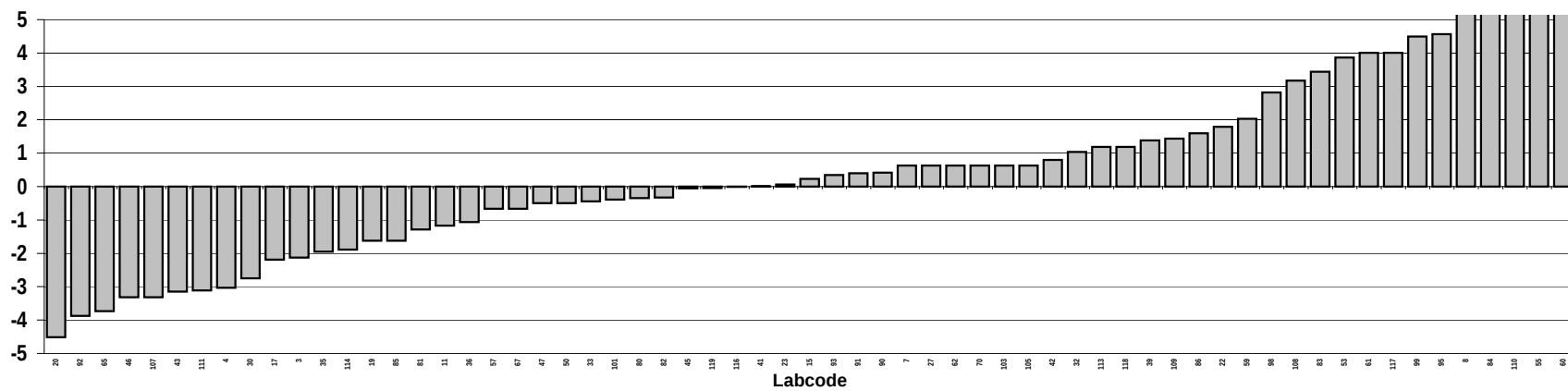
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.0051		93	0.0095	
4	0.0035	ND	95	0.017	ND
7	0.010	ND	98	0.014	
8	0.020	Outlier,ND	99	0.017	ND
11	0.0068		101	0.0082	
15	0.0093	ND	103	0.010	
17	0.0050	ND	105	0.010	ND
19	0.0060	ND	107	0.0030	
20	0.00087	ND	108	0.015	ND
22	0.012		109	0.011	
23	0.0090		110	0.022	Outlier
27	0.010		111	0.0034	ND
30	0.0040	ND	113	0.011	
32	0.011		114	0.0055	
33	0.0081		116	0.0089	
35	0.0054		117	0.016	ND
36	0.0070		118	0.011	
39	0.011		119	0.0088	
41	0.0089				
42	0.010				
43	0.0033				
45	0.0088				
46	0.0030				
47	0.0080				
50	0.0080				
53	0.016				
55	0.034	Outlier			
57	0.0077				
59	0.013				
60	0.061	Outlier,ND			
61	0.016				
62	0.010				
65	0.0023	ND			
67	0.0077				
70	0.010				
80	0.0083				
81	0.0066	ND			
82	0.0083				
83	0.015	ND			
84	0.021	Outlier			
85	0.0060				
86	0.012				
90	0.0096				
91	0.0096				
92	0.0020	ND			

Consensus statistics	
Consensus median, pg/g	0.0089
Median all values pg/g	0.0093
Consensus mean, pg/g	0.0088
Standard deviation, pg/g	0.0039
Relative standard deviation, %	44
No. of values reported	63
No. of values removed	5
No. of reported non-detects	19

2,3,7,8 TCDD



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



Beef

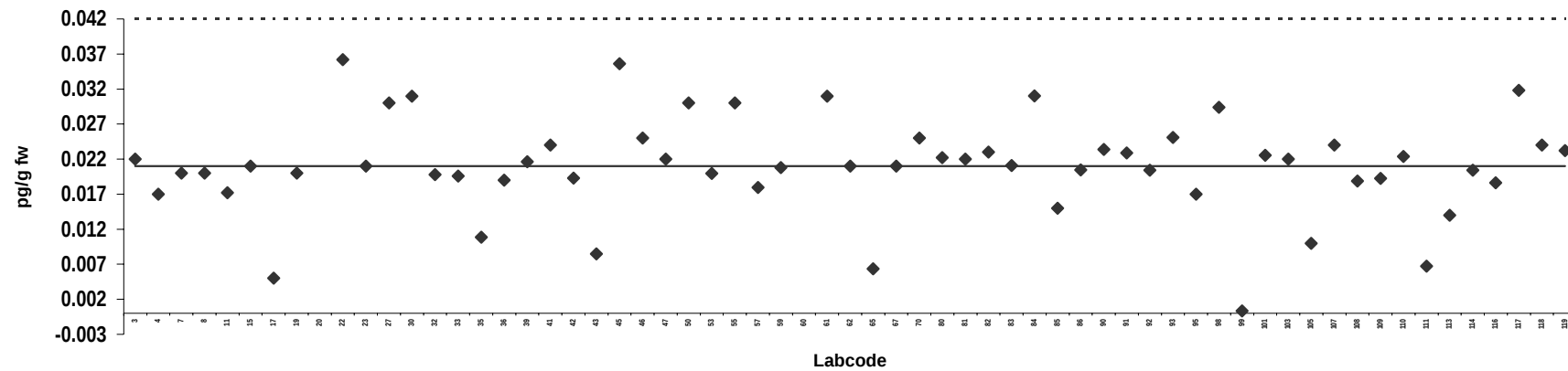
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.022		93	0.025	
4	0.017		95	0.017	ND
7	0.020		98	0.029	
8	0.020	ND	99	0.00033	ND
11	0.017		101	0.023	
15	0.021	ND	103	0.022	
17	0.0050	ND	105	0.010	ND
19	0.020		107	0.024	
20	0.053	Outlier	108	0.019	
22	0.036		109	0.019	
23	0.021		110	0.022	
27	0.030		111	0.0067	
30	0.031		113	0.014	
32	0.020		114	0.020	
33	0.020		116	0.019	
35	0.011		117	0.032	ND
36	0.019		118	0.024	
39	0.022		119	0.023	
41	0.024				
42	0.019				
43	0.0085				
45	0.036				
46	0.025				
47	0.022				
50	0.030				
53	0.020				
55	0.030				
57	0.018				
59	0.021				
60	0.066	Outlier,ND			
61	0.031				
62	0.021				
65	0.0063				
67	0.021				
70	0.025				
80	0.022				
81	0.022				
82	0.023				
83	0.021	ND			
84	0.031				
85	0.015				
86	0.020				
90	0.023				
91	0.023				
92	0.020				

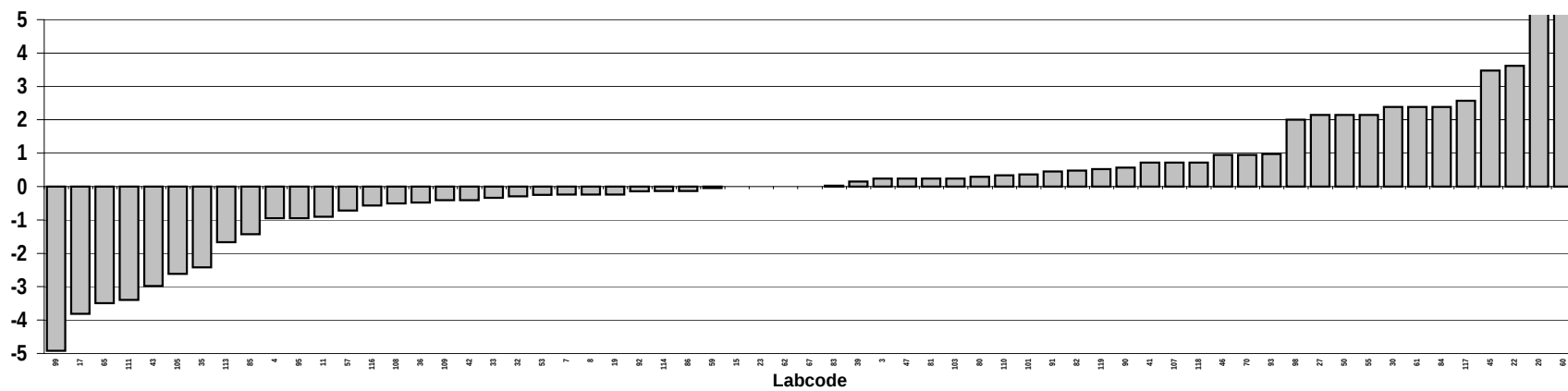
Consensus statistics

Consensus median, pg/g	0.021
Median all values pg/g	0.021
Consensus mean, pg/g	0.021
Standard deviation, pg/g	0.0070
Relative standard deviation, %	33
No. of values reported	63
No. of values removed	2
No. of reported non-detects	9

1,2,3,7,8 PeCDD



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

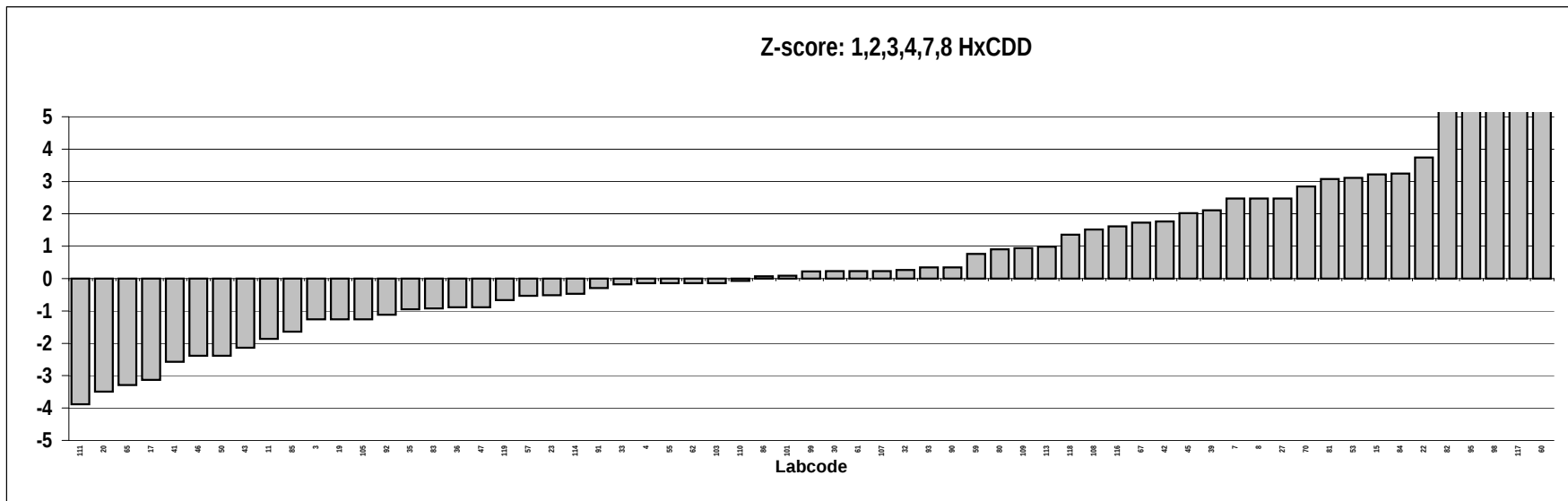
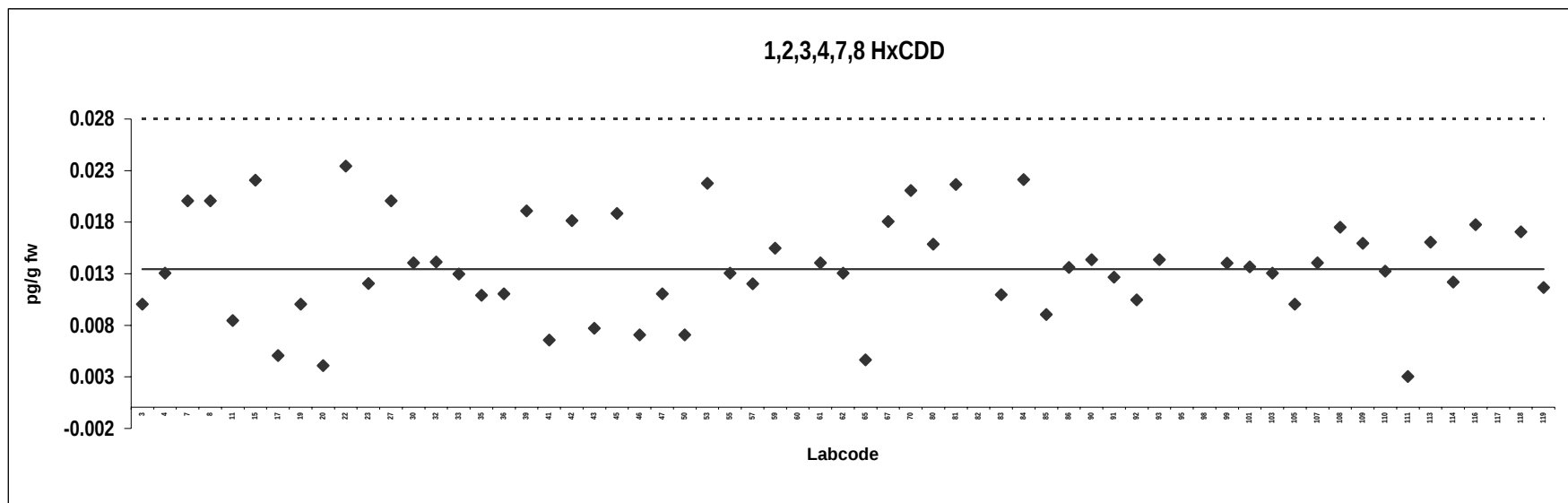


Beef

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.010		93	0.014	
4	0.013	ND	95	0.033	Outlier,ND
7	0.020		98	0.040	Outlier
8	0.020	ND	99	0.014	ND
11	0.0084	ND	101	0.014	
15	0.022	ND	103	0.013	
17	0.0050	ND	105	0.010	ND
19	0.010		107	0.014	
20	0.0040	ND	108	0.017	
22	0.023		109	0.016	
23	0.012		110	0.013	
27	0.020		111	0.0030	ND
30	0.014		113	0.016	
32	0.014		114	0.012	
33	0.013		116	0.018	
35	0.011		117	0.056	Outlier,ND
36	0.011		118	0.017	
39	0.019		119	0.012	
41	0.0065				
42	0.018				
43	0.0077				
45	0.019				
46	0.0070				
47	0.011				
50	0.0070				
53	0.022				
55	0.013				
57	0.012				
59	0.015				
60	0.32	Outlier			
61	0.014				
62	0.013				
65	0.0046				
67	0.018				
70	0.021				
80	0.016				
81	0.022				
82	0.032	Outlier			
83	0.011	ND			
84	0.022				
85	0.0090				
86	0.014				
90	0.014				
91	0.013				
92	0.010				

Consensus statistics	
Consensus median, pg/g	0.013
Median all values pg/g	0.014
Consensus mean, pg/g	0.014
Standard deviation, pg/g	0.0049
Relative standard deviation, %	36
No. of values reported	63
No. of values removed	5
No. of reported non-detects	12

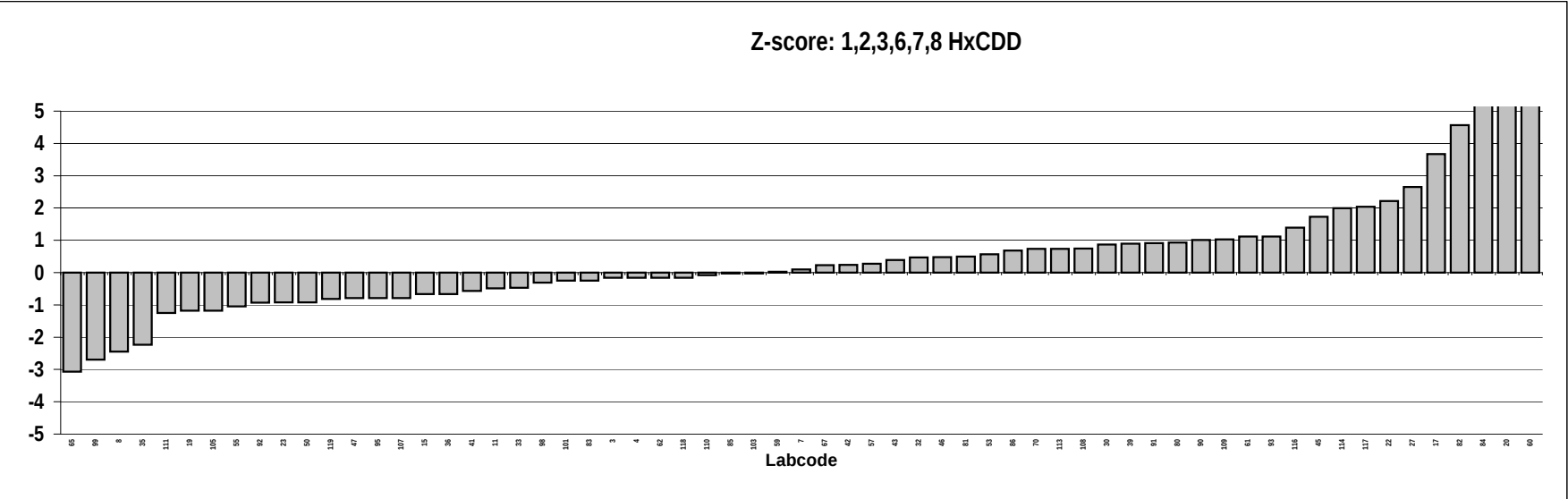
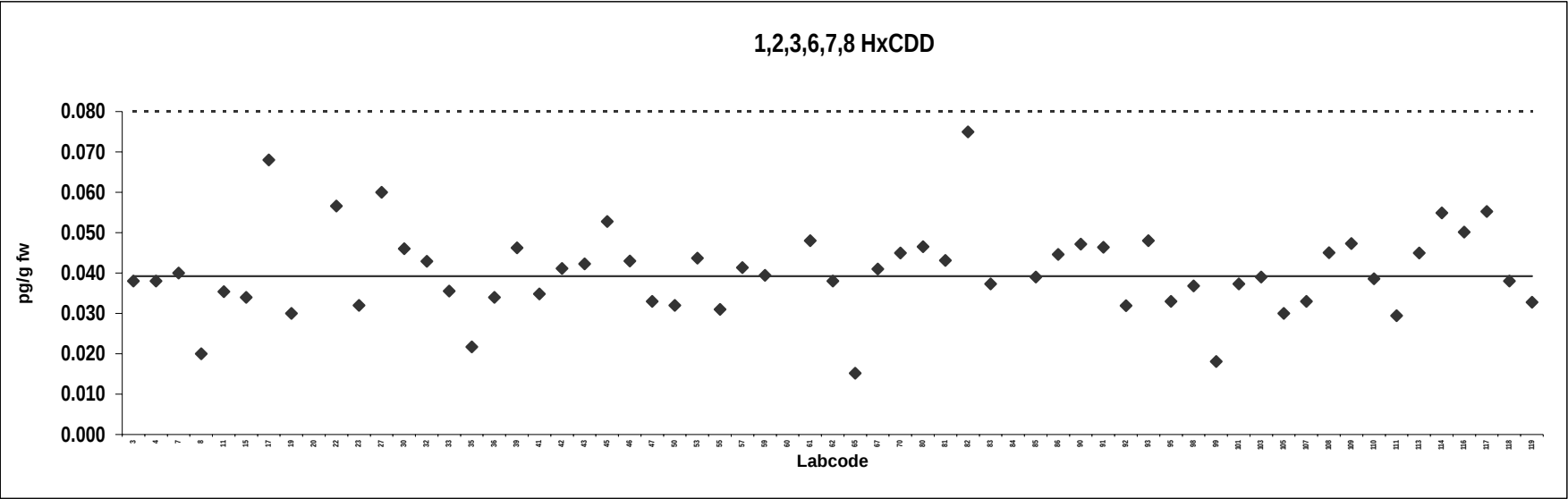


Beef

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.038	ND	93	0.048	ND
4	0.038		95	0.033	
7	0.040		98	0.037	
8	0.020		99	0.018	
11	0.035		101	0.037	
15	0.034	Outlier	103	0.039	ND
17	0.068		105	0.030	
19	0.030		107	0.033	
20	0.099		108	0.045	
22	0.057		109	0.047	
23	0.032		110	0.039	
27	0.060		111	0.029	
30	0.046		113	0.045	
32	0.043		114	0.055	
33	0.036		116	0.050	
35	0.022	Outlier	117	0.055	ND
36	0.034		118	0.038	
39	0.046		119	0.033	
41	0.035				
42	0.041				
43	0.042				
45	0.053				
46	0.043				
47	0.033				
50	0.032				
53	0.044	Outlier			
55	0.031				
57	0.041				
59	0.039				
60	0.24				
61	0.048				
62	0.038				
65	0.015				
67	0.041				
70	0.045				
80	0.047	Outlier			
81	0.043				
82	0.075				
83	0.037				
84	0.085				
85	0.039				
86	0.045				
90	0.047				
91	0.046				
92	0.032				

Consensus statistics	
Consensus median, pg/g	0.039
Median all values pg/g	0.040
Consensus mean, pg/g	0.040
Standard deviation, pg/g	0.011
Relative standard deviation, %	26
No. of values reported	63
No. of values removed	3
No. of reported non-detects	4

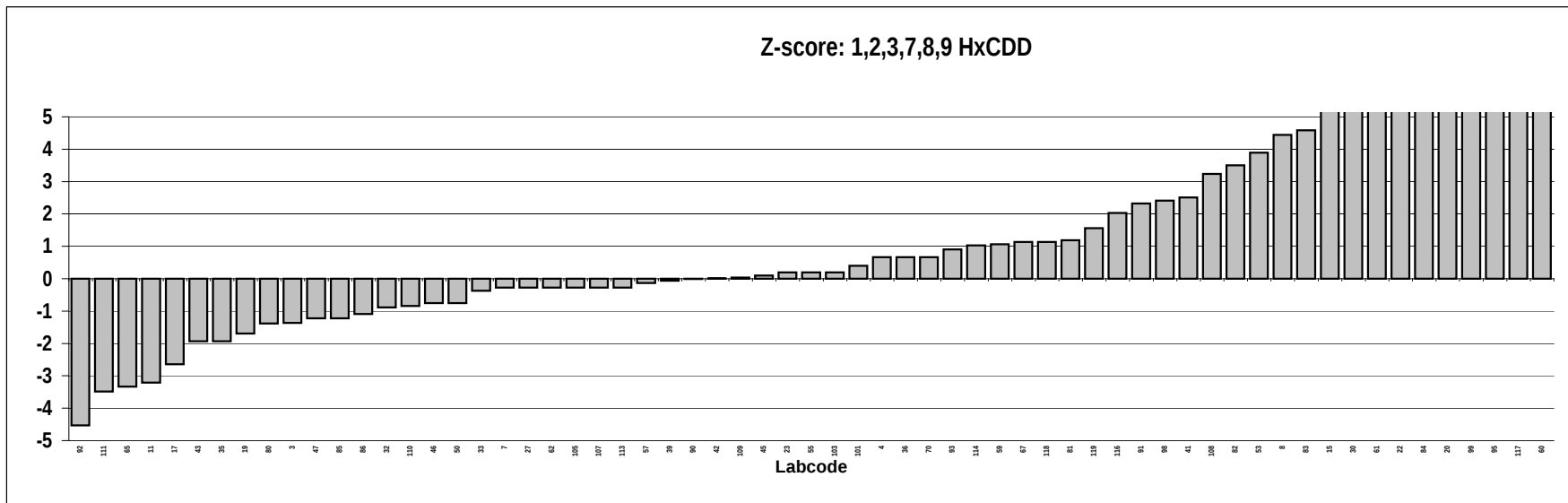
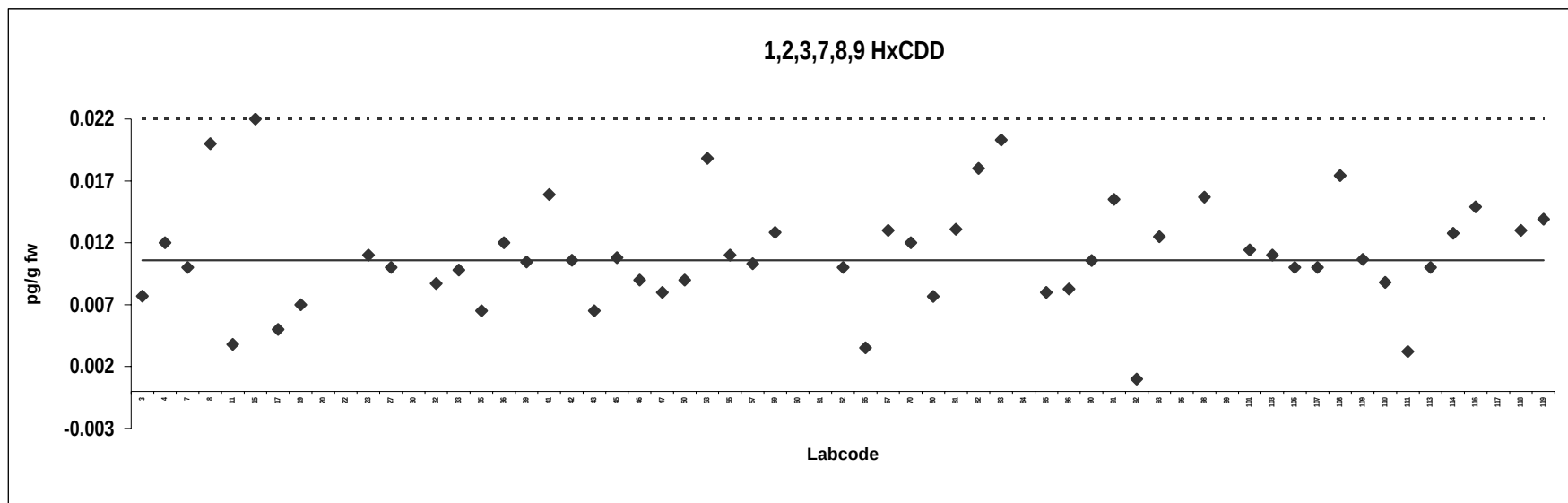


Beef

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.0077	ND	93	0.013	
4	0.012	ND	95	0.050	Outlier
7	0.010		98	0.016	
8	0.020	ND	99	0.045	Outlier,ND
11	0.0038	ND	101	0.011	
15	0.022	ND	103	0.011	
17	0.0050	ND	105	0.010	ND
19	0.0070		107	0.010	
20	0.039	Outlier	108	0.017	
22	0.028	Outlier	109	0.011	
23	0.011		110	0.0088	
27	0.010		111	0.0032	ND
30	0.023	Outlier	113	0.010	
32	0.0087		114	0.013	
33	0.0098		116	0.015	
35	0.0065		117	0.064	Outlier,ND
36	0.012		118	0.013	
39	0.010		119	0.014	
41	0.016				
42	0.011				
43	0.0065				
45	0.011				
46	0.0090				
47	0.0080				
50	0.0090				
53	0.019				
55	0.011				
57	0.010				
59	0.013				
60	0.18	Outlier			
61	0.025	Outlier,ND			
62	0.010				
65	0.0035				
67	0.013				
70	0.012				
80	0.0077				
81	0.013				
82	0.018				
83	0.020				
84	0.029	Outlier			
85	0.0080				
86	0.0083				
90	0.011				
91	0.016				
92	0.0010	ND			

Consensus statistics	
Consensus median, pg/g	0.011
Median all values pg/g	0.011
Consensus mean, pg/g	0.011
Standard deviation, pg/g	0.0043
Relative standard deviation, %	39
No. of values reported	63
No. of values removed	9
No. of reported non-detects	12

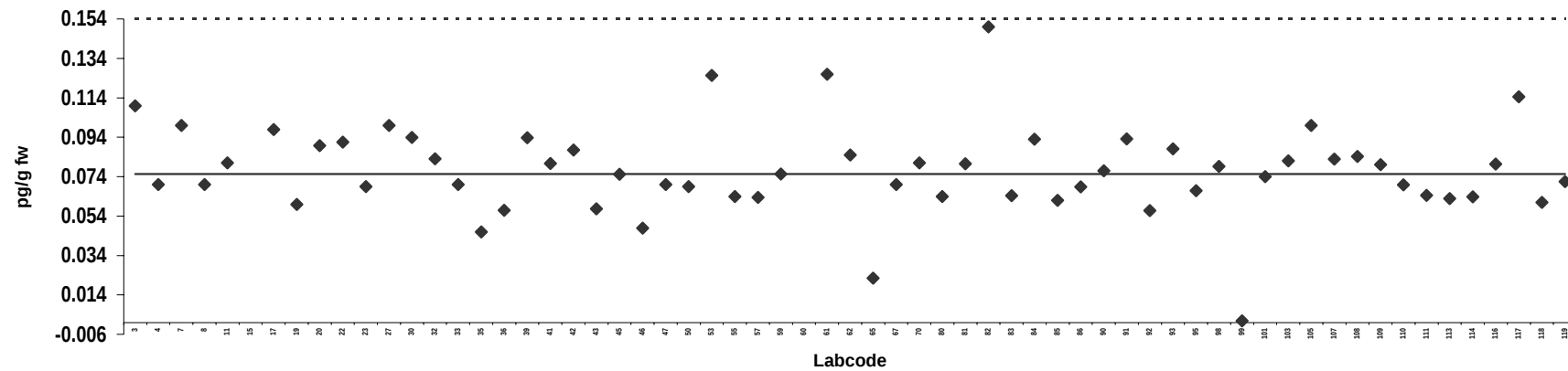


Beef
Congener: 1,2,3,4,6,7,8 HpCDD

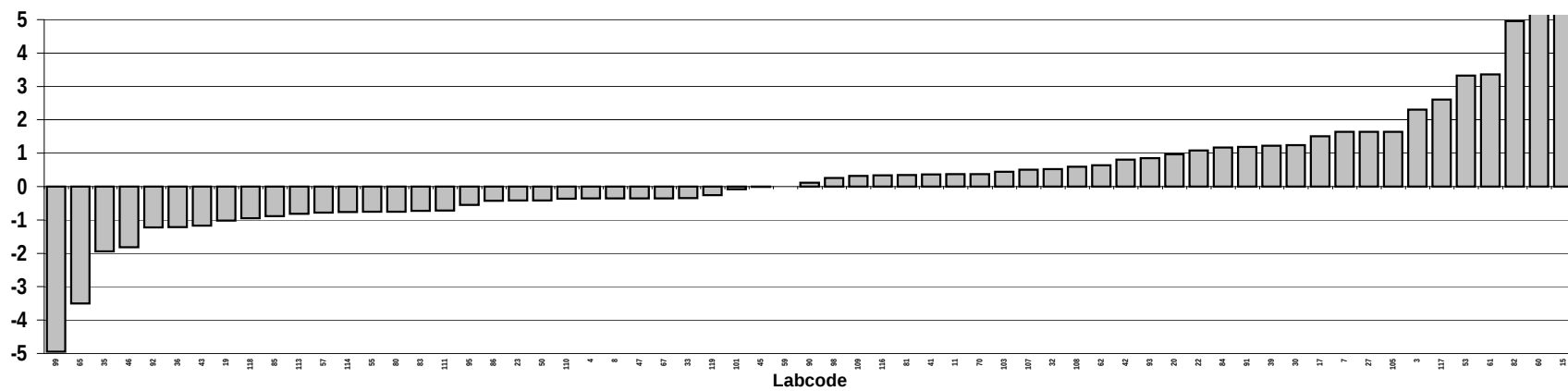
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.11	Outlier	93	0.088	ND
4	0.070		95	0.067	
7	0.10		98	0.079	ND
8	0.070		99	0.00086	
11	0.081		101	0.074	
15	0.30		103	0.082	
17	0.098		105	0.10	
19	0.060		107	0.083	
20	0.090		108	0.084	
22	0.092		109	0.080	
23	0.069	Outlier	110	0.070	
27	0.10		111	0.065	
30	0.094		113	0.063	
32	0.083		114	0.064	
33	0.070		116	0.080	
35	0.046		117	0.11	
36	0.057		118	0.061	
39	0.094		119	0.072	
41	0.081				
42	0.088				
43	0.058				
45	0.075				
46	0.048				
47	0.070				
50	0.069				
53	0.13				
55	0.064				
57	0.064				
59	0.075				
60	0.28				
61	0.13				
62	0.085				
65	0.023				
67	0.070				
70	0.081				
80	0.064				
81	0.081				
82	0.15				
83	0.064				
84	0.093				
85	0.062				
86	0.069				
90	0.077				
91	0.093				
92	0.057				

Consensus statistics	
Consensus median, pg/g	0.075
Median all values pg/g	0.077
Consensus mean, pg/g	0.077
Standard deviation, pg/g	0.023
Relative standard deviation, %	29
No. of values reported	63
No. of values removed	2
No. of reported non-detects	2

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



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

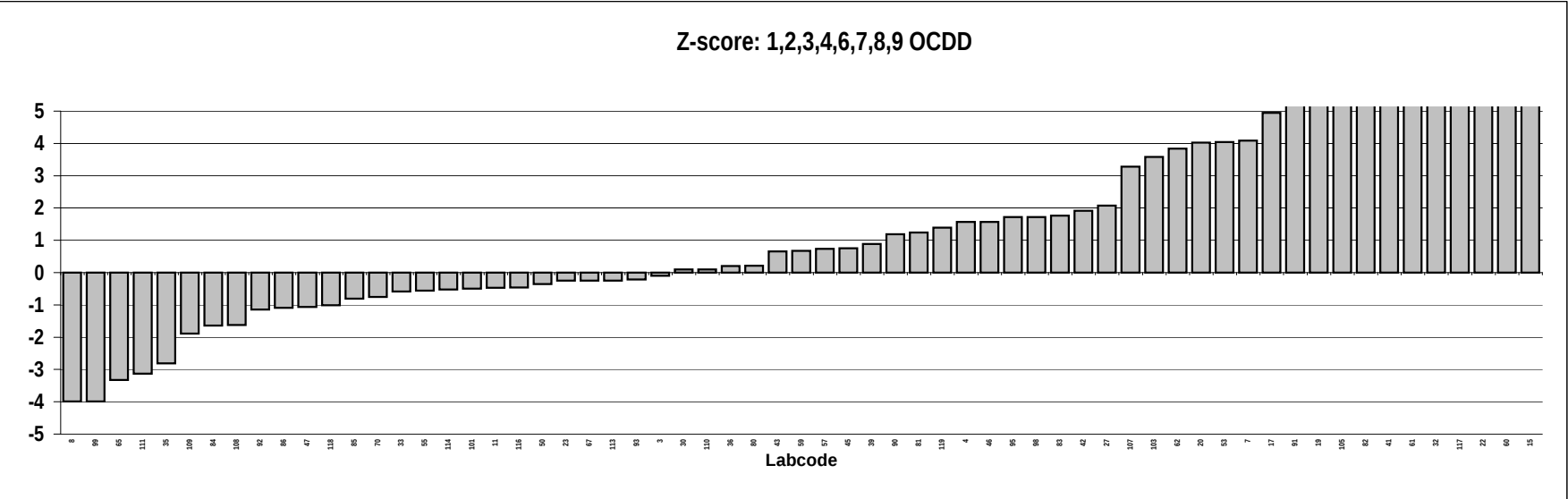
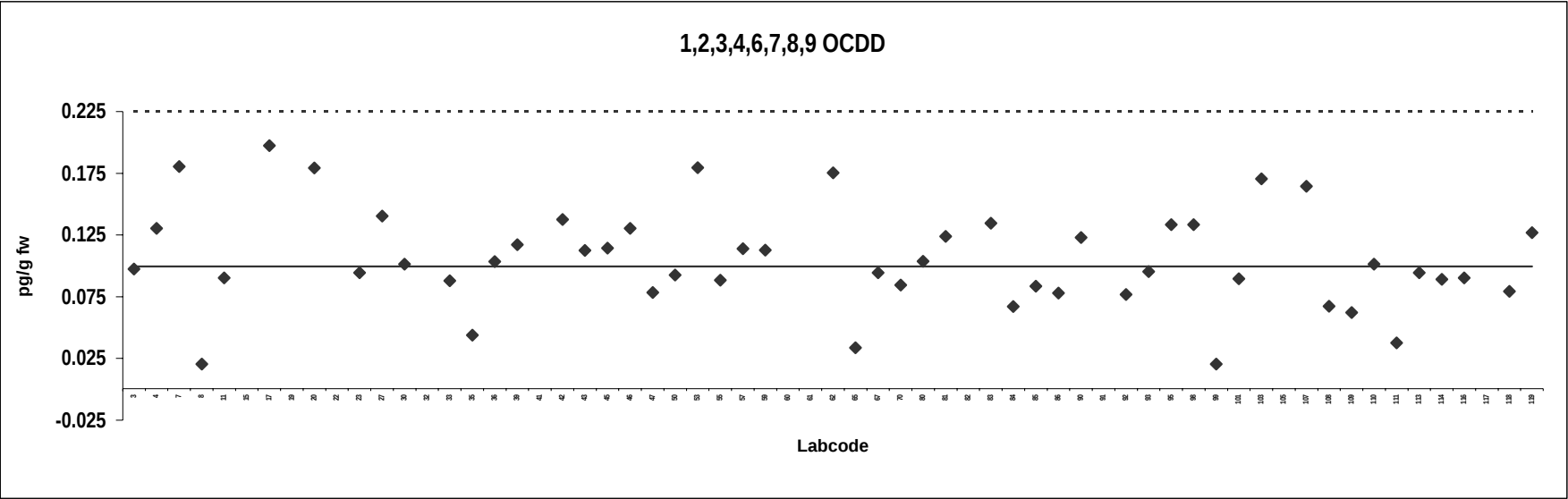


Beef

Congener: 1,2,3,4,6,7,8,9 OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.097		93	0.095	
4	0.13		95	0.13	ND
7	0.18		98	0.13	
8	0.020	ND	99	0.020	ND
11	0.090		101	0.089	
15	3.3	Outlier	103	0.17	
17	0.20		105	0.28	Outlier
19	0.28	Outlier,ND	107	0.16	
20	0.18		108	0.067	
22	0.36	Outlier	109	0.062	
23	0.094		110	0.10	
27	0.14		111	0.037	
30	0.10		113	0.094	
32	0.34	Outlier	114	0.089	
33	0.088		116	0.090	
35	0.043		117	0.35	Outlier,ND
36	0.10		118	0.079	
39	0.12		119	0.13	
41	0.30	Outlier			
42	0.14				
43	0.11				
45	0.11				
46	0.13				
47	0.078				
50	0.092				
53	0.18				
55	0.088				
57	0.11				
59	0.11				
60	2.3	Outlier			
61	0.30	Outlier			
62	0.18				
65	0.033				
67	0.094				
70	0.084				
80	0.10				
81	0.12				
82	0.29	Outlier			
83	0.13				
84	0.067				
85	0.083				
86	0.077				
90	0.12				
91	0.25	Outlier			
92	0.076				

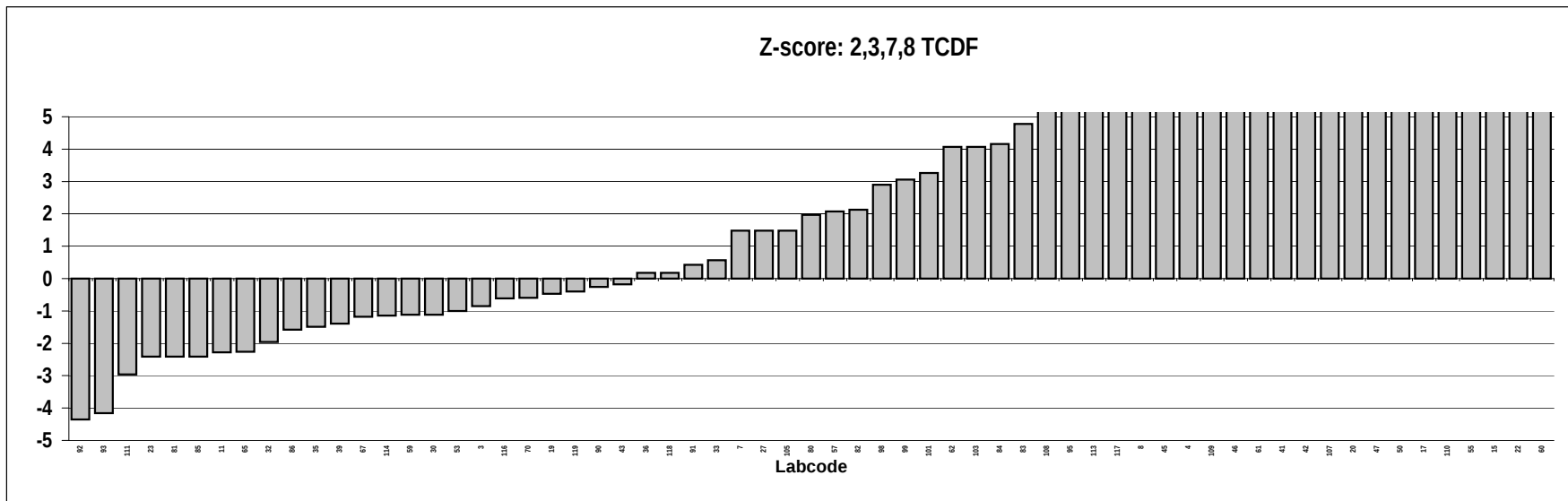
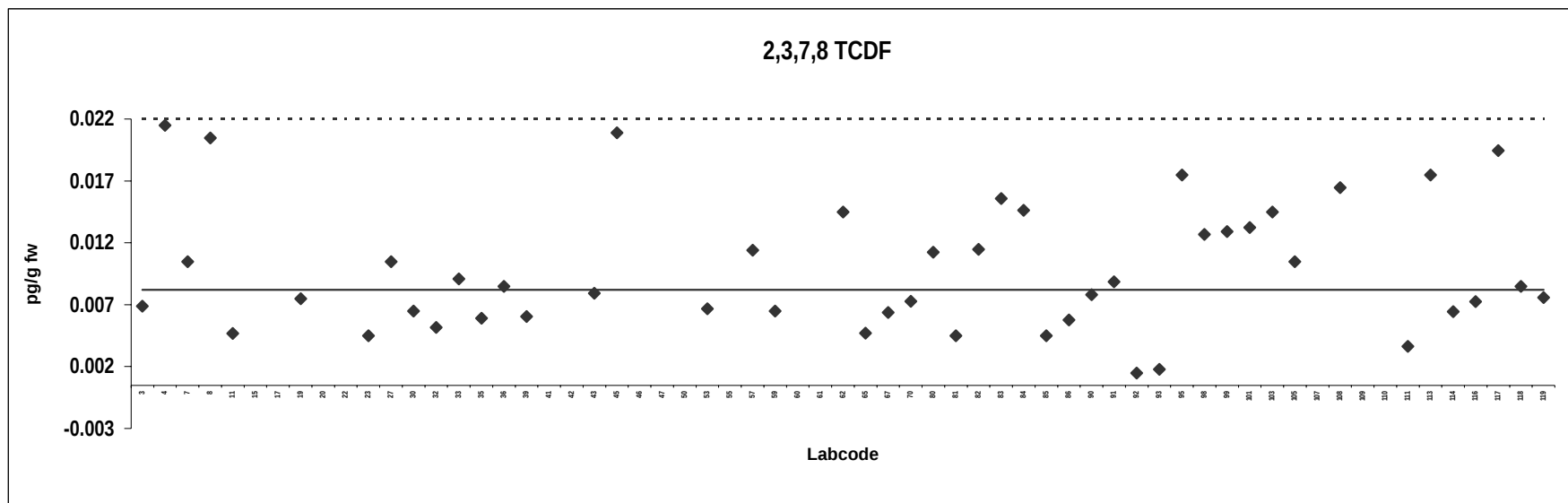
Consensus statistics	
Consensus median, pg/g	0.099
Median all values pg/g	0.11
Consensus mean, pg/g	0.10
Standard deviation, pg/g	0.041
Relative standard deviation, %	39
No. of values reported	63
No. of values removed	11
No. of reported non-detects	5



Beef
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.0064		93	0.0013	ND
4	0.021		95	0.017	ND
7	0.010	ND	98	0.012	
8	0.020		99	0.012	ND
11	0.0042	ND	101	0.013	
15	0.079	Outlier	103	0.014	
17	0.046	Outlier	105	0.010	ND
19	0.0070		107	0.034	Outlier
20	0.034	Outlier	108	0.016	
22	0.099	Outlier	109	0.023	Outlier
23	0.0040		110	0.055	Outlier
27	0.010		111	0.0032	ND
30	0.0060	ND	113	0.017	
32	0.0047		114	0.0060	
33	0.0086		116	0.0068	
35	0.0054		117	0.019	ND
36	0.0080		118	0.0080	
39	0.0056		119	0.0071	
41	0.029	Outlier			
42	0.029	Outlier			
43	0.0074				
45	0.020				
46	0.025	Outlier			
47	0.035	Outlier			
50	0.041	Outlier			
53	0.0062				
55	0.077	Outlier			
57	0.011				
59	0.0060				
60	0.23	Outlier			
61	0.026	Outlier			
62	0.014				
65	0.0042				
67	0.0059				
70	0.0068	ND			
80	0.011				
81	0.0040	ND			
82	0.011				
83	0.015	ND			
84	0.014				
85	0.0040				
86	0.0053	ND			
90	0.0073				
91	0.0084				
92	0.0010	ND			

Consensus statistics	
Consensus median, pg/g	0.0077
Median all values pg/g	0.011
Consensus mean, pg/g	0.0093
Standard deviation, pg/g	0.0051
Relative standard deviation, %	55
No. of values reported	63
No. of values removed	15
No. of reported non-detects	14

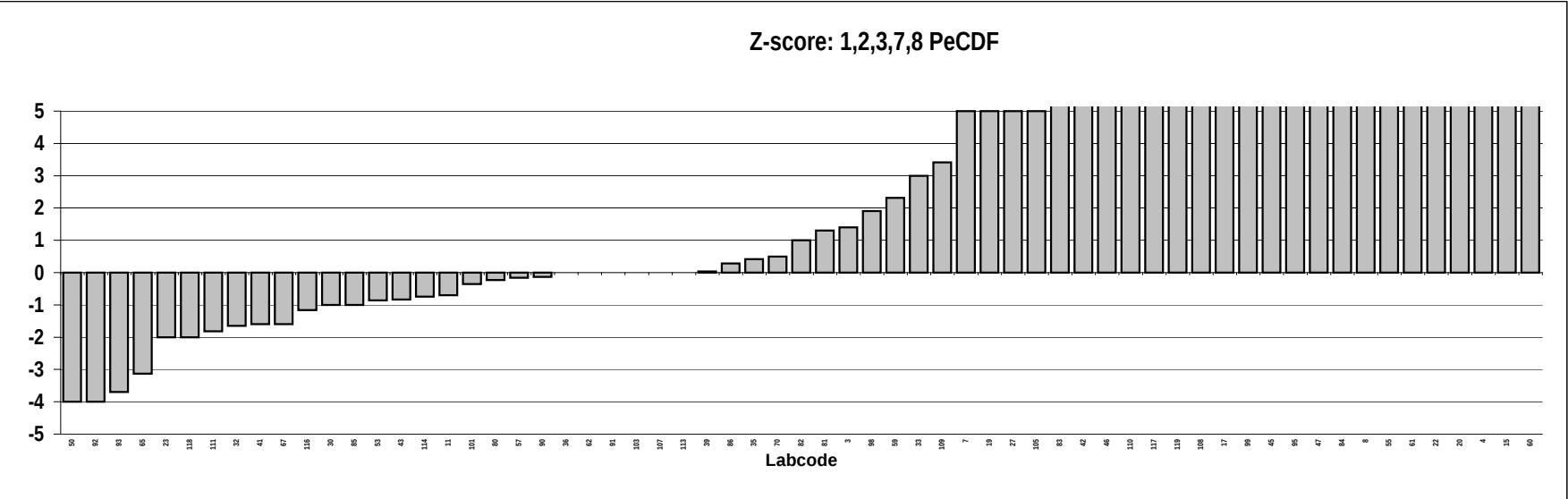
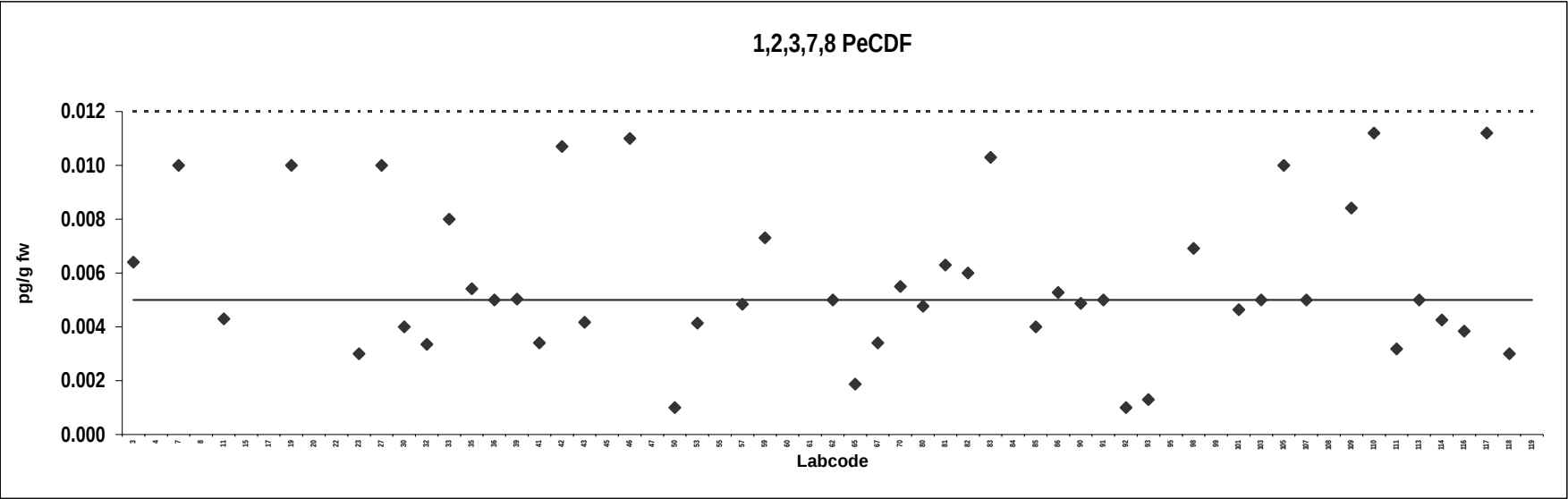


Beef

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.0064	ND	93	0.0013	ND
4	0.073	Outlier,ND	95	0.017	Outlier,ND
7	0.010	ND	98	0.0069	
8	0.020	Outlier,ND	99	0.015	Outlier,ND
11	0.0043	ND	101	0.0046	
15	0.14	Outlier,ND	103	0.0050	
17	0.015	Outlier	105	0.010	ND
19	0.010	ND	107	0.0050	
20	0.055	Outlier	108	0.015	Outlier,ND
22	0.026	Outlier	109	0.0084	
23	0.0030		110	0.011	
27	0.010		111	0.0032	ND
30	0.0040	ND	113	0.0050	ND
32	0.0034		114	0.0043	
33	0.0080	ND	116	0.0038	
35	0.0054		117	0.011	ND
36	0.0050	ND	118	0.0030	ND
39	0.0050		119	0.013	Outlier
41	0.0034	ND			
42	0.011				
43	0.0042				
45	0.016	Outlier			
46	0.011				
47	0.018	Outlier			
50	0.0010				
53	0.0041				
55	0.024	Outlier			
57	0.0048				
59	0.0073				
60	0.16	Outlier			
61	0.025	Outlier,ND			
62	0.0050				
65	0.0019	ND			
67	0.0034				
70	0.0055				
80	0.0048	ND			
81	0.0063	ND			
82	0.0060				
83	0.010	ND			
84	0.018	Outlier			
85	0.0040	ND			
86	0.0053	ND			
90	0.0049				
91	0.0050	ND			
92	0.0010	ND			

Consensus statistics	
Consensus median, pg/g	0.0050
Median all values pg/g	0.0060
Consensus mean, pg/g	0.0057
Standard deviation, pg/g	0.0028
Relative standard deviation, %	50
No. of values reported	63
No. of values removed	16
No. of reported non-detects	29



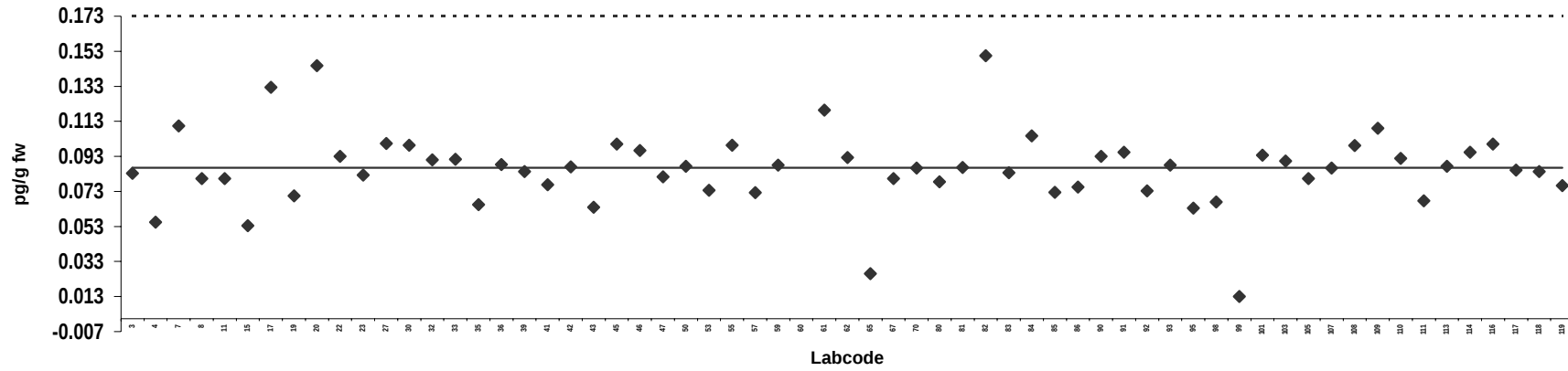
Beef

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

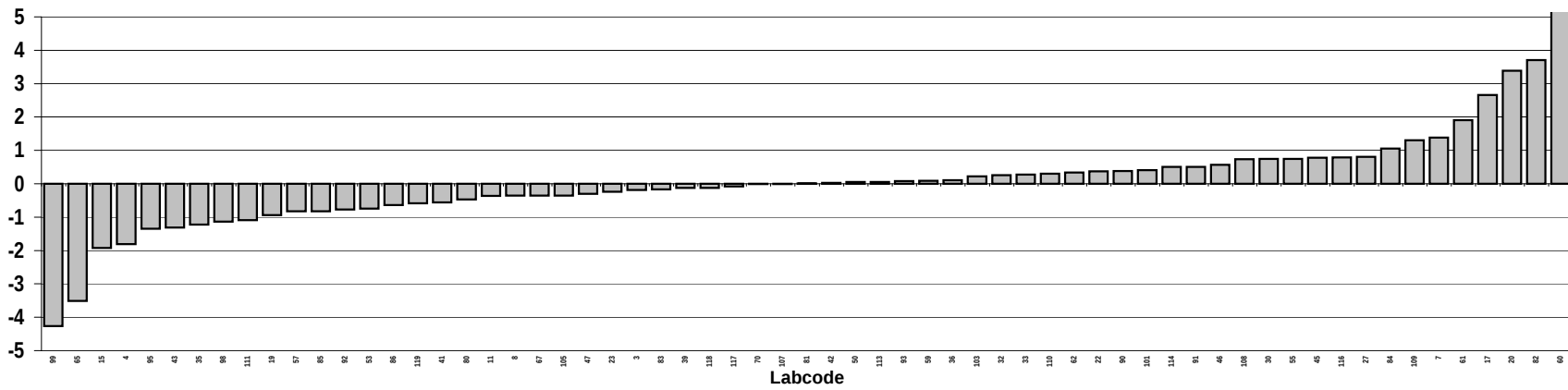
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.083	Outlier	93	0.088	ND
4	0.055		95	0.063	
7	0.11		98	0.067	
8	0.080		99	0.013	
11	0.080		101	0.093	
15	0.053		103	0.090	
17	0.13		105	0.080	
19	0.070		107	0.086	
20	0.14		108	0.099	
22	0.093		109	0.11	
23	0.082		110	0.091	
27	0.10		111	0.067	
30	0.099		113	0.087	
32	0.091		114	0.095	
33	0.091		116	0.100	
35	0.065		117	0.085	
36	0.088		118	0.084	
39	0.084		119	0.076	
41	0.077				
42	0.087				
43	0.064				
45	0.100				
46	0.096				
47	0.081				
50	0.087				
53	0.073				
55	0.099				
57	0.072				
59	0.088				
60	0.78				
61	0.12				
62	0.092				
65	0.026				
67	0.080				
70	0.086				
80	0.078				
81	0.086				
82	0.15				
83	0.083				
84	0.10				
85	0.072				
86	0.075				
90	0.093				
91	0.095				
92	0.073				

Consensus statistics	
Consensus median, pg/g	0.086
Median all values pg/g	0.086
Consensus mean, pg/g	0.086
Standard deviation, pg/g	0.022
Relative standard deviation, %	25
No. of values reported	63
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

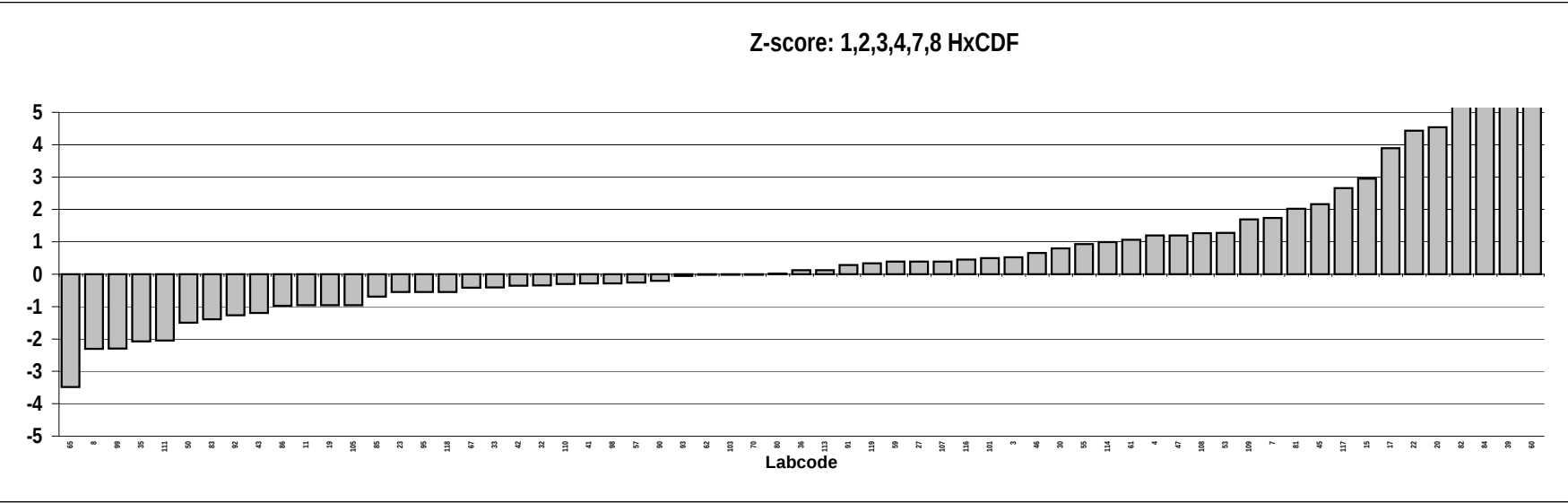
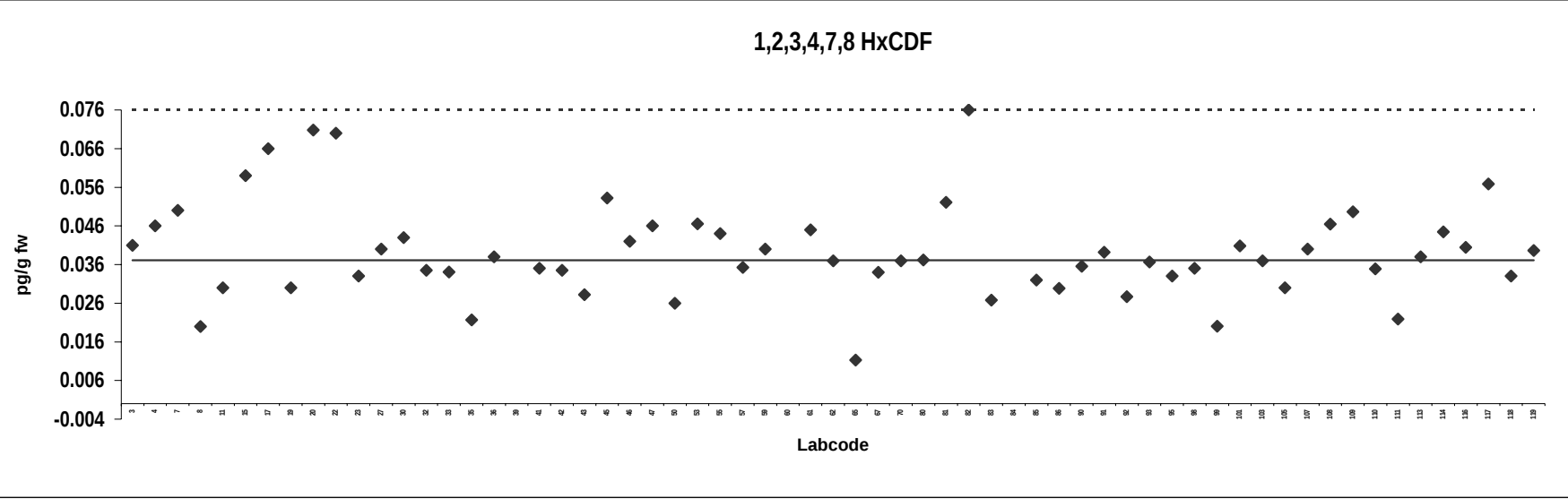


Beef

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.041	ND	93	0.037	ND
4	0.046		95	0.033	
7	0.050		98	0.035	
8	0.020		99	0.020	
11	0.030		101	0.041	
15	0.059		103	0.037	
17	0.066		105	0.030	
19	0.030		107	0.040	
20	0.071		108	0.046	
22	0.070		109	0.050	
23	0.033	Outlier	110	0.035	
27	0.040		111	0.022	
30	0.043		113	0.038	
32	0.035		114	0.044	
33	0.034		116	0.040	
35	0.022		117	0.057	
36	0.038		118	0.033	
39	0.086		119	0.040	
41	0.035	Outlier			
42	0.035				
43	0.028				
45	0.053				
46	0.042				
47	0.046				
50	0.026				
53	0.047				
55	0.044				
57	0.035				
59	0.040	Outlier			
60	1.5				
61	0.045				
62	0.037				
65	0.011				
67	0.034				
70	0.037				
80	0.037				
81	0.052				
82	0.076				
83	0.027	Outlier			
84	0.078				
85	0.032				
86	0.030				
90	0.036				
91	0.039				
92	0.028				

Consensus statistics	
Consensus median, pg/g	0.037
Median all values pg/g	0.038
Consensus mean, pg/g	0.039
Standard deviation, pg/g	0.012
Relative standard deviation, %	32
No. of values reported	63
No. of values removed	3
No. of reported non-detects	3



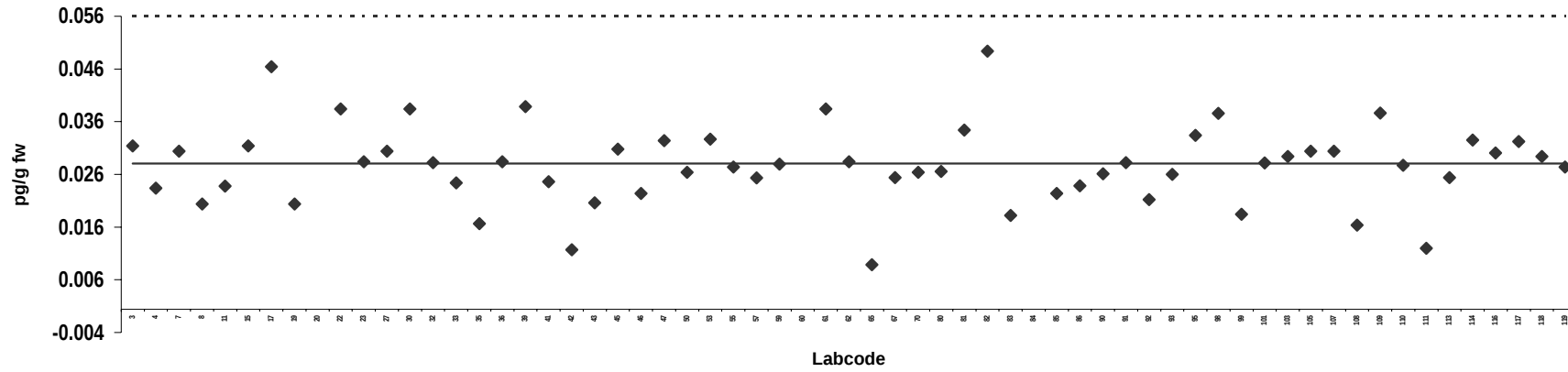
Beef

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

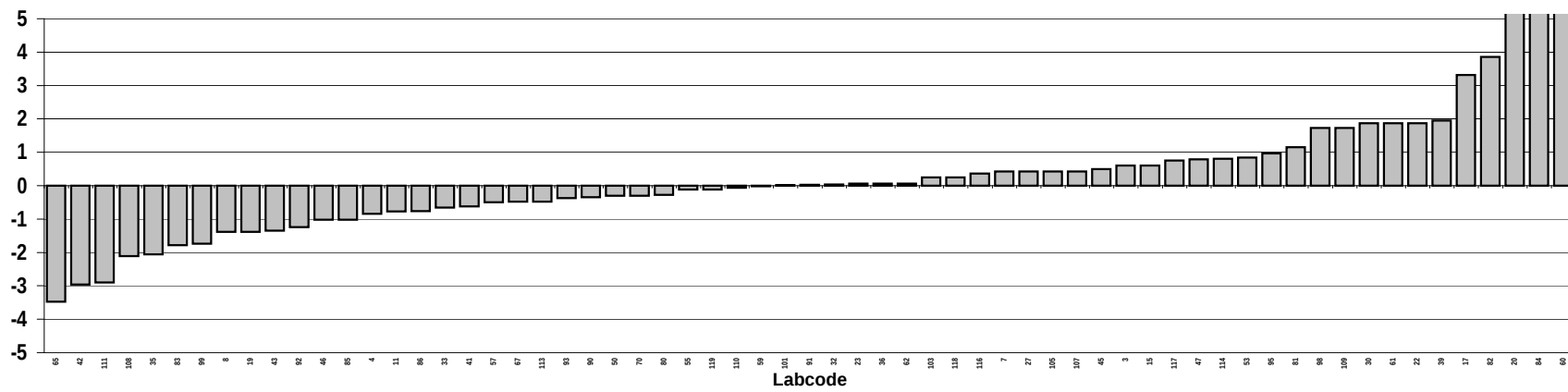
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.031		93	0.026	
4	0.023		95	0.033	ND
7	0.030		98	0.037	
8	0.020	ND	99	0.018	ND
11	0.023		101	0.028	
15	0.031	ND	103	0.029	
17	0.046		105	0.030	
19	0.020		107	0.030	
20	0.062	Outlier	108	0.016	
22	0.038		109	0.037	
23	0.028		110	0.027	
27	0.030		111	0.012	
30	0.038		113	0.025	
32	0.028		114	0.032	
33	0.024		116	0.030	
35	0.016		117	0.032	
36	0.028		118	0.029	
39	0.038		119	0.027	
41	0.024				
42	0.011				
43	0.020				
45	0.030				
46	0.022				
47	0.032				
50	0.026				
53	0.032				
55	0.027				
57	0.025				
59	0.028				
60	0.16	Outlier			
61	0.038				
62	0.028				
65	0.0085				
67	0.025				
70	0.026				
80	0.026				
81	0.034				
82	0.049				
83	0.018				
84	0.070	Outlier			
85	0.022				
86	0.023				
90	0.026				
91	0.028				
92	0.021				

Consensus statistics	
Consensus median, pg/g	0.028
Median all values pg/g	0.028
Consensus mean, pg/g	0.027
Standard deviation, pg/g	0.0076
Relative standard deviation, %	28
No. of values reported	63
No. of values removed	3
No. of reported non-detects	4

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



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



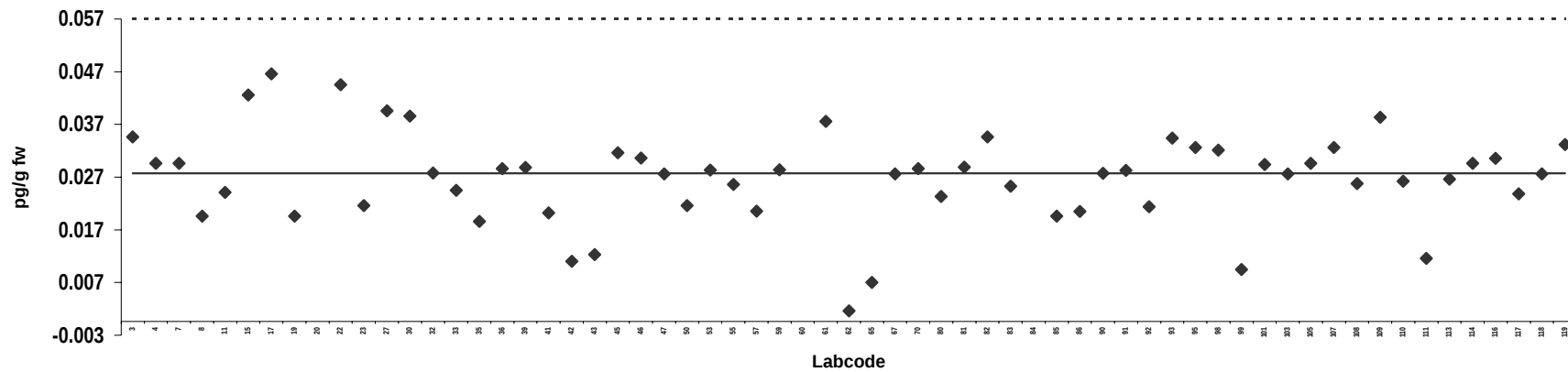
Beef

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

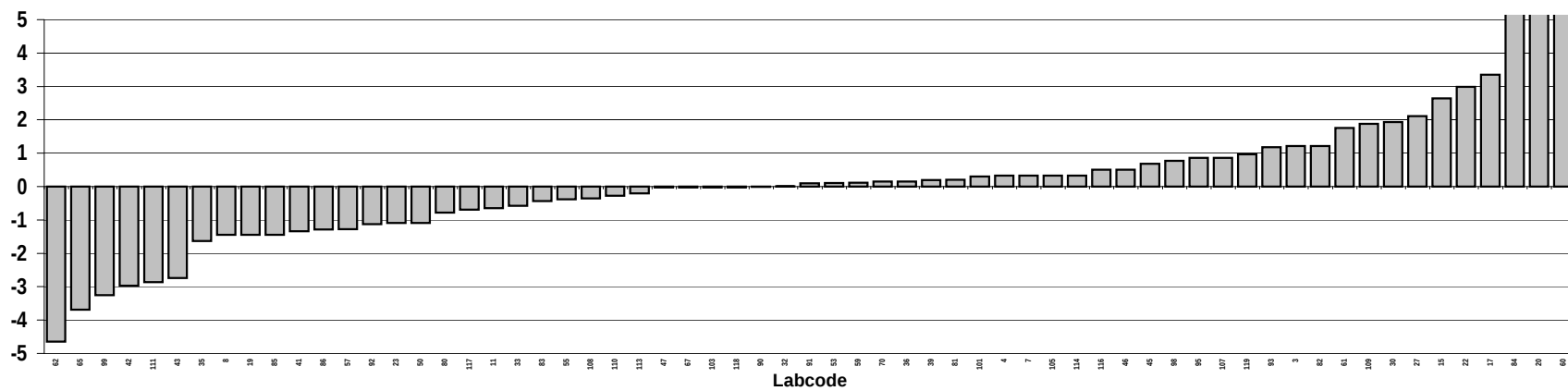
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.035		93	0.035	
4	0.030		95	0.033	ND
7	0.030		98	0.033	
8	0.020	ND	99	0.0099	ND
11	0.025		101	0.030	
15	0.043		103	0.028	
17	0.047		105	0.030	
19	0.020		107	0.033	
20	0.096	Outlier	108	0.026	
22	0.045		109	0.039	
23	0.022		110	0.027	
27	0.040		111	0.012	
30	0.039		113	0.027	
32	0.028		114	0.030	
33	0.025		116	0.031	
35	0.019		117	0.024	ND
36	0.029		118	0.028	
39	0.029		119	0.034	
41	0.021				
42	0.011				
43	0.013				
45	0.032				
46	0.031				
47	0.028				
50	0.022				
53	0.029				
55	0.026				
57	0.021				
59	0.029				
60	0.47	Outlier			
61	0.038				
62	0.0020	ND			
65	0.0074				
67	0.028				
70	0.029				
80	0.024				
81	0.029				
82	0.035				
83	0.026				
84	0.072	Outlier			
85	0.020				
86	0.021				
90	0.028				
91	0.029				
92	0.022				

Consensus statistics	
Consensus median, pg/g	0.028
Median all values pg/g	0.029
Consensus mean, pg/g	0.027
Standard deviation, pg/g	0.0087
Relative standard deviation, %	32
No. of values reported	63
No. of values removed	3
No. of reported non-detects	5

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



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



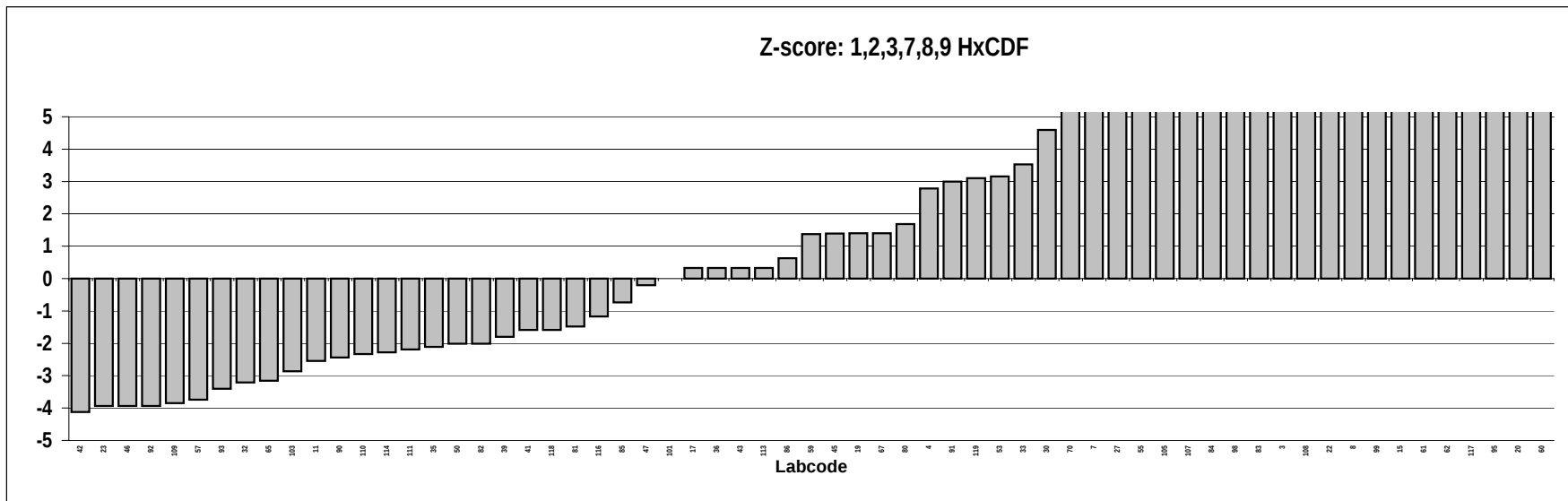
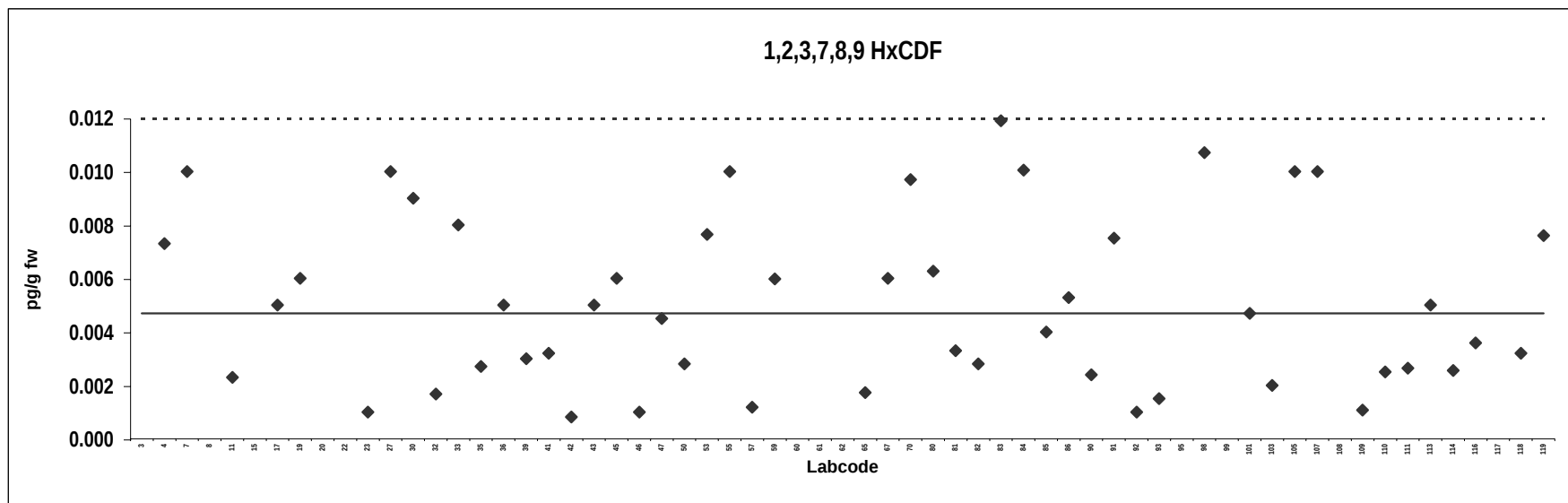
Beef

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.012	Outlier,ND	93	0.0015	ND
4	0.0073	ND	95	0.033	Outlier,ND
7	0.010	ND	98	0.011	
8	0.020	Outlier,ND	99	0.021	Outlier,ND
11	0.0023	ND	101	0.0047	
15	0.021	Outlier,ND	103	0.0020	ND
17	0.0050	ND	105	0.010	ND
19	0.0060	ND	107	0.010	
20	0.082	Outlier	108	0.015	Outlier,ND
22	0.015	Outlier	109	0.0011	ND
23	0.0010		110	0.0025	ND
27	0.010	ND	111	0.0026	ND
30	0.0090		113	0.0050	ND
32	0.0017		114	0.0026	
33	0.0080	ND	116	0.0036	
35	0.0027		117	0.032	Outlier,ND
36	0.0050	ND	118	0.0032	ND
39	0.0030	ND	119	0.0076	
41	0.0032	ND			
42	0.00082	ND			
43	0.0050	ND			
45	0.0060				
46	0.0010				
47	0.0045	ND			
50	0.0028	ND			
53	0.0077				
55	0.010	ND			
57	0.0012	ND			
59	0.0060	ND			
60	0.19	Outlier			
61	0.025	Outlier,ND			
62	0.026	Outlier			
65	0.0017	ND			
67	0.0060	ND			
70	0.0097	ND			
80	0.0063	ND			
81	0.0033	ND			
82	0.0028				
83	0.012	ND			
84	0.010				
85	0.0040	ND			
86	0.0053	ND			
90	0.0024	ND			
91	0.0075	ND			
92	0.0010	ND			

Consensus statistics

Consensus median, pg/g	0.0047
Median all values pg/g	0.0060
Consensus mean, pg/g	0.0051
Standard deviation, pg/g	0.0032
Relative standard deviation, %	63
No. of values reported	63
No. of values removed	12
No. of reported non-detects	44

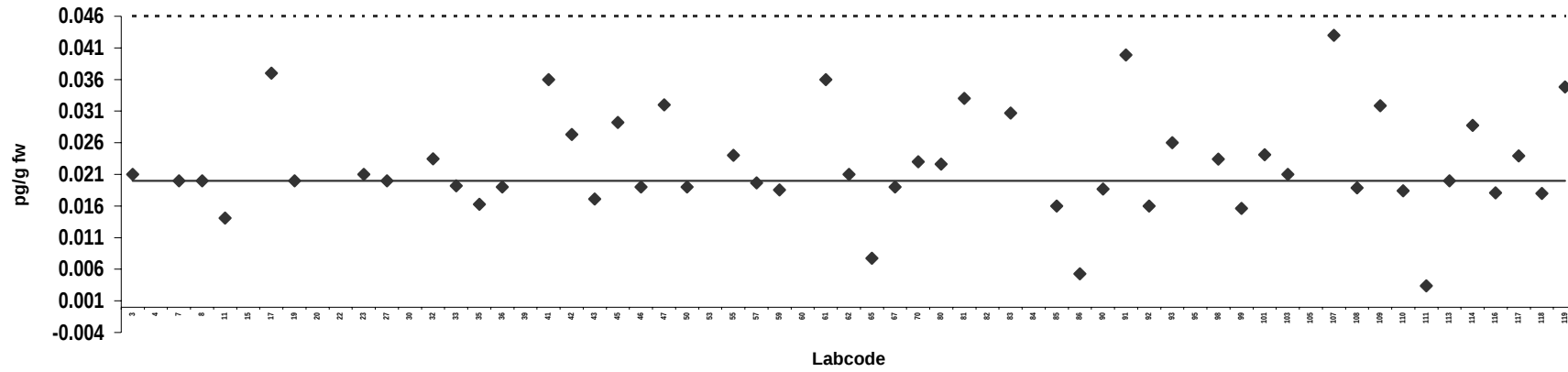


Beef
Congener: 1,2,3,4,6,7,8 HpCDF

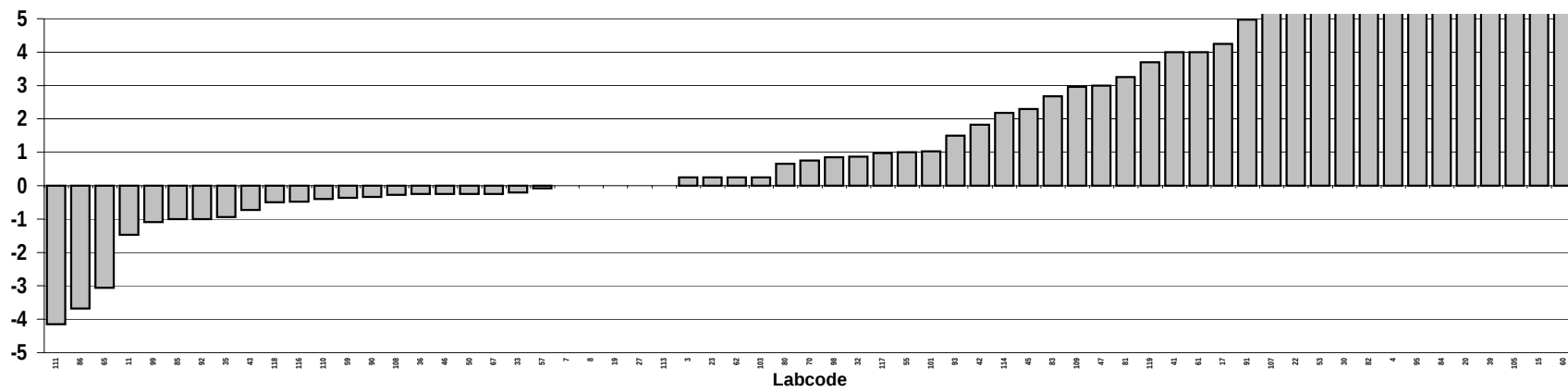
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.021		93	0.026	
4	0.061	Outlier	95	0.067	Outlier,ND
7	0.020		98	0.023	
8	0.020	ND	99	0.016	ND
11	0.014		101	0.024	
15	0.17	Outlier	103	0.021	
17	0.037		105	0.11	Outlier
19	0.020		107	0.043	
20	0.071	Outlier	108	0.019	
22	0.050	Outlier	109	0.032	
23	0.021		110	0.018	
27	0.020		111	0.0034	ND
30	0.055	Outlier	113	0.020	
32	0.023		114	0.029	
33	0.019		116	0.018	
35	0.016		117	0.024	
36	0.019		118	0.018	
39	0.081	Outlier	119	0.035	
41	0.036				
42	0.027				
43	0.017				
45	0.029				
46	0.019				
47	0.032				
50	0.019				
53	0.051	Outlier			
55	0.024				
57	0.020				
59	0.019				
60	2.9	Outlier			
61	0.036				
62	0.021				
65	0.0078				
67	0.019				
70	0.023				
80	0.023				
81	0.033				
82	0.057	Outlier			
83	0.031				
84	0.069	Outlier			
85	0.016				
86	0.0053	ND			
90	0.019				
91	0.040				
92	0.016				

Consensus statistics	
Consensus median, pg/g	0.020
Median all values pg/g	0.023
Consensus mean, pg/g	0.023
Standard deviation, pg/g	0.0081
Relative standard deviation, %	36
No. of values reported	63
No. of values removed	12
No. of reported non-detects	5

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



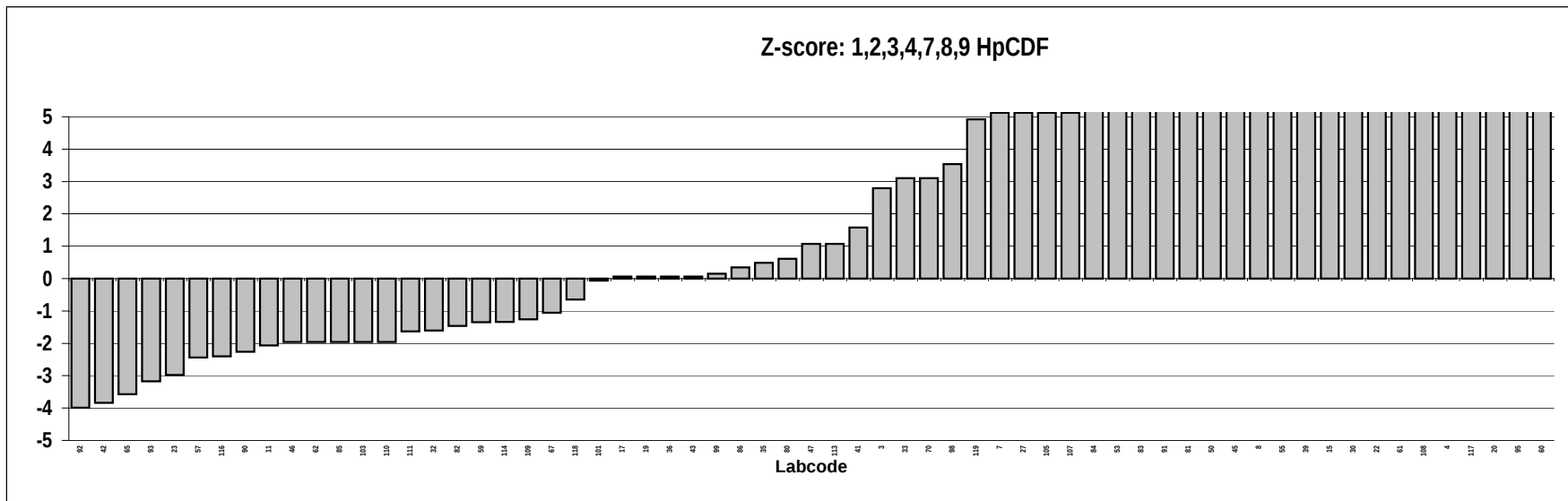
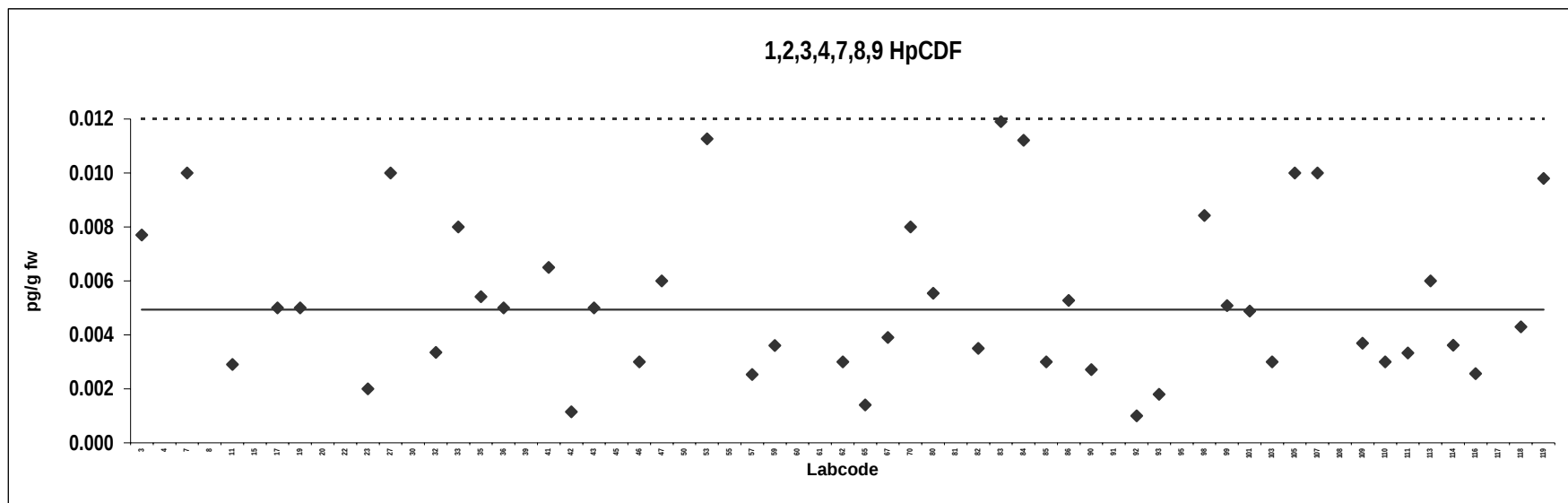
Z-score: 1,2,3,4,6,7,8 HpCDF



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.0077	ND	93	0.0018	ND
4	0.038	Outlier	95	0.067	Outlier,ND
7	0.010	ND	98	0.0084	
8	0.020	Outlier,ND	99	0.0051	ND
11	0.0029	ND	101	0.0049	
15	0.022	Outlier,ND	103	0.0030	ND
17	0.0050	ND	105	0.010	ND
19	0.0050	ND	107	0.010	
20	0.062	Outlier	108	0.026	Outlier
22	0.022	Outlier	109	0.0037	
23	0.0020		110	0.0030	ND
27	0.010		111	0.0033	ND
30	0.022	Outlier	113	0.0060	ND
32	0.0034		114	0.0036	
33	0.0080	ND	116	0.0026	
35	0.0054		117	0.044	Outlier
36	0.0050	ND	118	0.0043	ND
39	0.021	Outlier	119	0.0098	
41	0.0065	ND			
42	0.0012	ND			
43	0.0050	ND			
45	0.017	Outlier			
46	0.0030				
47	0.0060				
50	0.013	Outlier			
53	0.011				
55	0.020	Outlier,ND			
57	0.0025				
59	0.0036	ND			
60	0.69	Outlier			
61	0.025	Outlier,ND			
62	0.0030	ND			
65	0.0014	ND			
67	0.0039				
70	0.0080	ND			
80	0.0055	ND			
81	0.013	Outlier			
82	0.0035	ND			
83	0.012	ND			
84	0.011				
85	0.0030	ND			
86	0.0053	ND			
90	0.0027				
91	0.013	Outlier,ND			
92	0.0010	ND			

Consensus statistics	
Consensus median, pg/g	0.0049
Median all values pg/g	0.0060
Consensus mean, pg/g	0.0053
Standard deviation, pg/g	0.0030
Relative standard deviation, %	57
No. of values reported	63
No. of values removed	17
No. of reported non-detects	34



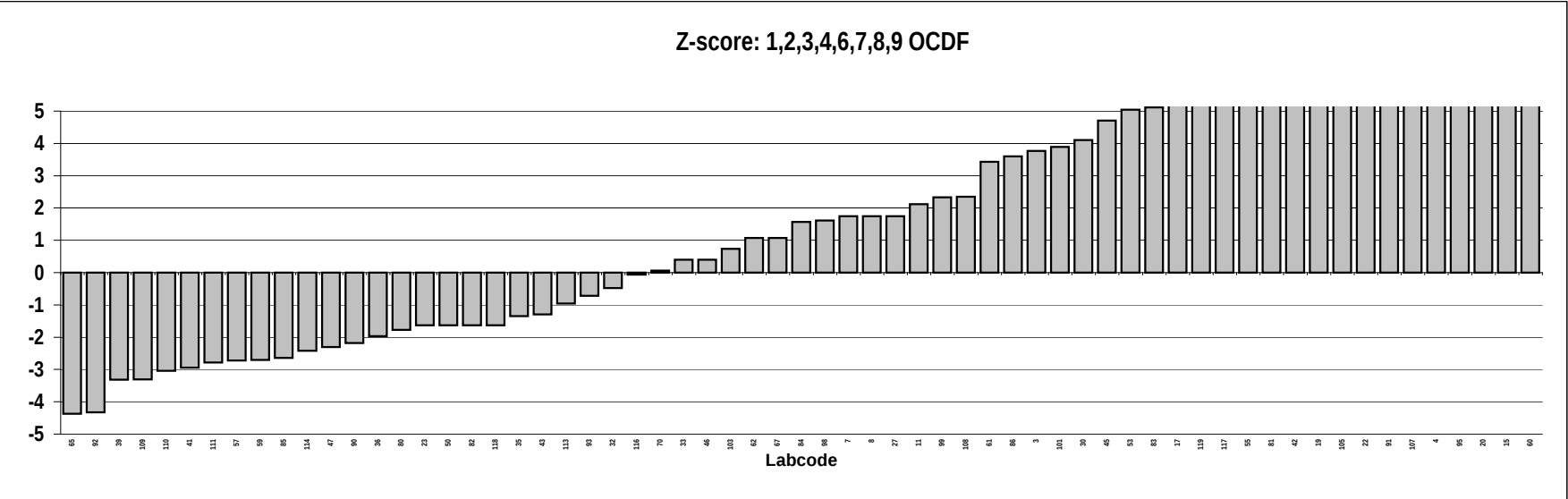
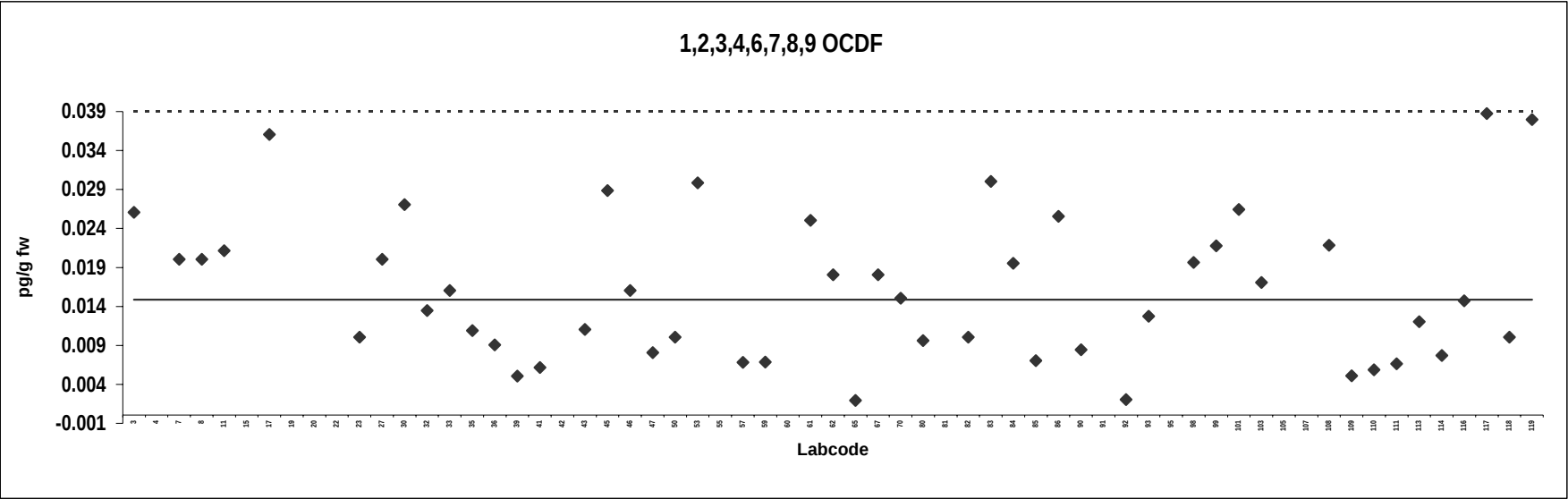
Beef

Congener: 1,2,3,4,6,7,8,9 OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.026	ND	93	0.013	
4	0.075	Outlier	95	0.13	Outlier,ND
7	0.020	ND	98	0.020	
8	0.020	ND	99	0.022	ND
11	0.021		101	0.026	
15	0.26	Outlier	103	0.017	
17	0.036		105	0.050	Outlier,ND
19	0.050	Outlier,ND	107	0.073	Outlier
20	0.15	Outlier	108	0.022	ND
22	0.069	Outlier	109	0.0050	
23	0.010		110	0.0058	
27	0.020		111	0.0066	ND
30	0.027		113	0.012	
32	0.013		114	0.0077	
33	0.016	ND	116	0.015	
35	0.011		117	0.039	ND
36	0.0090		118	0.010	ND
39	0.0050		119	0.038	
41	0.0061	ND			
42	0.049	Outlier			
43	0.011				
45	0.029				
46	0.016				
47	0.0080				
50	0.010				
53	0.030				
55	0.040	Outlier,ND			
57	0.0068				
59	0.0068				
60	5.4	Outlier			
61	0.025	ND			
62	0.018				
65	0.0019	ND			
67	0.018	ND			
70	0.015	ND			
80	0.0096				
81	0.041	Outlier			
82	0.010				
83	0.030				
84	0.019				
85	0.0070	ND			
86	0.026	ND			
90	0.0084				
91	0.072	Outlier			
92	0.0020	ND			

Consensus statistics

Consensus median, pg/g	0.015
Median all values pg/g	0.019
Consensus mean, pg/g	0.016
Standard deviation, pg/g	0.0094
Relative standard deviation, %	58
No. of values reported	63
No. of values removed	13
No. of reported non-detects	21

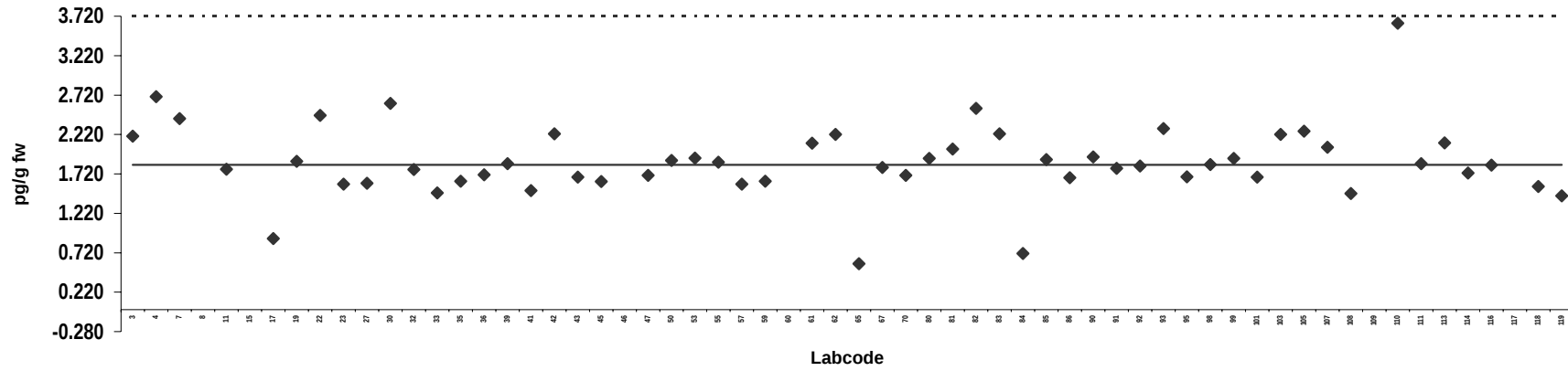


Beef
Congener: PCB 77

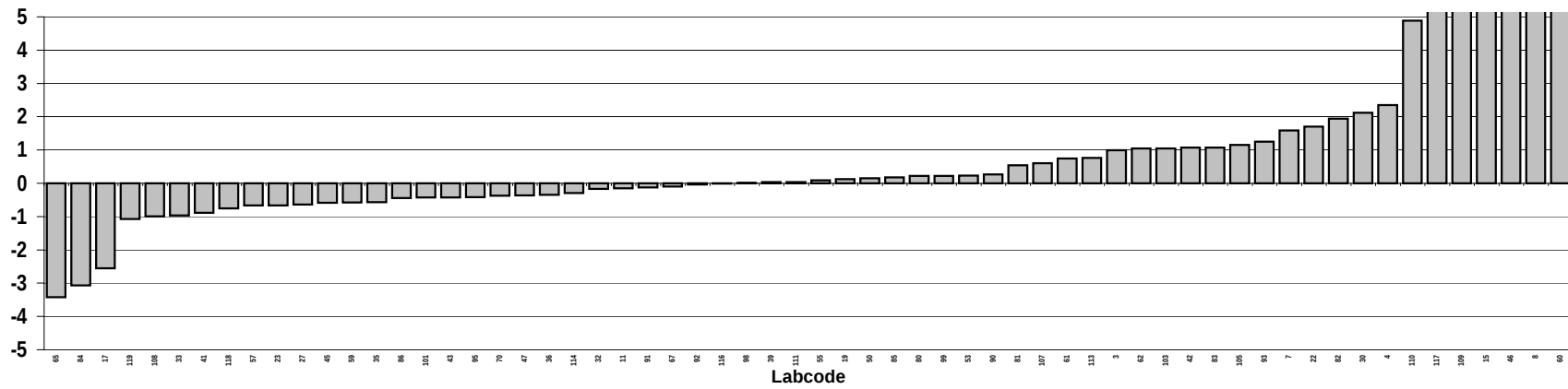
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	2.2		95	1.7	
4	2.7		98	1.8	
7	2.4		99	1.9	
8	5.7	Outlier	101	1.7	
11	1.8		103	2.2	
15	4.1	Outlier	105	2.3	
17	0.90		107	2.1	
19	1.9		108	1.5	
22	2.5		109	4.0	Outlier
23	1.6		110	3.6	
27	1.6		111	1.9	
30	2.6		113	2.1	
32	1.8		114	1.7	
33	1.5		116	1.8	
35	1.6		117	4.0	Outlier
36	1.7		118	1.6	
39	1.8		119	1.4	
41	1.5				
42	2.2				
43	1.7				
45	1.6				
46	4.9	Outlier			
47	1.7				
50	1.9				
53	1.9				
55	1.9				
57	1.6				
59	1.6				
60	9.0	Outlier			
61	2.1				
62	2.2				
65	0.58				
67	1.8				
70	1.7				
80	1.9				
81	2.0				
82	2.6				
83	2.2				
84	0.71				
85	1.9				
86	1.7				
90	1.9				
91	1.8				
92	1.8				
93	2.3				

Consensus statistics	
Consensus median, pg/g	1.8
Median all values pg/g	1.9
Consensus mean, pg/g	1.9
Standard deviation, pg/g	0.47
Relative standard deviation, %	25
No. of values reported	62
No. of values removed	6
No. of reported non-detects	0

PCB 77



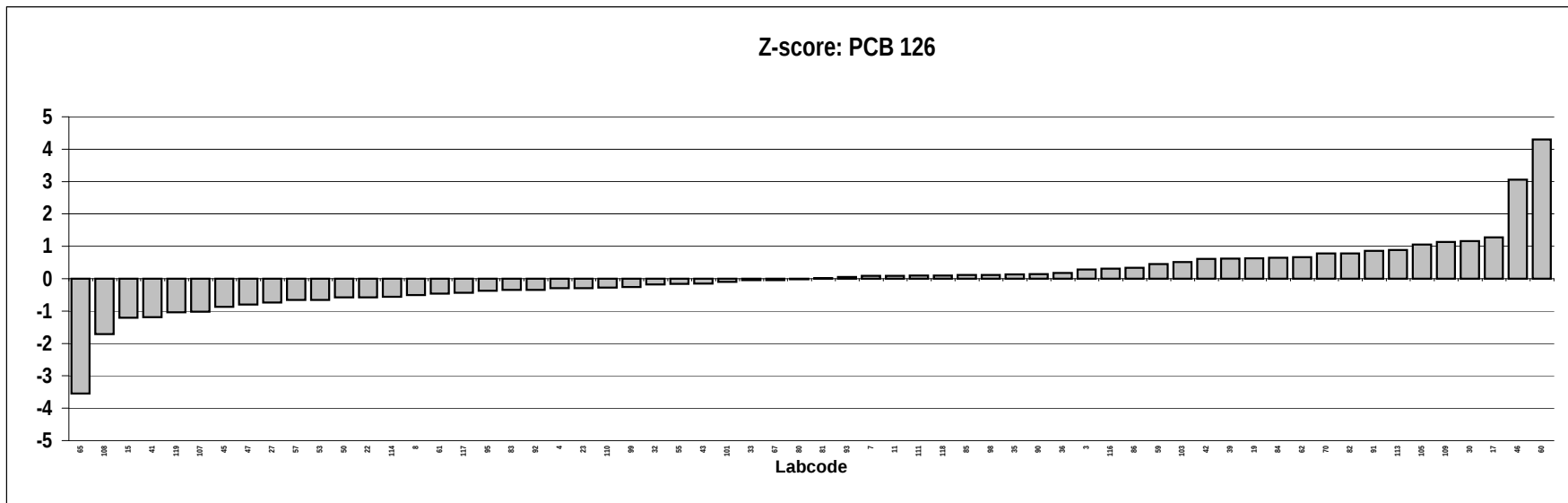
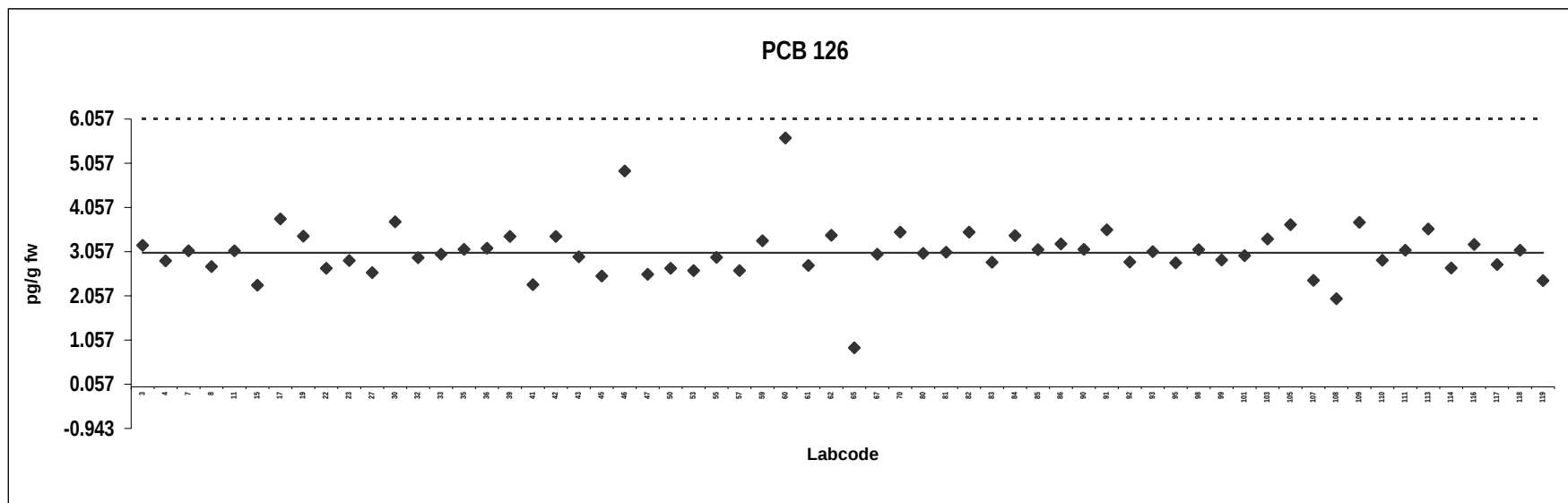
Z-score: PCB 77



Beef
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	3.2		95	2.8	
4	2.9		98	3.1	
7	3.1		99	2.9	
8	2.7		101	3.0	
11	3.1		103	3.3	
15	2.3		105	3.7	
17	3.8		107	2.4	
19	3.4		108	2.0	
22	2.7		109	3.7	
23	2.9		110	2.9	
27	2.6		111	3.1	
30	3.7		113	3.6	
32	2.9		114	2.7	
33	3.0		116	3.2	
35	3.1		117	2.8	
36	3.1		118	3.1	
39	3.4		119	2.4	
41	2.3				
42	3.4				
43	2.9				
45	2.5				
46	4.9				
47	2.5				
50	2.7				
53	2.6				
55	2.9				
57	2.6				
59	3.3				
60	5.6				
61	2.7				
62	3.4				
65	0.88				
67	3.0				
70	3.5				
80	3.0				
81	3.0				
82	3.5				
83	2.8				
84	3.4				
85	3.1				
86	3.2				
90	3.1				
91	3.6				
92	2.8				
93	3.1				

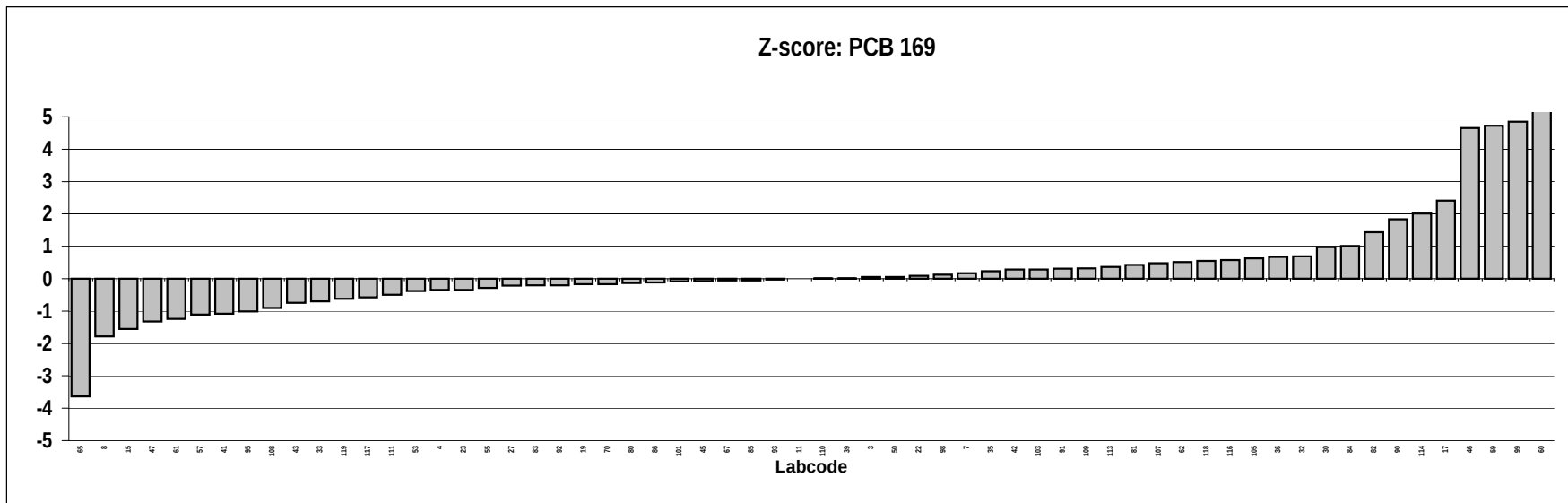
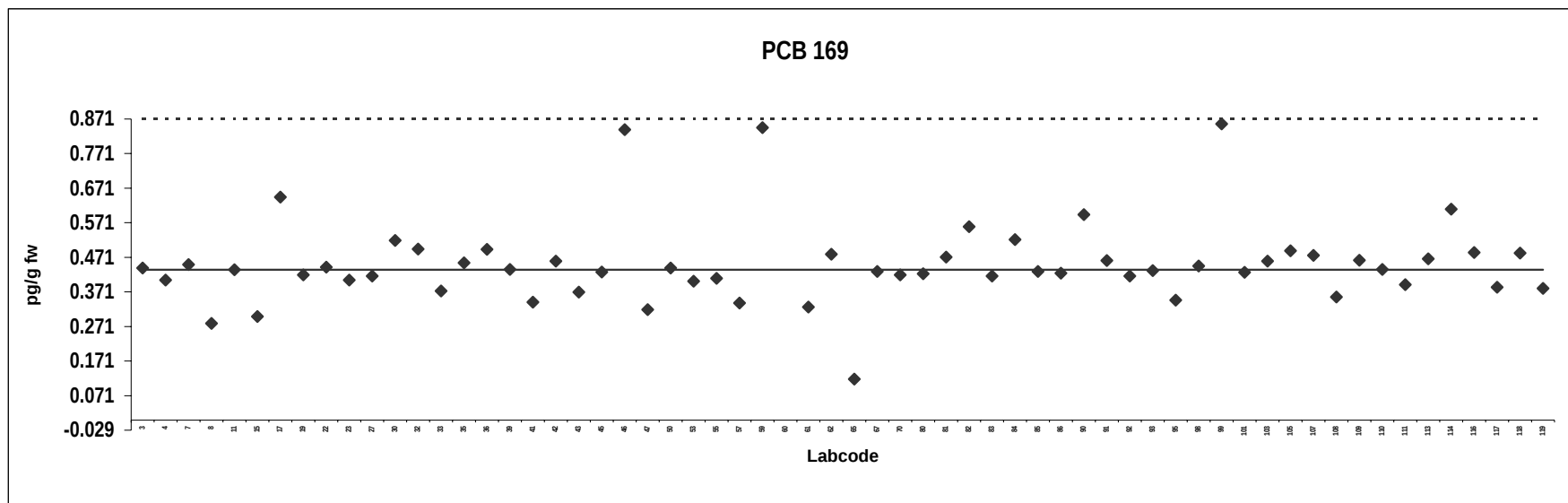
Consensus statistics	
Consensus median, pg/g	3.0
Median all values pg/g	3.0
Consensus mean, pg/g	3.0
Standard deviation, pg/g	0.62
Relative standard deviation, %	20
No. of values reported	62
No. of values removed	0
No. of reported non-detects	0



Beef
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.44	ND Outlier	95	0.35	
4	0.41		98	0.45	
7	0.45		99	0.86	
8	0.28		101	0.43	
11	0.44		103	0.46	
15	0.30		105	0.49	
17	0.65		107	0.48	
19	0.42		108	0.36	
22	0.44		109	0.46	
23	0.41		110	0.44	
27	0.42		111	0.39	
30	0.52		113	0.47	
32	0.50		114	0.61	
33	0.37		116	0.48	
35	0.46		117	0.38	
36	0.49		118	0.48	
39	0.44		119	0.38	
41	0.34				
42	0.46				
43	0.37				
45	0.43				
46	0.84				
47	0.32				
50	0.44				
53	0.40				
55	0.41				
57	0.34				
59	0.85				
60	1.1				
61	0.33				
62	0.48				
65	0.12				
67	0.43				
70	0.42				
80	0.42				
81	0.47				
82	0.56				
83	0.42				
84	0.52				
85	0.43				
86	0.43				
90	0.59				
91	0.46				
92	0.42				
93	0.43				

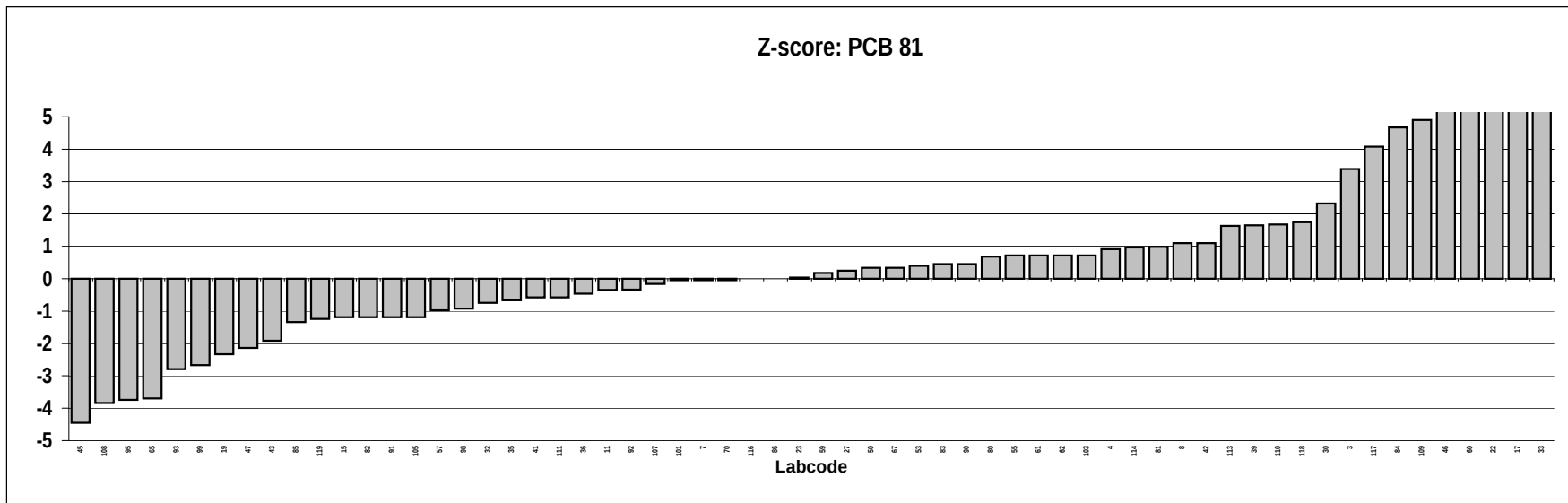
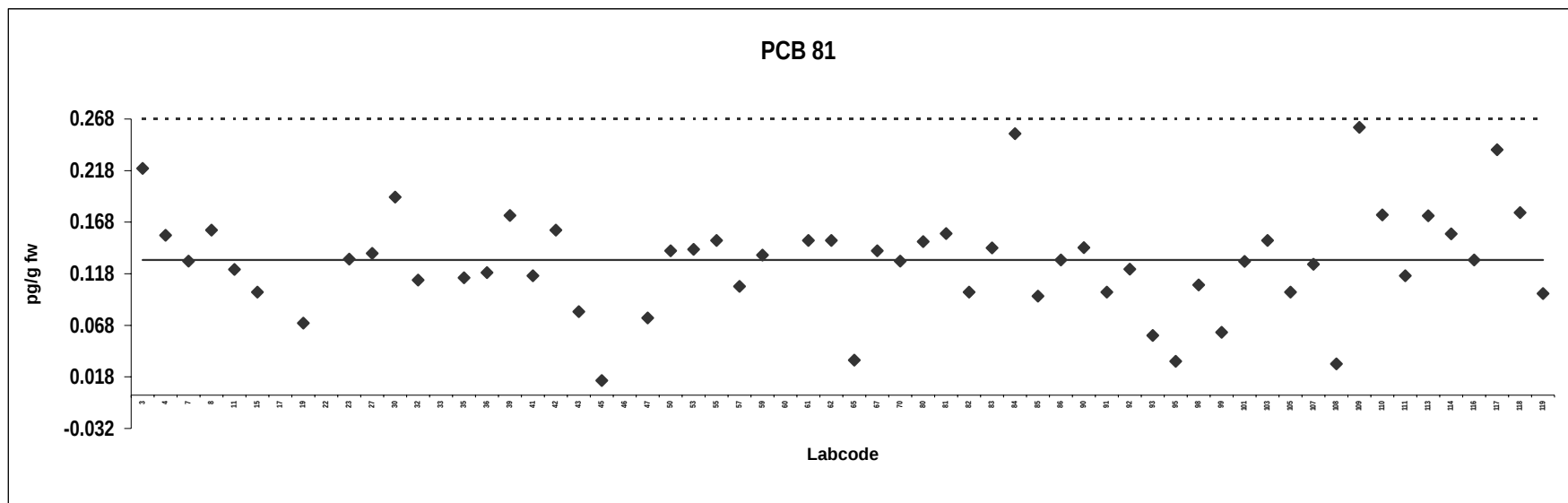
Consensus statistics	
Consensus median, pg/g	0.44
Median all values pg/g	0.44
Consensus mean, pg/g	0.45
Standard deviation, pg/g	0.12
Relative standard deviation, %	27
No. of values reported	62
No. of values removed	1
No. of reported non-detects	1



Beef
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.22		95	0.033	ND
4	0.16		98	0.11	
7	0.13		99	0.061	
8	0.16		101	0.13	
11	0.12	ND	103	0.15	
15	0.10		105	0.10	ND
17	0.52	Outlier	107	0.13	
19	0.070		108	0.031	
22	0.40	Outlier	109	0.26	
23	0.13		110	0.18	
27	0.14		111	0.12	
30	0.19		113	0.17	
32	0.11		114	0.16	
33	0.56	Outlier	116	0.13	
35	0.11		117	0.24	ND
36	0.12		118	0.18	
39	0.17		119	0.099	
41	0.12				
42	0.16				
43	0.081				
45	0.014				
46	0.29	Outlier			
47	0.075				
50	0.14				
53	0.14				
55	0.15				
57	0.11				
59	0.14	ND			
60	0.34	Outlier			
61	0.15				
62	0.15				
65	0.034				
67	0.14				
70	0.13				
80	0.15				
81	0.16				
82	0.10				
83	0.14				
84	0.25				
85	0.096				
86	0.13				
90	0.14				
91	0.10				
92	0.12				
93	0.058	ND			

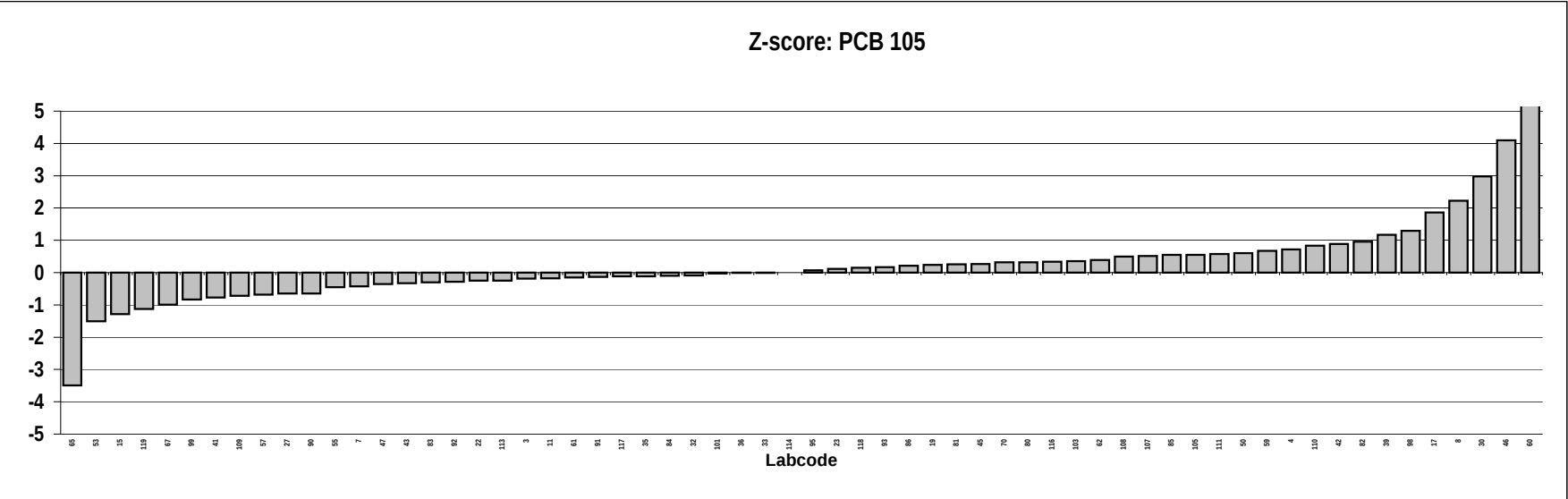
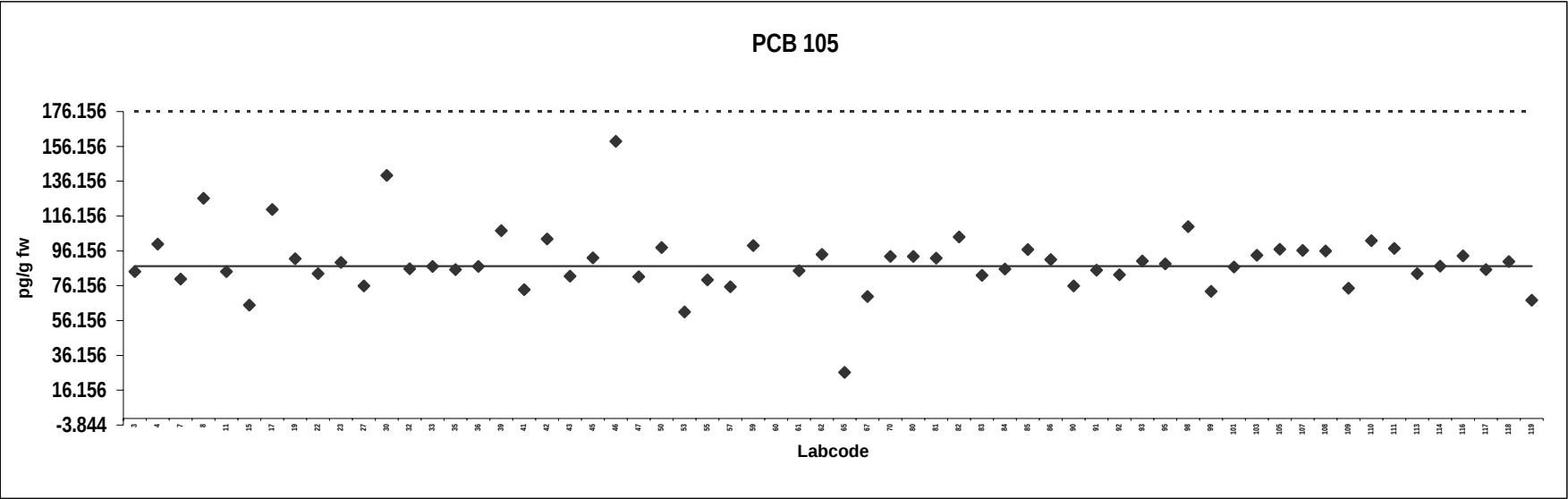
Consensus statistics	
Consensus median, pg/g	0.13
Median all values pg/g	0.13
Consensus mean, pg/g	0.13
Standard deviation, pg/g	0.050
Relative standard deviation, %	39
No. of values reported	62
No. of values removed	5
No. of reported non-detects	6



Beef
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	84	Outlier	95	89	
4	100		98	110	
7	80		99	73	
8	126		101	87	
11	84		103	94	
15	65		105	97	
17	120		107	96	
19	92		108	96	
22	83		109	75	
23	89		110	102	
27	76		111	98	
30	140		113	83	
32	86		114	87	
33	87		116	93	
35	85		117	85	
36	87		118	90	
39	108		119	68	
41	74				
42	103				
43	82				
45	92				
46	159				
47	81				
50	98				
53	61				
55	80				
57	75				
59	99				
60	201				
61	85				
62	94				
65	26				
67	70				
70	93				
80	93				
81	92				
82	104				
83	82				
84	86				
85	97				
86	91				
90	76				
91	85				
92	82				
93	90				

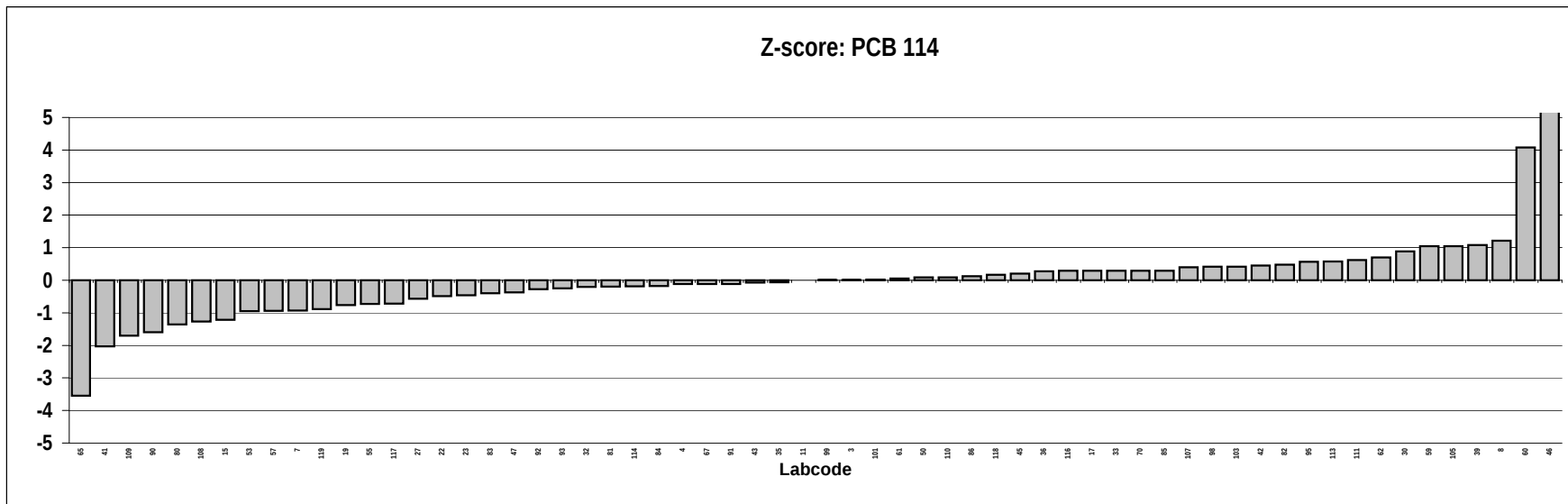
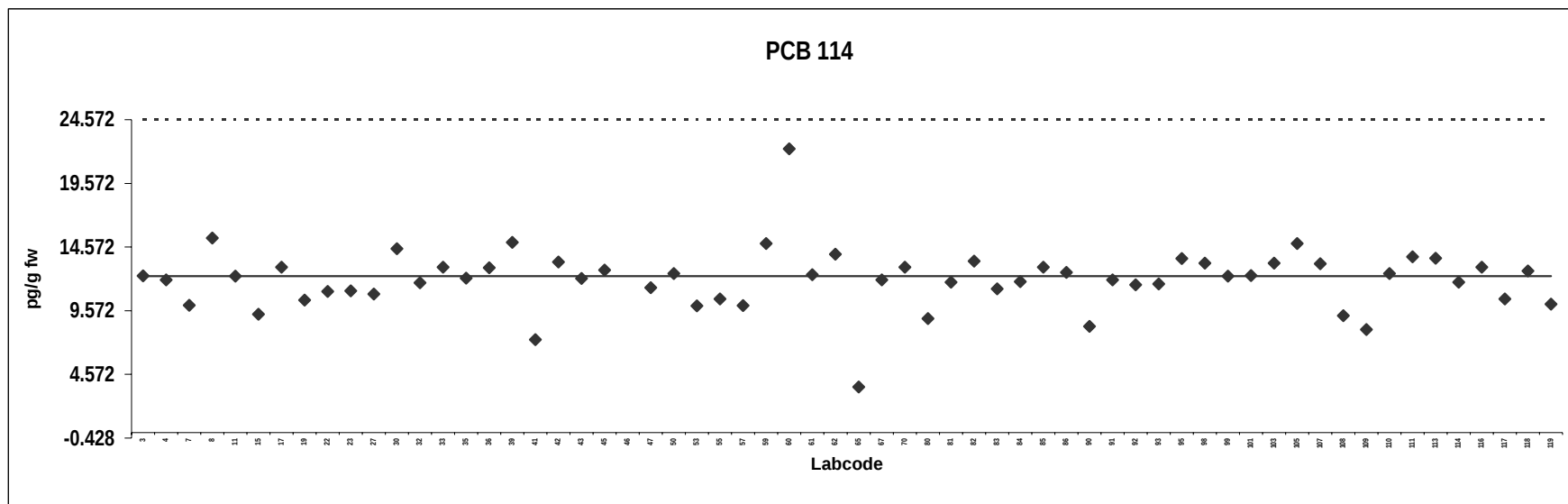
Consensus statistics	
Consensus median, pg/g	87
Median all values pg/g	88
Consensus mean, pg/g	90
Standard deviation, pg/g	18
Relative standard deviation, %	20
No. of values reported	62
No. of values removed	1
No. of reported non-detects	0



Beef
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	12	Outlier	95	14	
4	12		98	13	
7	10		99	12	
8	15		101	12	
11	12		103	13	
15	9.3		105	15	
17	13		107	13	
19	10		108	9.2	
22	11		109	8.1	
23	11		110	13	
27	11		111	14	
30	14		113	14	
32	12		114	12	
33	13		116	13	
35	12		117	11	
36	13		118	13	
39	15		119	10	
41	7.3				
42	13				
43	12				
45	13				
46	26				
47	11				
50	13				
53	9.9				
55	11				
57	10				
59	15				
60	22				
61	12				
62	14				
65	3.6				
67	12				
70	13				
80	9.0				
81	12				
82	13				
83	11				
84	12				
85	13				
86	13				
90	8.4				
91	12				
92	12				
93	12				

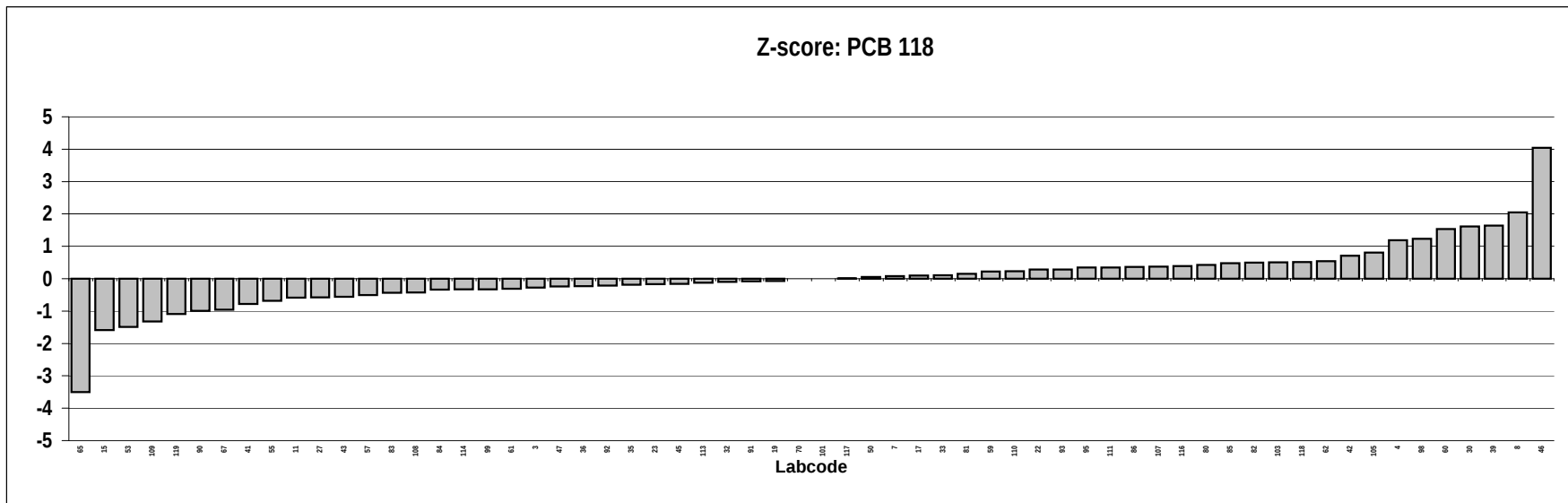
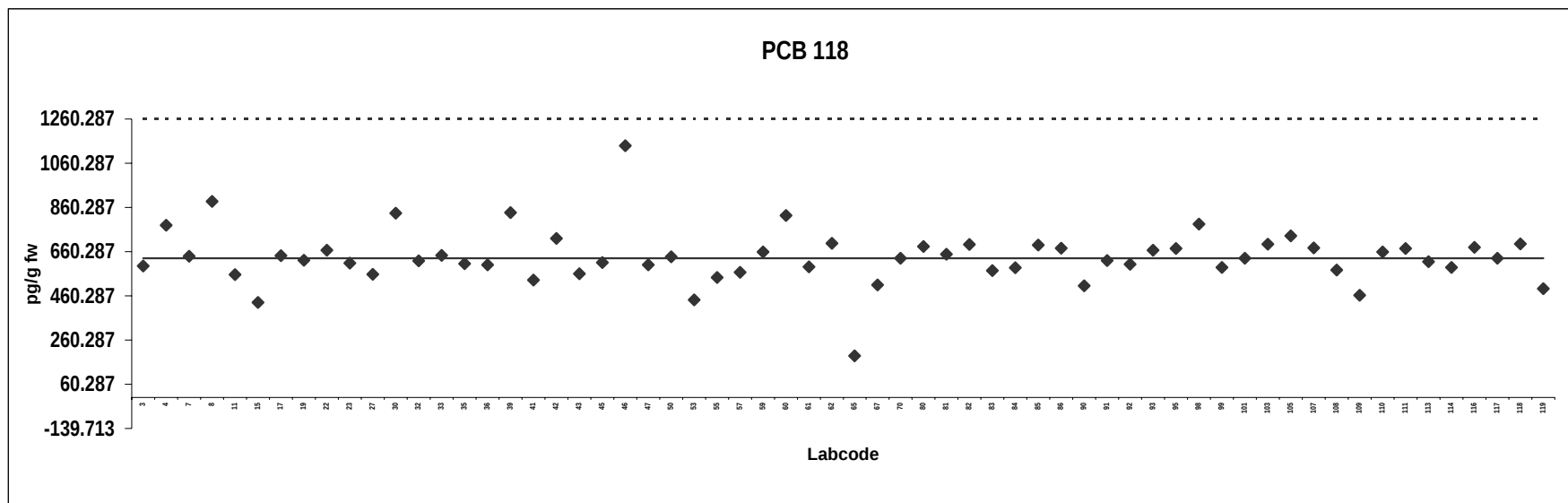
Consensus statistics	
Consensus median, pg/g	12
Median all values pg/g	12
Consensus mean, pg/g	12
Standard deviation, pg/g	2.4
Relative standard deviation, %	20
No. of values reported	62
No. of values removed	1
No. of reported non-detects	0



Beef
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	596		95	674	
4	780		98	785	
7	640		99	589	
8	888		101	630	
11	557		103	694	
15	430		105	731	
17	642		107	677	
19	621		108	577	
22	666		109	463	
23	609		110	660	
27	557		111	674	
30	834		113	615	
32	618		114	589	
33	644		116	680	
35	606		117	631	
36	601		118	695	
39	837		119	493	
41	532				
42	720				
43	560				
45	611				
46	1140				
47	600				
50	637				
53	442				
55	544				
57	566				
59	658				
60	824				
61	591				
62	698				
65	189				
67	510				
70	630				
80	684				
81	649				
82	693				
83	575				
84	587				
85	690				
86	676				
90	505				
91	620				
92	603				
93	666				

Consensus statistics	
Consensus median, pg/g	630
Median all values pg/g	630
Consensus mean, pg/g	635
Standard deviation, pg/g	125
Relative standard deviation, %	20
No. of values reported	62
No. of values removed	0
No. of reported non-detects	0

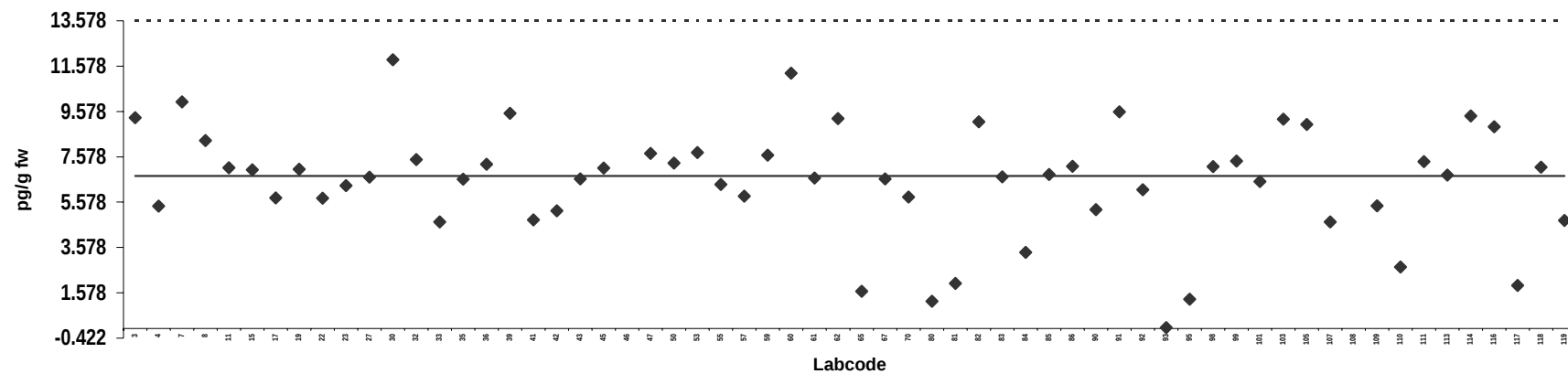


Beef
Congener: PCB 123

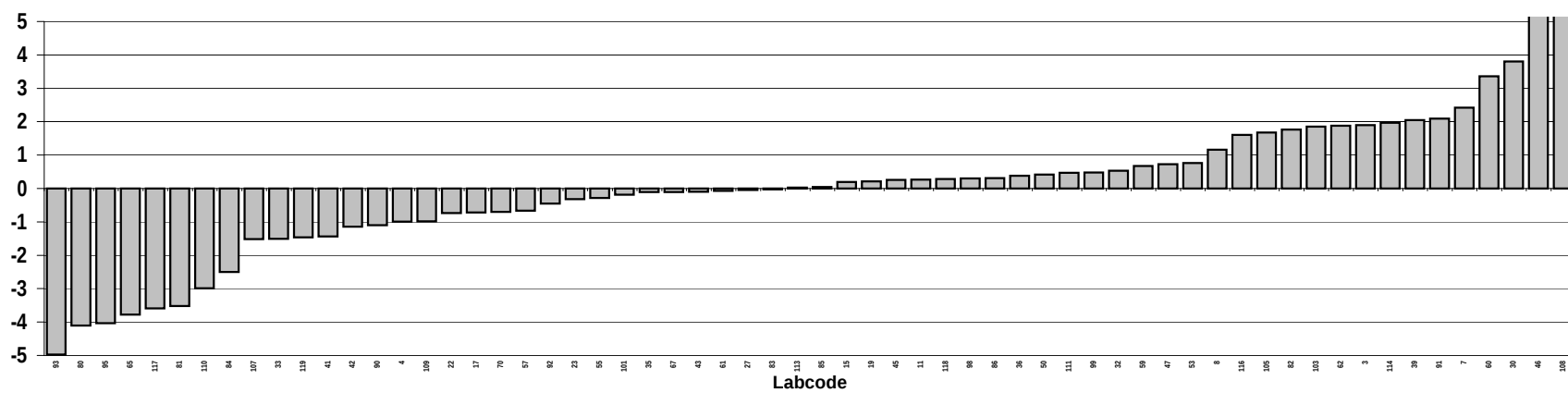
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	9.3		95	1.3	ND
4	5.4		98	7.2	
7	10	ND	99	7.4	
8	8.3		101	6.5	
11	7.1		103	9.2	
15	7.0	ND	105	9.0	
17	5.8		107	4.7	
19	7.0		108	16	Outlier
22	5.7		109	5.4	
23	6.3		110	2.7	
27	6.7		111	7.4	
30	12		113	6.8	
32	7.5		114	9.4	
33	4.7		116	8.9	
35	6.6		117	1.9	
36	7.3		118	7.1	
39	9.5		119	4.8	
41	4.8				
42	5.2				
43	6.6				
45	7.1				
46	15	Outlier			
47	7.7				
50	7.3				
53	7.8				
55	6.4				
57	5.8				
59	7.7				
60	11				
61	6.6				
62	9.3				
65	1.6				
67	6.6				
70	5.8				
80	1.2				
81	2.0				
82	9.1				
83	6.7				
84	3.4				
85	6.8				
86	7.2				
90	5.3				
91	9.6				
92	6.1				
93	0.040	ND			

Consensus statistics	
Consensus median, pg/g	6.7
Median all values pg/g	6.8
Consensus mean, pg/g	6.5
Standard deviation, pg/g	2.4
Relative standard deviation, %	38
No. of values reported	62
No. of values removed	2
No. of reported non-detects	4

PCB 123



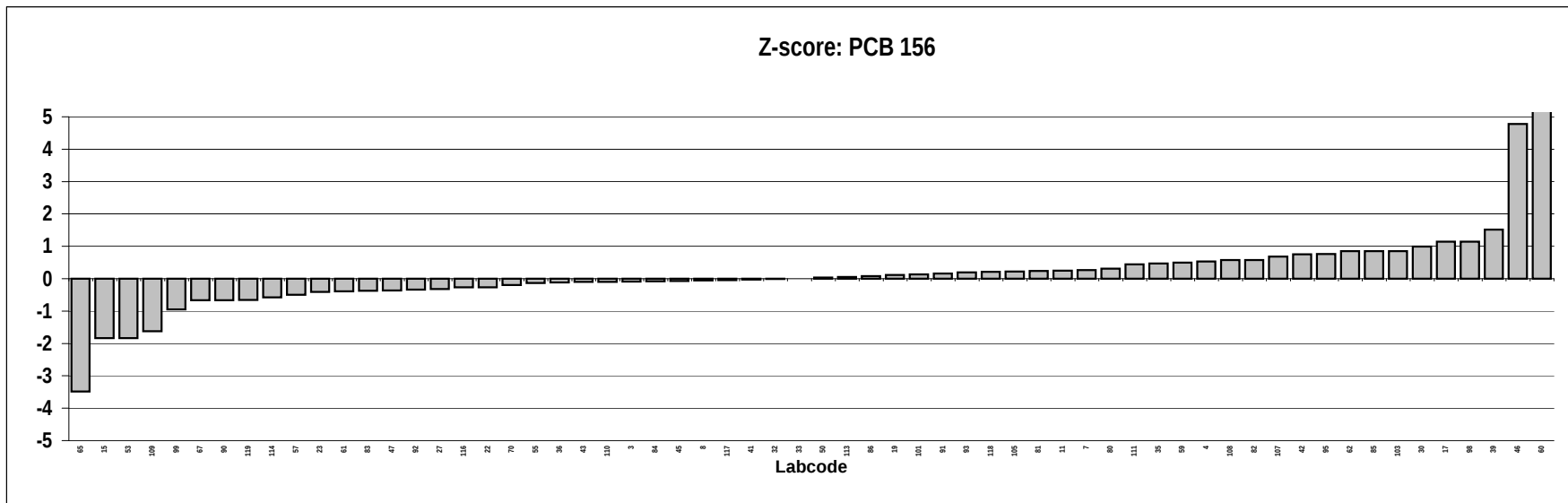
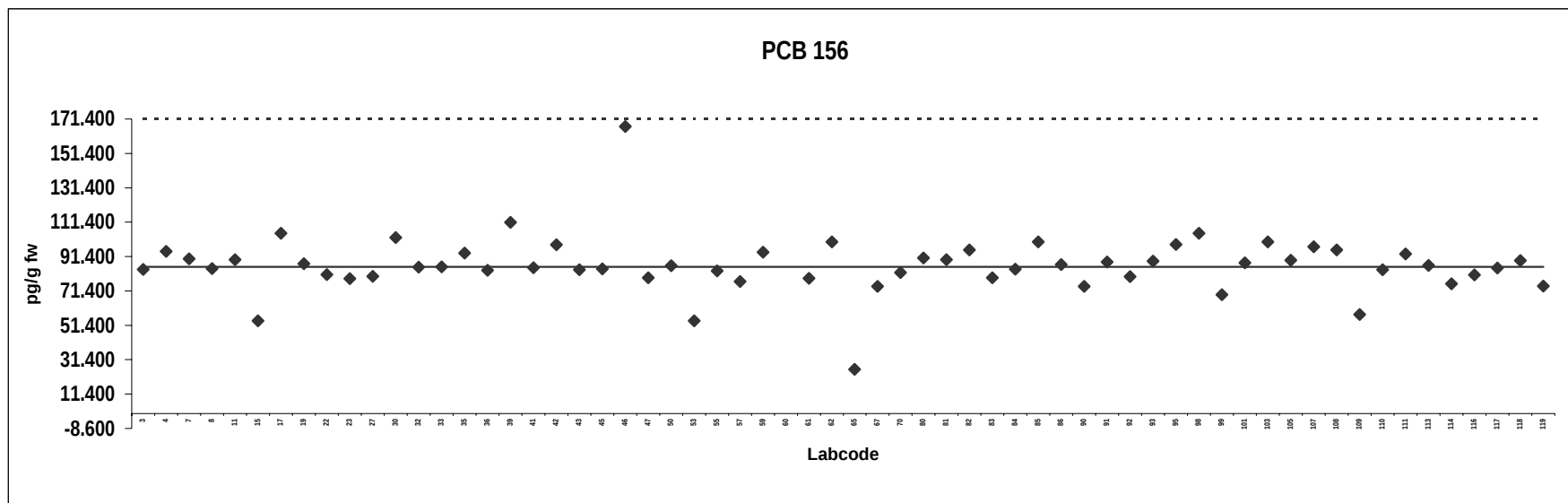
Z-score: PCB 123



Beef
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	84	Outlier	95	98	
4	95		98	105	
7	90		99	69	
8	84		101	88	
11	90		103	100	
15	54		105	89	
17	105		107	97	
19	87		108	95	
22	81		109	58	
23	78		110	84	
27	80		111	93	
30	102		113	86	
32	85		114	75	
33	85		116	81	
35	93		117	85	
36	83		118	89	
39	111		119	74	
41	85				
42	98				
43	84				
45	84				
46	167				
47	79				
50	86				
53	54				
55	83				
57	77				
59	94				
60	180				
61	79				
62	100				
65	26				
67	74				
70	82				
80	91				
81	90				
82	95				
83	79				
84	84				
85	100				
86	87				
90	74				
91	88				
92	80				
93	89				

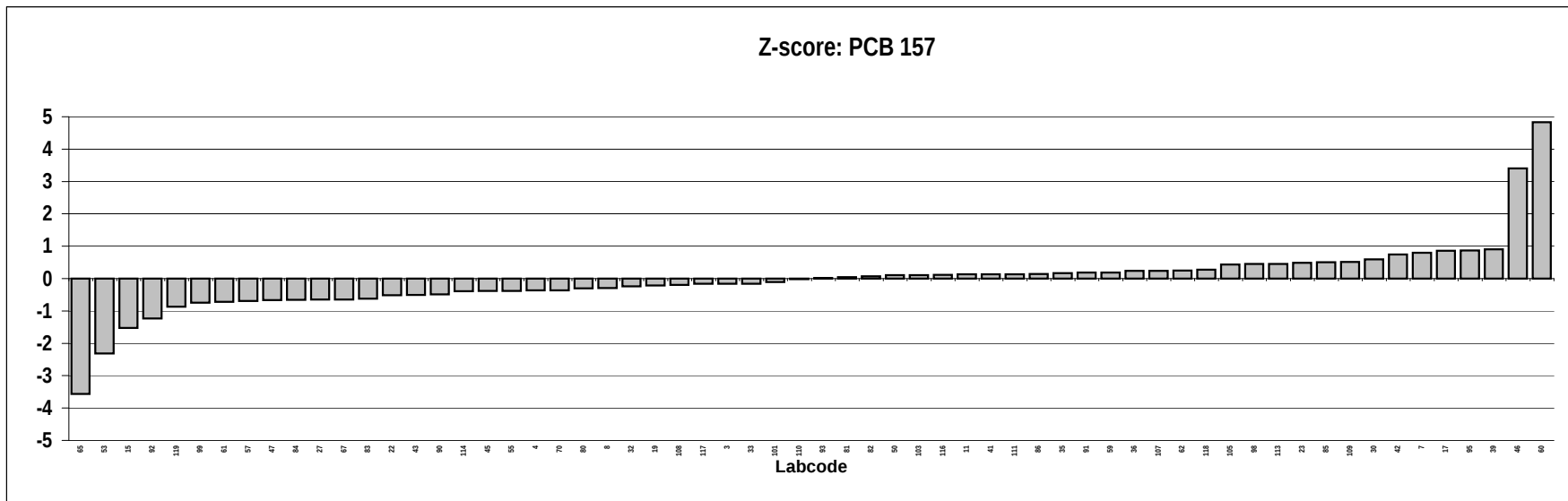
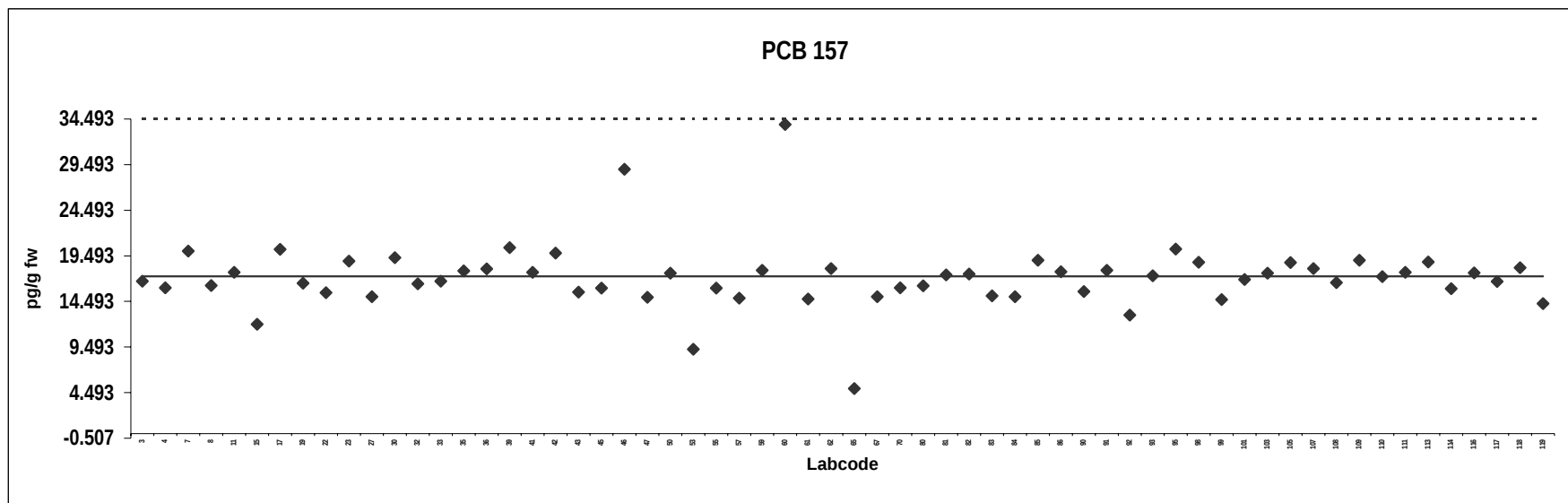
Consensus statistics	
Consensus median, pg/g	85
Median all values pg/g	86
Consensus mean, pg/g	86
Standard deviation, pg/g	17
Relative standard deviation, %	20
No. of values reported	62
No. of values removed	1
No. of reported non-detects	0



Beef
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	17		95	20	
4	16		98	19	
7	20		99	15	
8	16		101	17	
11	18		103	18	
15	12		105	19	
17	20		107	18	
19	17		108	17	
22	15		109	19	
23	19		110	17	
27	15		111	18	
30	19		113	19	
32	16		114	16	
33	17		116	18	
35	18		117	17	
36	18		118	18	
39	20		119	14	
41	18				
42	20				
43	16				
45	16				
46	29				
47	15				
50	18				
53	9.3				
55	16				
57	15				
59	18				
60	34				
61	15				
62	18				
65	4.9				
67	15				
70	16				
80	16				
81	17				
82	17				
83	15				
84	15				
85	19				
86	18				
90	16				
91	18				
92	13				
93	17				

Consensus statistics	
Consensus median, pg/g	17
Median all values pg/g	17
Consensus mean, pg/g	17
Standard deviation, pg/g	3.7
Relative standard deviation, %	21
No. of values reported	62
No. of values removed	0
No. of reported non-detects	0

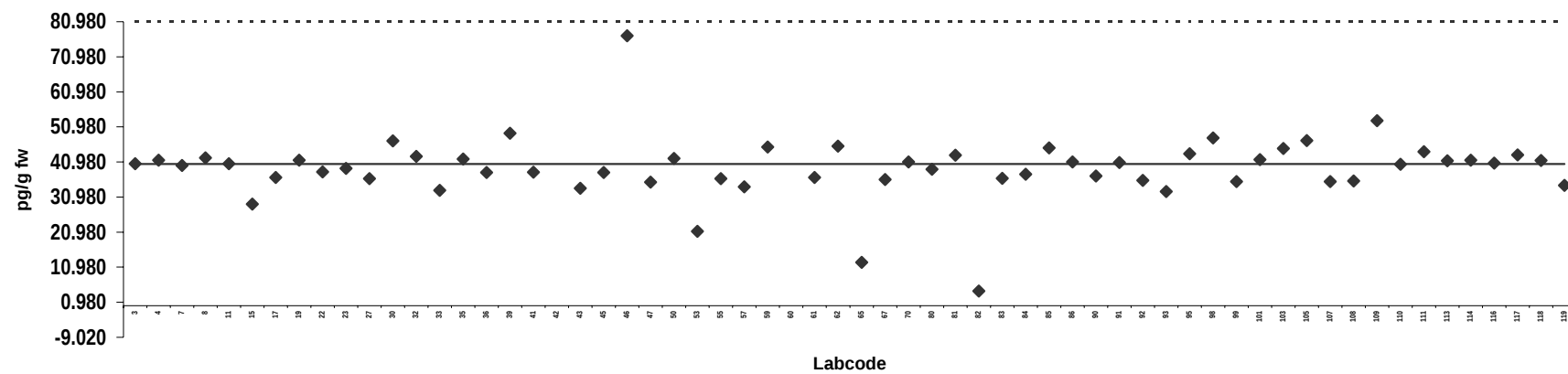


Beef
Congener: PCB 167

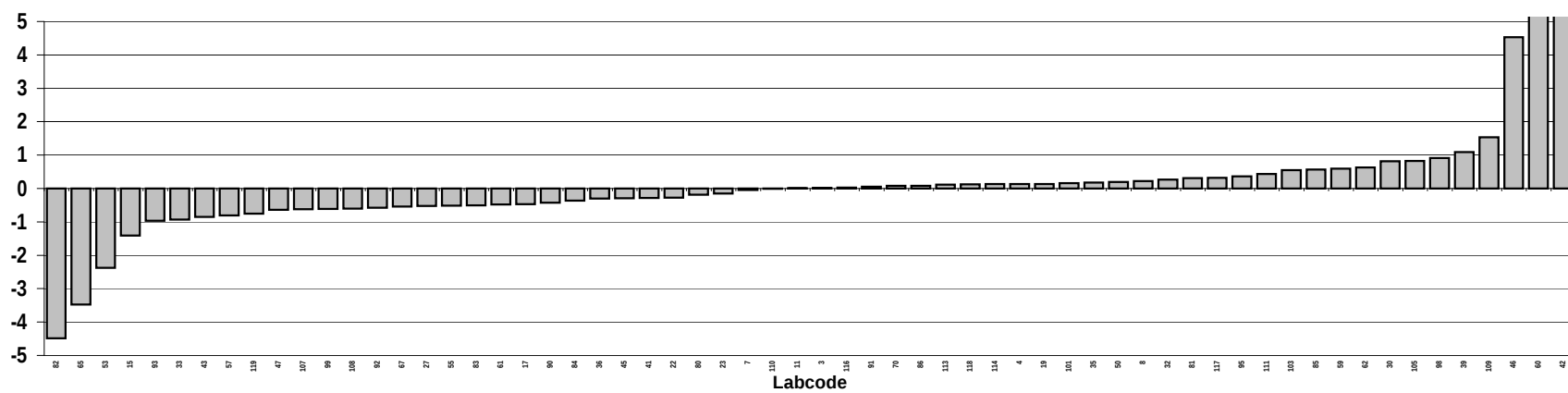
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	41		95	43	
4	42		98	48	
7	40		99	35	
8	42		101	42	
11	40		103	45	
15	29		105	47	
17	37		107	35	
19	42		108	36	
22	38		109	53	
23	39		110	40	
27	36		111	44	
30	47		113	41	
32	43		114	41	
33	33		116	41	
35	42		117	43	
36	38		118	41	
39	49		119	34	
41	38				
42	131	Outlier			
43	34				
45	38				
46	77				
47	35				
50	42				
53	21				
55	36				
57	34				
59	45				
60	88	Outlier			
61	37				
62	46				
65	12				
67	36				
70	41				
80	39				
81	43				
82	4.1				
83	36				
84	37				
85	45				
86	41				
90	37				
91	41				
92	36				
93	33				

Consensus statistics	
Consensus median, pg/g	40
Median all values pg/g	40
Consensus mean, pg/g	39
Standard deviation, pg/g	9.1
Relative standard deviation, %	23
No. of values reported	62
No. of values removed	2
No. of reported non-detects	0

PCB 167



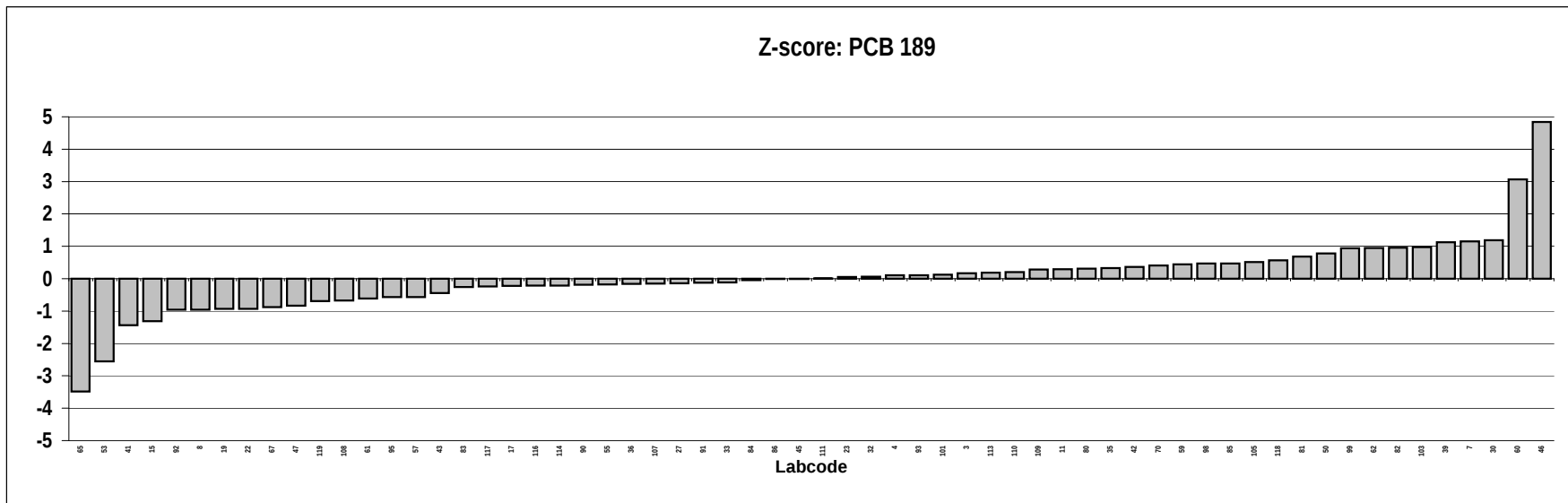
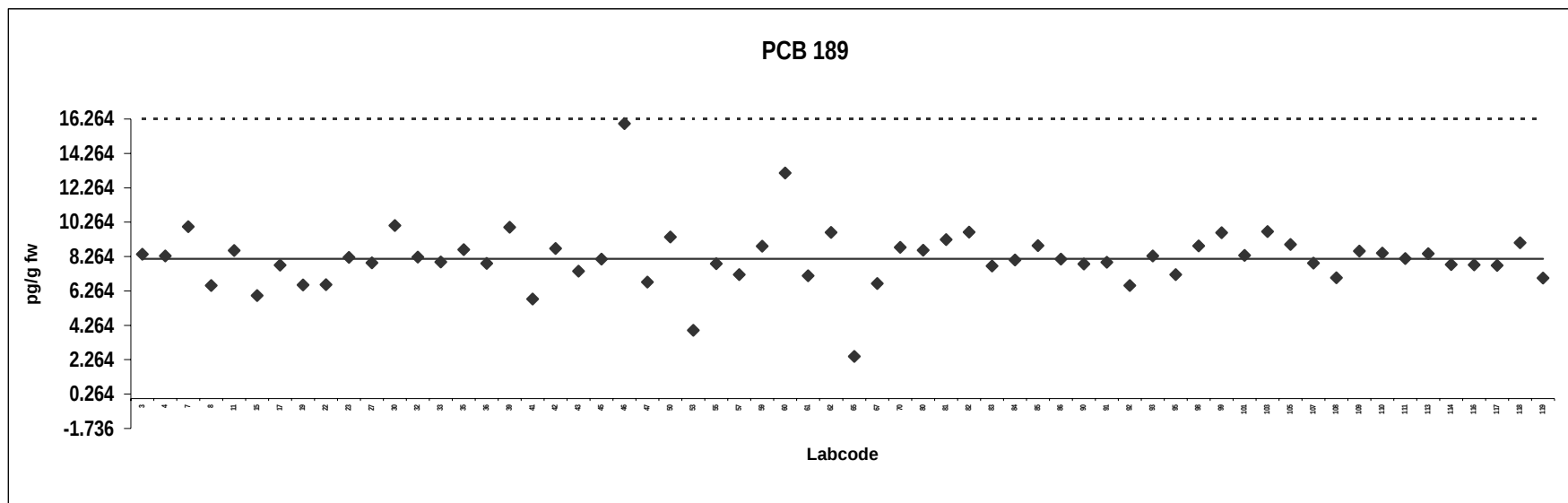
Z-score: PCB 167



Beef
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	8.4	ND	95	7.2	
4	8.3		98	8.9	
7	10		99	9.7	
8	6.6		101	8.3	
11	8.6		103	9.7	
15	6.0		105	9.0	
17	7.8		107	7.9	
19	6.6		108	7.0	
22	6.6		109	8.6	
23	8.2		110	8.5	
27	7.9		111	8.2	
30	10		113	8.4	
32	8.2		114	7.8	
33	8.0		116	7.8	
35	8.7		117	7.7	
36	7.9		118	9.1	
39	10		119	7.0	
41	5.8				
42	8.7				
43	7.4				
45	8.1				
46	16				
47	6.8				
50	9.4				
53	4.0				
55	7.9				
57	7.2				
59	8.9				
60	13				
61	7.1				
62	9.7				
65	2.5				
67	6.7				
70	8.8				
80	8.6				
81	9.2				
82	9.7				
83	7.7				
84	8.1				
85	8.9				
86	8.1				
90	7.8				
91	7.9				
92	6.6				
93	8.3				

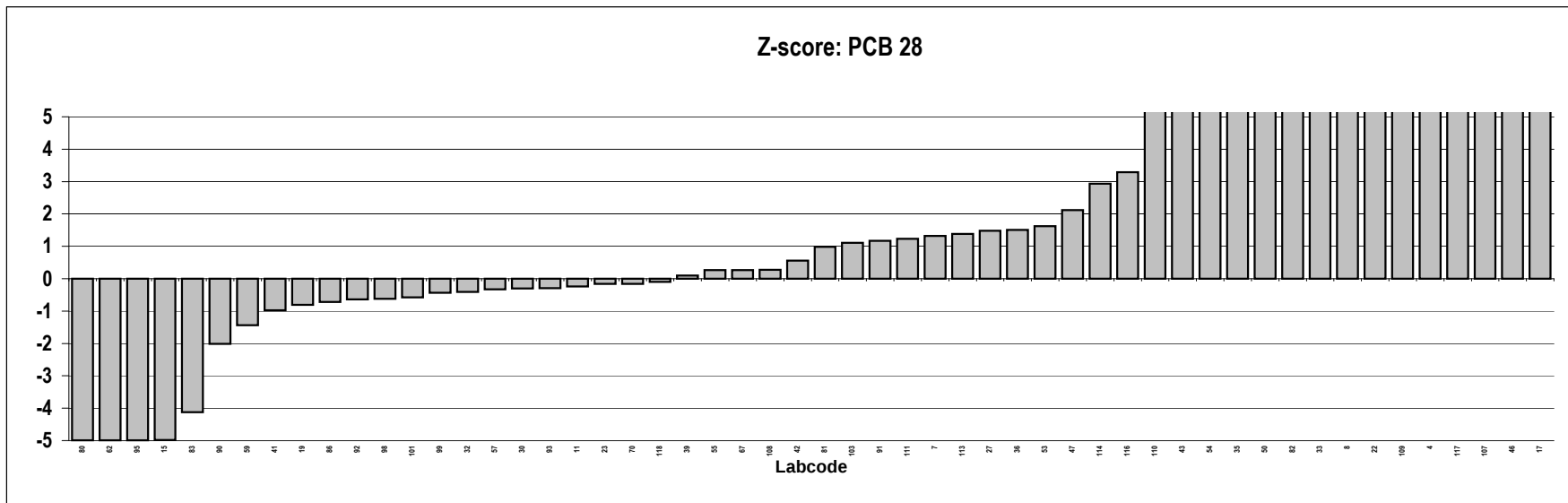
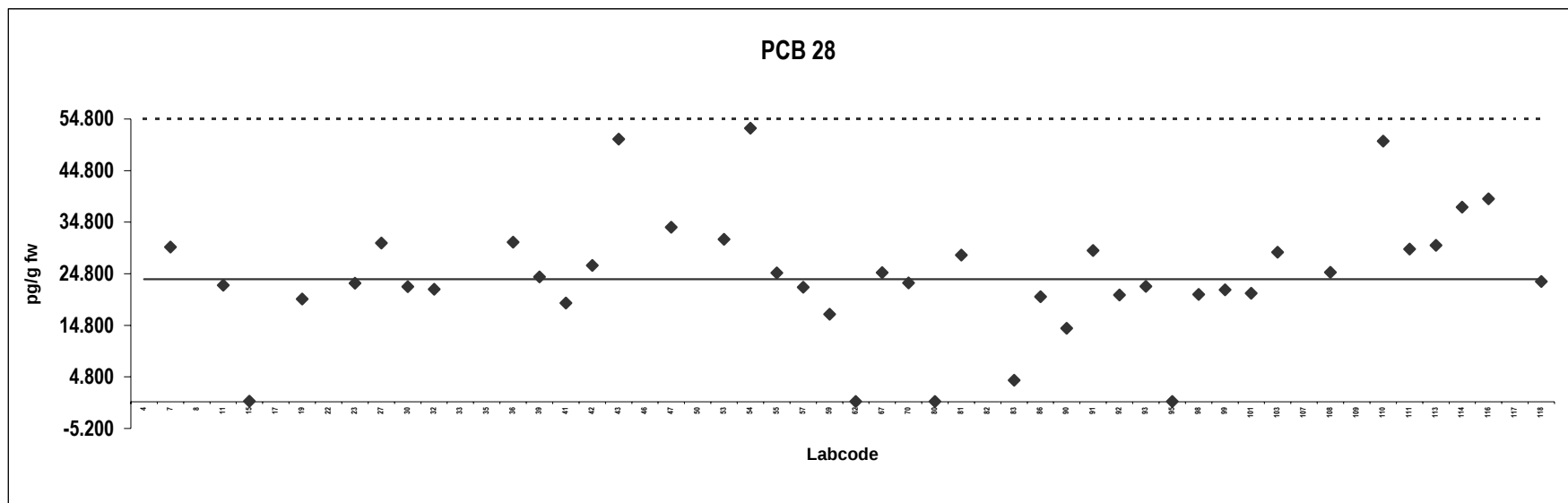
Consensus statistics	
Consensus median, pg/g	8.1
Median all values pg/g	8.1
Consensus mean, pg/g	8.2
Standard deviation, pg/g	1.8
Relative standard deviation, %	22
No. of values reported	62
No. of values removed	0
No. of reported non-detects	1



Beef
Congener: PCB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	98	Outlier	108	25	
7	30		109	97	Outlier
8	79	Outlier	110	51	
11	23		111	30	
15	0.10	ND	113	30	
17	3550	Outlier	114	38	
19	20		116	39	
22	84	Outlier	117	117	Outlier
23	23		118	23	
27	31				
30	22				
32	22				
33	77	Outlier			
35	56	Outlier			
36	31				
39	24				
41	19				
42	26				
43	51				
46	161	Outlier			
47	34				
50	57	Outlier			
53	31				
54	53				
55	25				
57	22				
59	17				
62	0.030				
67	25				
70	23				
80	0.026				
81	28				
82	68	Outlier			
83	4.2	ND			
86	20				
90	14				
91	29				
92	21				
93	22				
95	0.030				
98	21				
99	22				
101	21				
103	29				
107	138	Outlier			

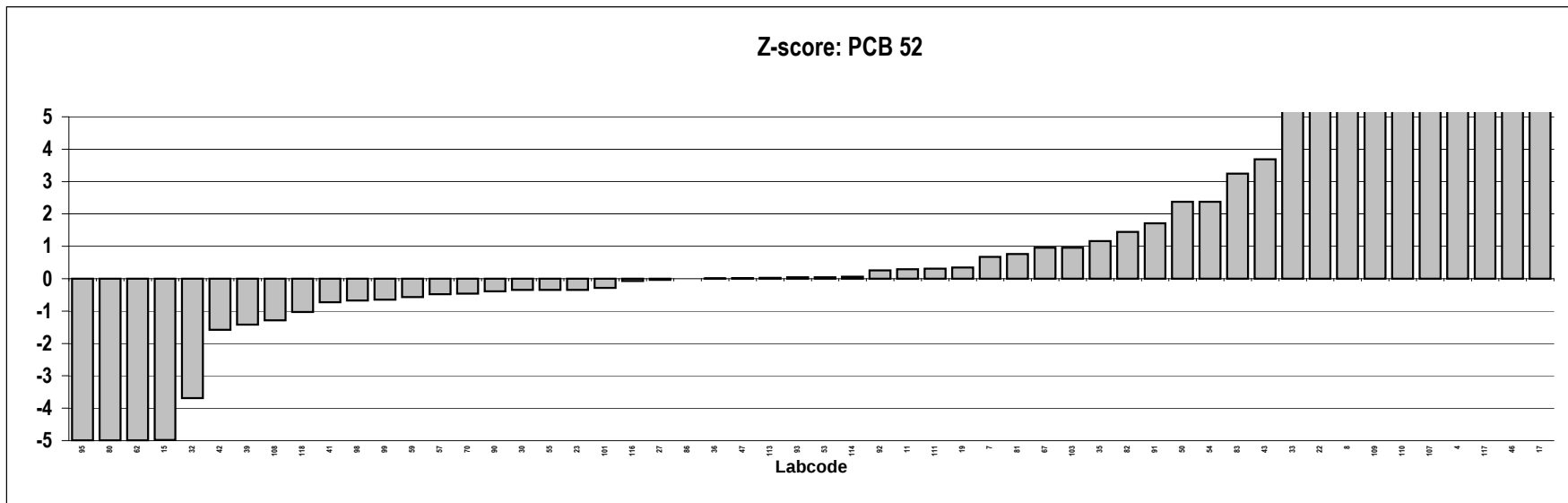
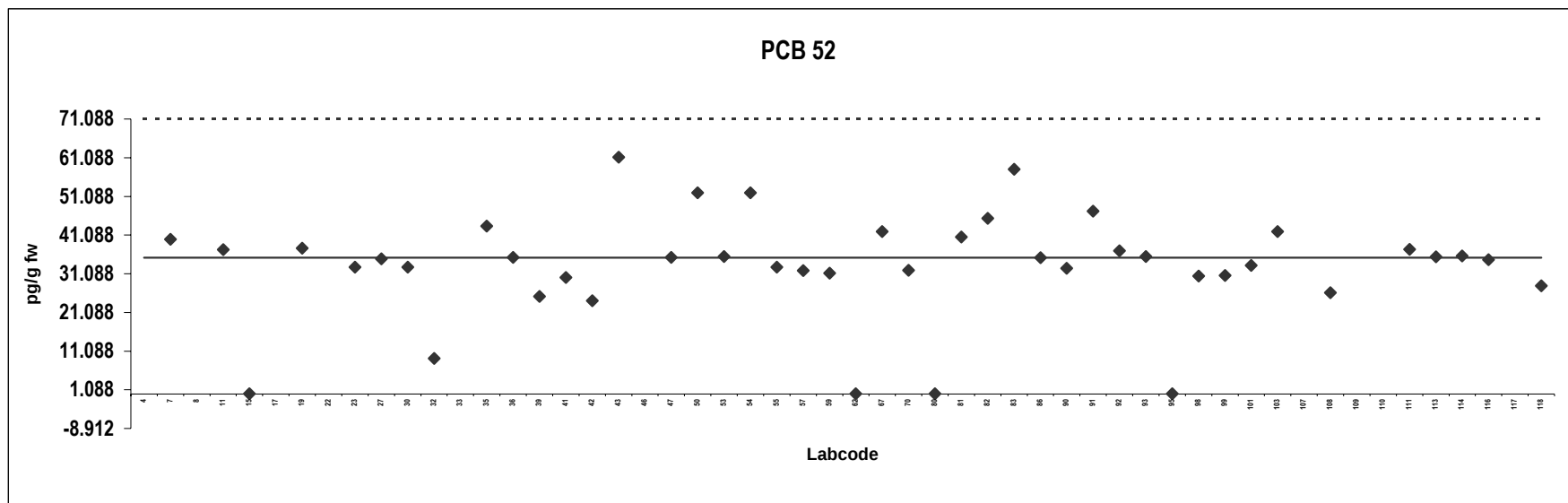
Consensus statistics	
Consensus median, pg/g	24
Median all values pg/g	27
Consensus mean, pg/g	24
Standard deviation, pg/g	12
Relative standard deviation, %	50
No. of values reported	54
No. of values removed	12
No. of reported non-detects	2



Beef
Congener: PCB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	165	Outlier	108	26	
7	40		109	135	Outlier
8	104	Outlier	110	143	Outlier
11	37		111	37	
15	0.10	ND	113	35	
17	11200	Outlier	114	36	
19	38		116	35	
22	90	Outlier	117	257	Outlier
23	33		118	28	
27	35				
30	33				
32	9.2				
33	77	Outlier			
35	43				
36	35				
39	25				
41	30				
42	24				
43	61				
46	614	Outlier			
47	35				
50	52				
53	36				
54	52				
55	33				
57	32				
59	31				
62	0.042				
67	42				
70	32				
80	0.041				
81	41				
82	45				
83	58				
86	35				
90	32				
91	47				
92	37				
93	36				
95	0.035				
98	31				
99	31				
101	33				
103	42				
107	164	Outlier			

Consensus statistics	
Consensus median, pg/g	35
Median all values pg/g	36
Consensus mean, pg/g	33
Standard deviation, pg/g	14
Relative standard deviation, %	42
No. of values reported	54
No. of values removed	10
No. of reported non-detects	1



Beef
Congener: PCB 101

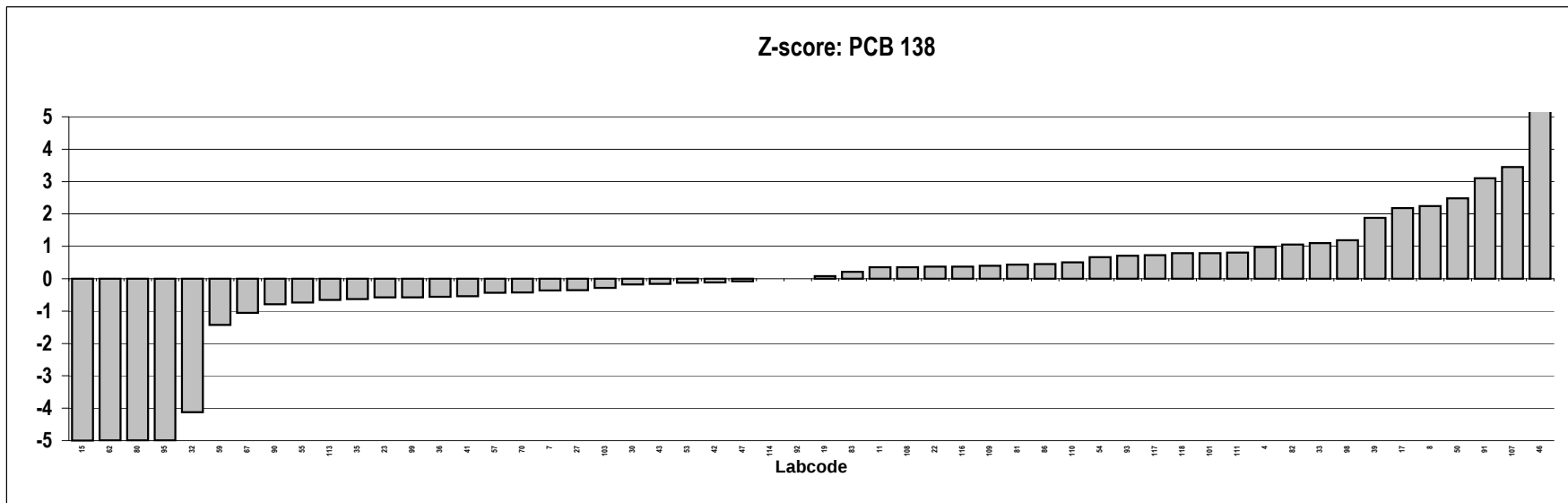
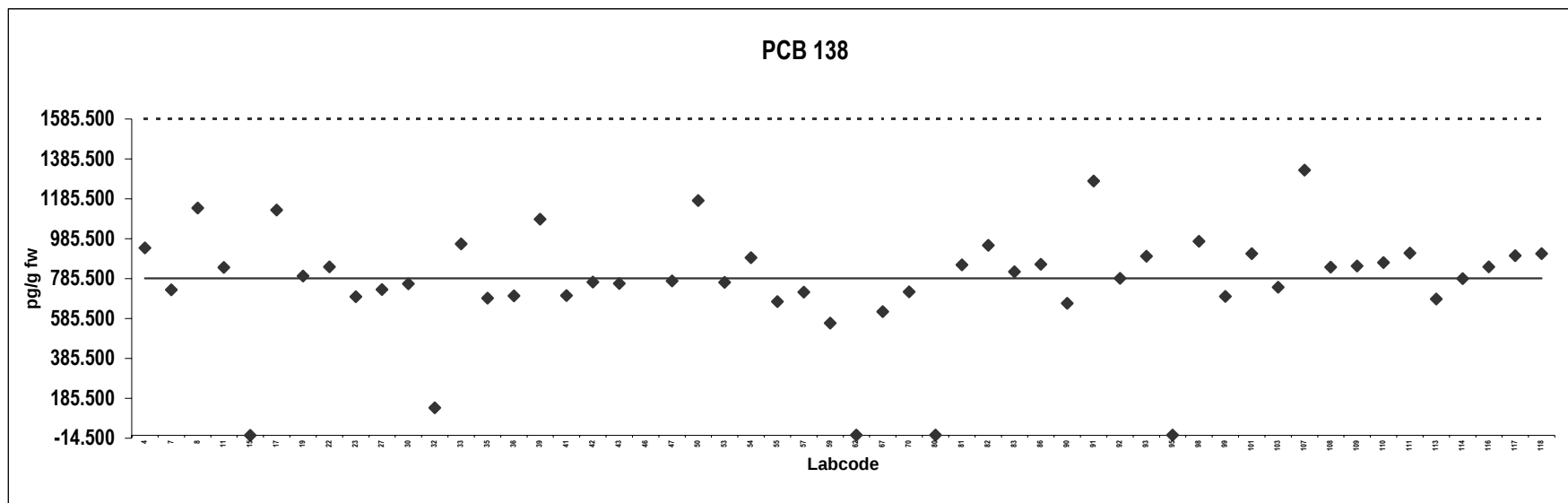
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	290	Outlier	108	96	
7	110		109	170	
8	535	Outlier	110	279	Outlier
11	103		111	112	
15	0.10	ND	113	101	
17	3550	Outlier	114	101	
19	105		116	107	
22	141		117	151	
23	94		118	91	
27	87				
30	66				
32	107				
33	91				
35	94				
36	88				
39	103				
41	78				
42	88				
43	112				
46	384	Outlier			
47	105				
50	172				
53	100				
54	113				
55	92				
57	92				
59	86				
62	0.10				
67	90				
70	96				
80	0.096				
81	117				
82	124				
83	139				
86	93				
90	88				
91	96				
92	113				
93	117				
95	0.12				
98	91				
99	97				
101	110				
103	101				
107	250	Outlier			

Consensus statistics	
Consensus median, pg/g	100
Median all values pg/g	101
Consensus mean, pg/g	96
Standard deviation, pg/g	36
Relative standard deviation, %	37
No. of values reported	54
No. of values removed	6
No. of reported non-detects	1

Beef
Congener: PCB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	940	Outlier	108	843	
7	730		109	849	
8	1140		110	866	
11	842		111	913	
15	0.50		113	683	
17	1130		114	786	
19	799		116	845	
22	844		117	901	
23	695		118	910	
27	731				
30	759				
32	138				
33	960				
35	688				
36	699				
39	1083				
41	701				
42	768				
43	761				
46	2140				
47	774				
50	1177				
53	767				
54	891				
55	671				
57	718				
59	562				
62	0.76				
67	620				
70	720				
80	0.79				
81	855				
82	953				
83	820				
86	857				
90	662				
91	1274				
92	787				
93	898				
95	0.85				
98	973				
99	696				
101	910				
103	742				
107	1329				

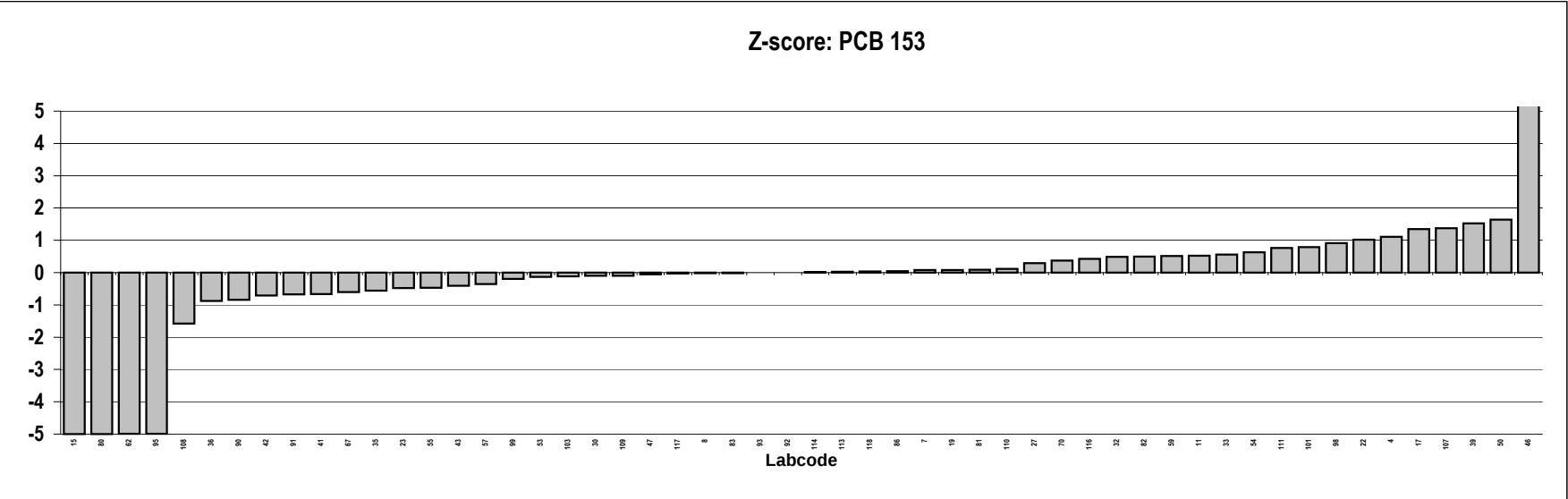
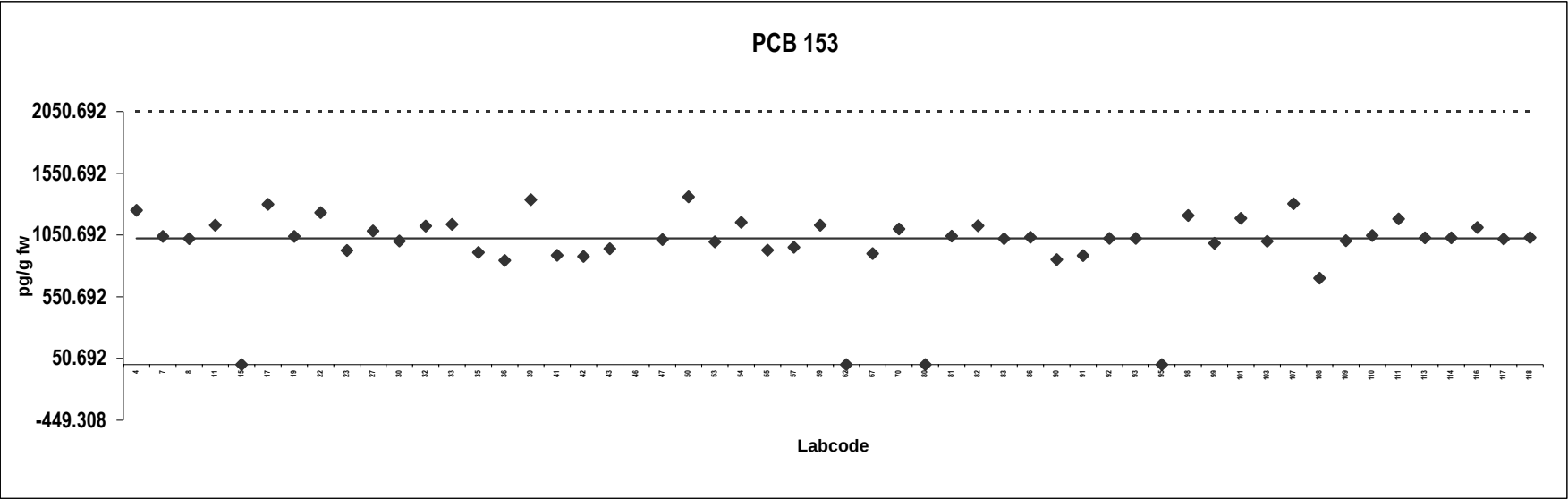
Consensus statistics	
Consensus median, pg/g	787
Median all values pg/g	793
Consensus mean, pg/g	767
Standard deviation, pg/g	287
Relative standard deviation, %	37
No. of values reported	54
No. of values removed	1
No. of reported non-detects	0



Beef
Congener: PCB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	1250	Outlier	108	701	
7	1040		109	1004	
8	1020		110	1047	
11	1130		111	1180	
15	0.70		113	1029	
17	1300		114	1027	
19	1040		116	1110	
22	1233		117	1018	
23	926		118	1030	
27	1083				
30	1003				
32	1123				
33	1138				
35	909				
36	844				
39	1335				
41	887				
42	878				
43	940				
46	2520				
47	1013				
50	1359				
53	996				
54	1153				
55	928				
57	951				
59	1130				
62	1.0				
67	900				
70	1100				
80	0.88				
81	1042				
82	1126				
83	1020				
86	1032				
90	851				
91	885				
92	1023				
93	1023				
95	1.1				
98	1210				
99	983				
101	1185				
103	1000				
107	1305				

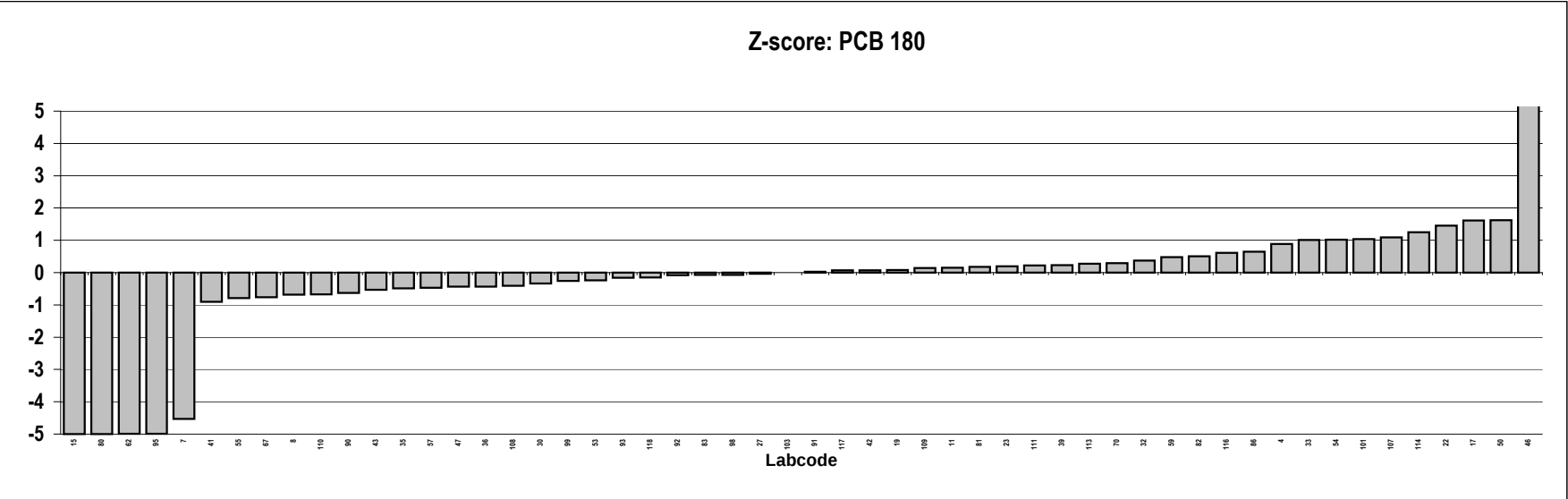
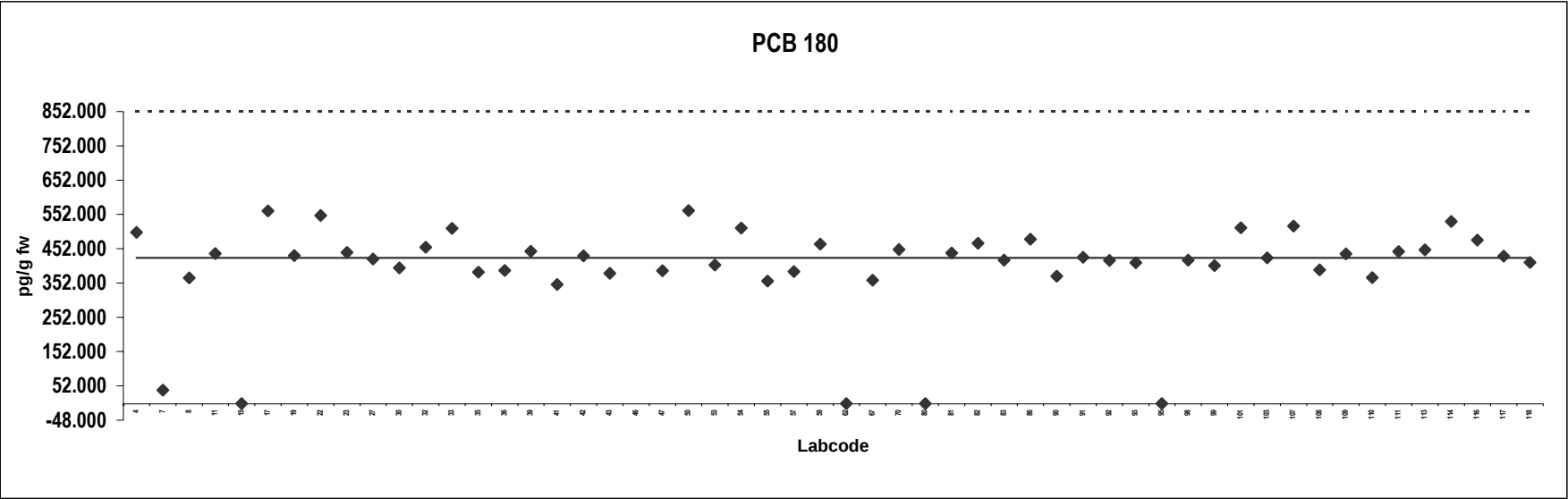
Consensus statistics	
Consensus median, pg/g	1023
Median all values pg/g	1025
Consensus mean, pg/g	971
Standard deviation, pg/g	309
Relative standard deviation, %	32
No. of values reported	54
No. of values removed	1
No. of reported non-detects	0



Beef
Congener: PCB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	500	Outlier	108	390	
7	40		109	437	
8	367		110	368	
11	438		111	444	
15	0.30		113	449	
17	562		114	531	
19	432		116	477	
22	549		117	431	
23	441		118	412	
27	422				
30	396				
32	456				
33	511				
35	384				
36	388				
39	445				
41	348				
42	431				
43	380				
46	961				
47	388				
50	563				
53	404				
54	512				
55	358				
57	385				
59	466				
62	0.43				
67	360				
70	450				
80	0.37				
81	440				
82	468				
83	419				
86	480				
90	372				
91	427				
92	418				
93	411				
95	0.46				
98	419				
99	403				
101	513				
103	425				
107	518				

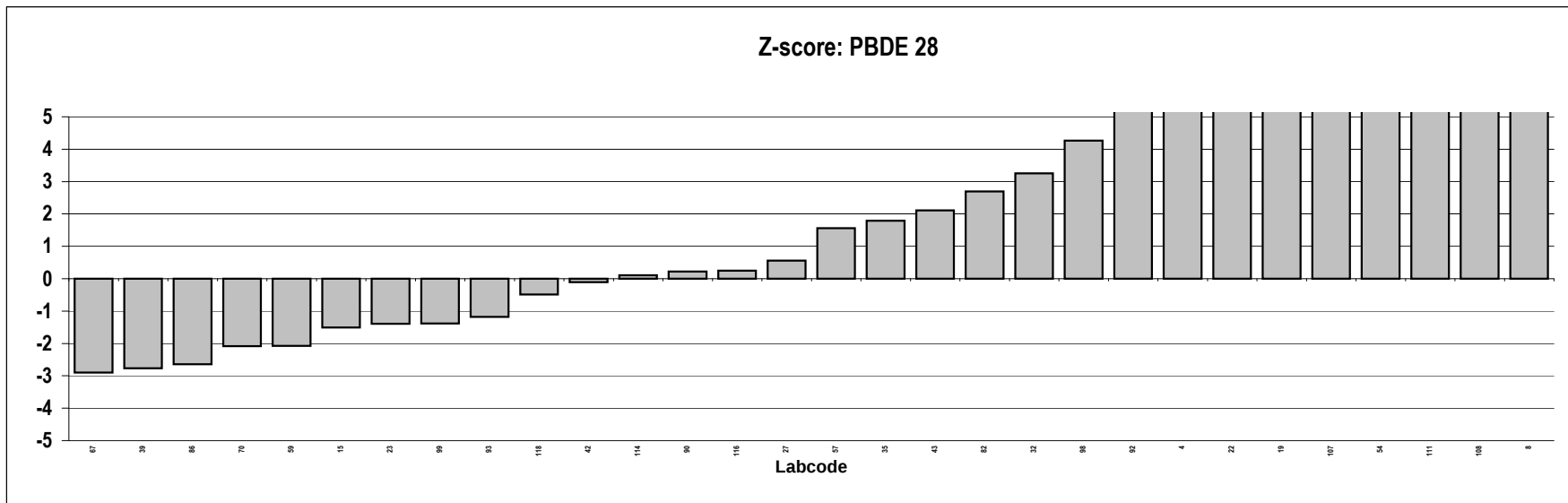
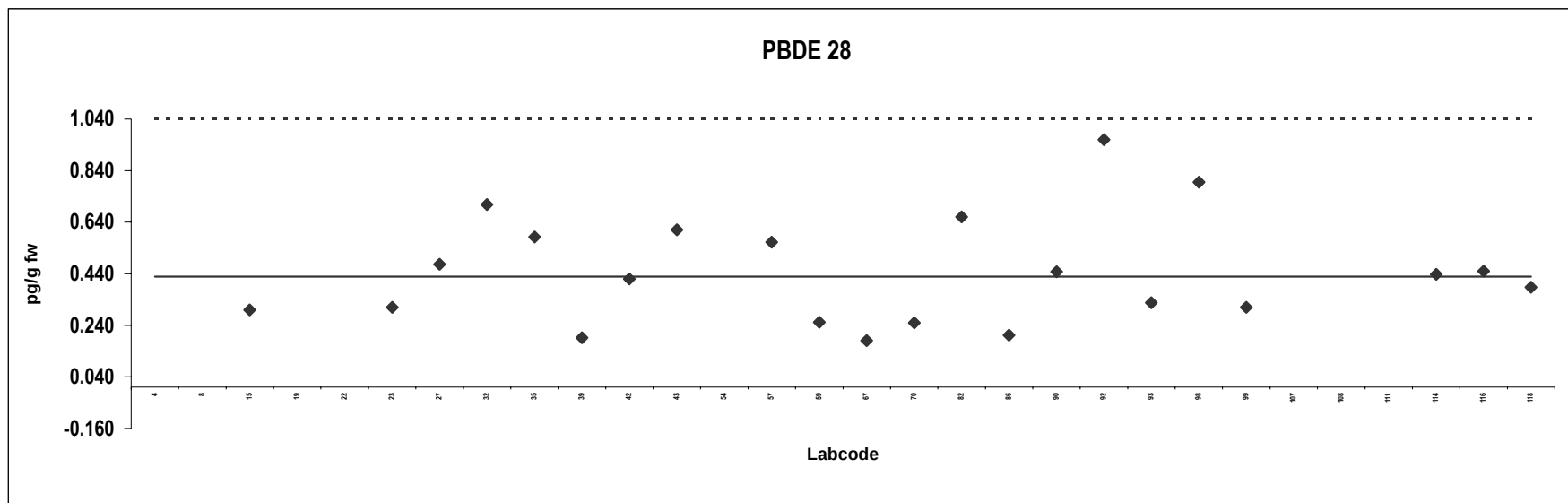
Consensus statistics	
Consensus median, pg/g	425
Median all values pg/g	426
Consensus mean, pg/g	397
Standard deviation, pg/g	137
Relative standard deviation, %	35
No. of values reported	54
No. of values removed	1
No. of reported non-detects	0



Beef
Congener: PBDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	1.1	Outlier			
8	27	Outlier			
15	0.30				
19	1.5	Outlier			
22	1.2	Outlier			
23	0.31				
27	0.48				
32	0.71				
35	0.58				
39	0.19				
42	0.42				
43	0.61				
54	2.5	Outlier,ND			
57	0.56				
59	0.25				
67	0.18				
70	0.25				
82	0.66				
86	0.20				
90	0.45				
92	0.96				
93	0.33				
98	0.80				
99	0.31				
107	2.1	Outlier			
108	7.3	Outlier,ND			
111	4.0	Outlier,ND			
114	0.44				
116	0.45				
118	0.39				

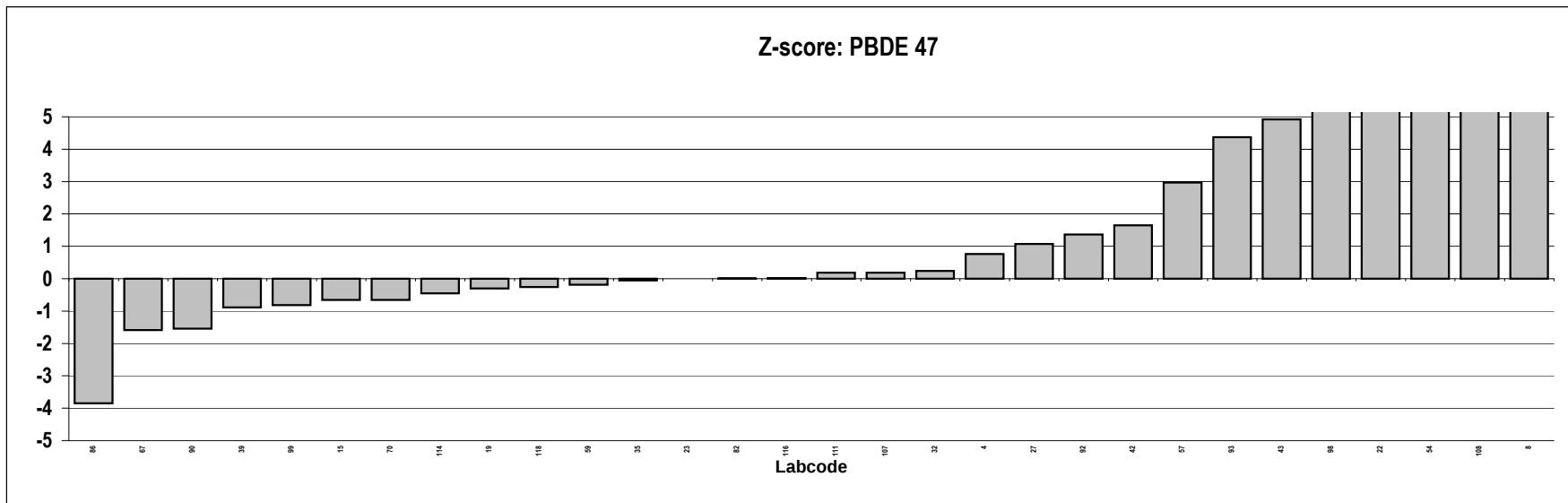
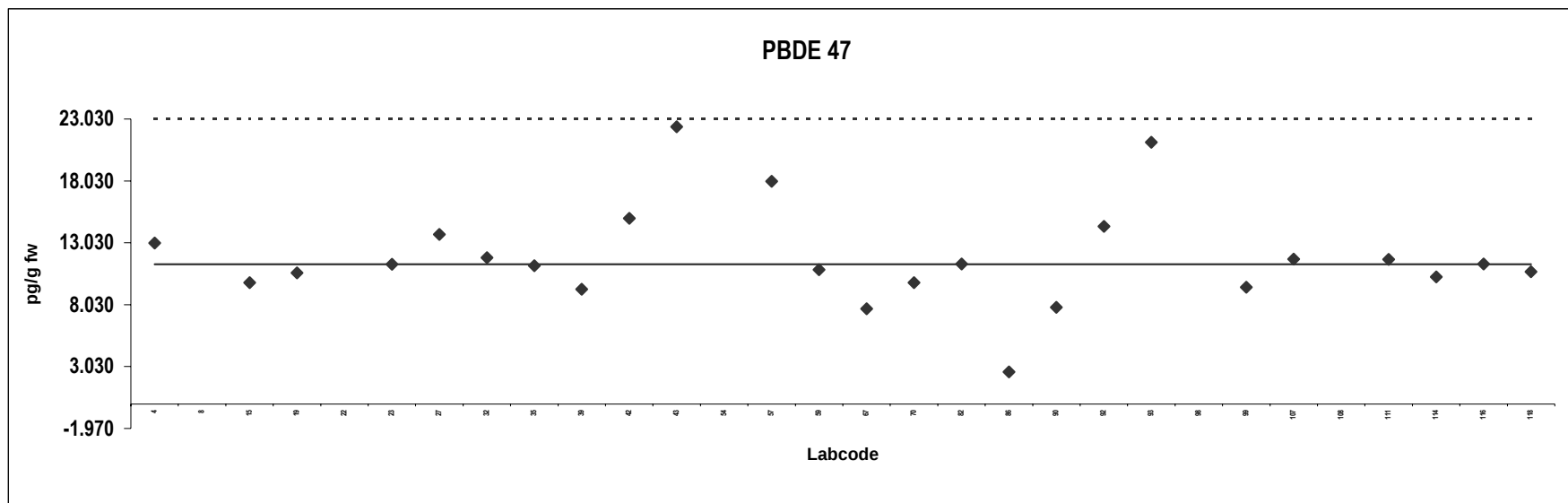
Consensus statistics	
Consensus median, pg/g	0.43
Median all values pg/g	0.52
Consensus mean, pg/g	0.45
Standard deviation, pg/g	0.21
Relative standard deviation, %	47
No. of values reported	30
No. of values removed	8
No. of reported non-detects	3



Beef
Congener: PBDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	13				
8	601	Outlier			
15	9.8				
19	11				
22	26	Outlier			
23	11				
27	14				
32	12				
35	11				
39	9.3				
42	15				
43	22				
54	43	Outlier			
57	18				
59	11				
67	7.7				
70	9.8				
82	11				
86	2.6				
90	7.8				
92	14				
93	21				
98	24	Outlier			
99	9.5				
107	12				
108	152	Outlier			
111	12				
114	10				
116	11				
118	11				

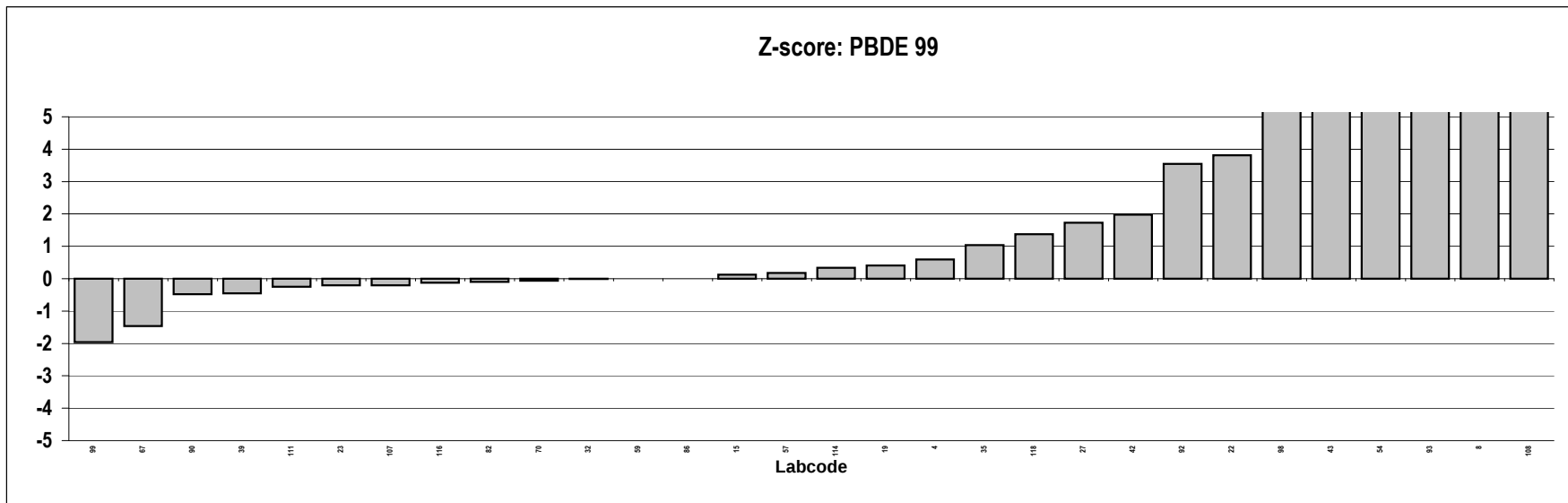
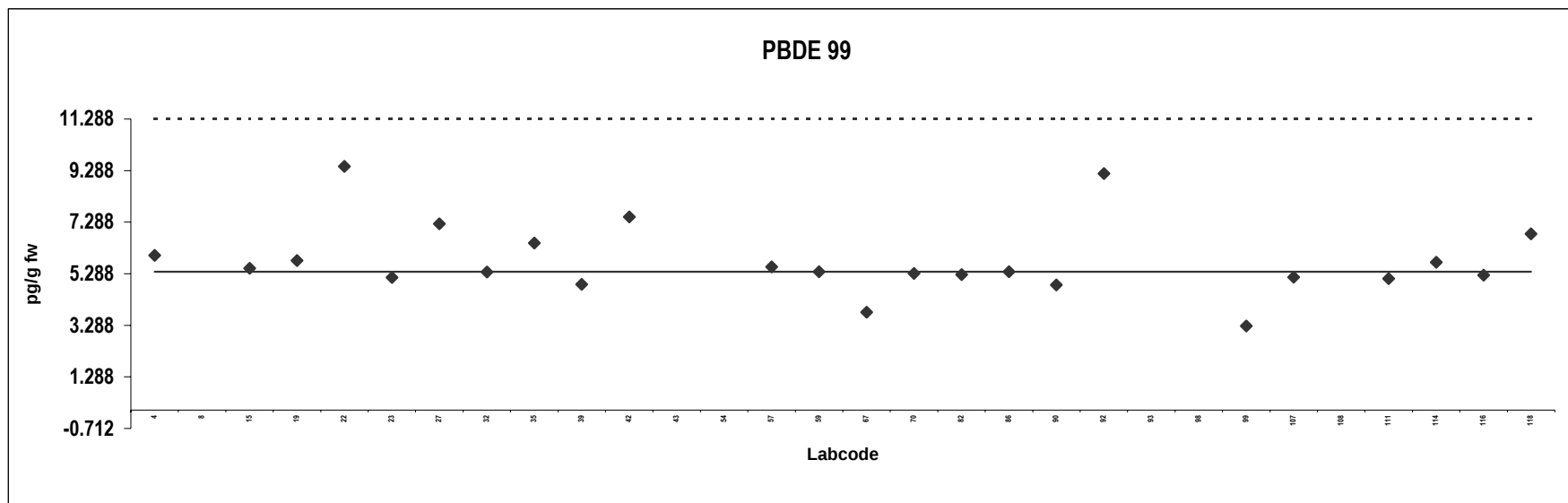
Consensus statistics	
Consensus median, pg/g	11
Median all values pg/g	12
Consensus mean, pg/g	12
Standard deviation, pg/g	4.1
Relative standard deviation, %	35
No. of values reported	30
No. of values removed	5
No. of reported non-detects	0



Beef
Congener: PBDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	6.0				
8	98	Outlier			
15	5.5				
19	5.8				
22	9.5				
23	5.1				
27	7.2				
32	5.4				
35	6.5				
39	4.9				
42	7.5				
43	15	Outlier			
54	15	Outlier			
57	5.6				
59	5.4				
67	3.8				
70	5.3				
82	5.3				
86	5.4				
90	4.8				
92	9.2				
93	20	Outlier			
98	15	Outlier			
99	3.3				
107	5.2				
108	129	Outlier			
111	5.1				
114	5.7				
116	5.2				
118	6.8				

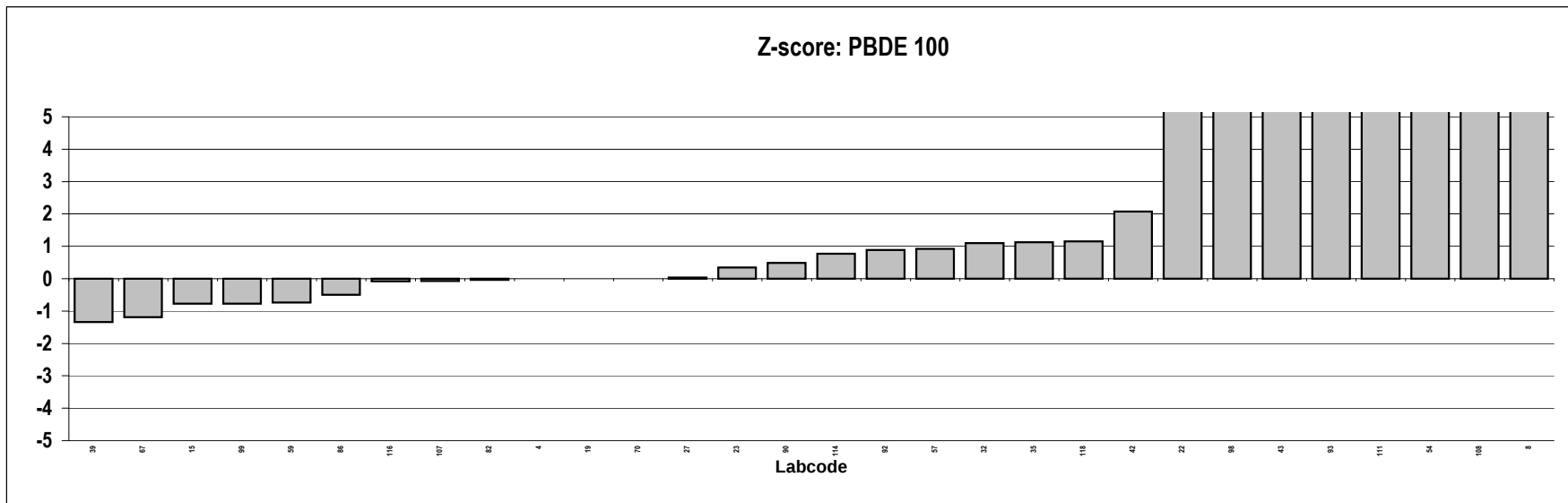
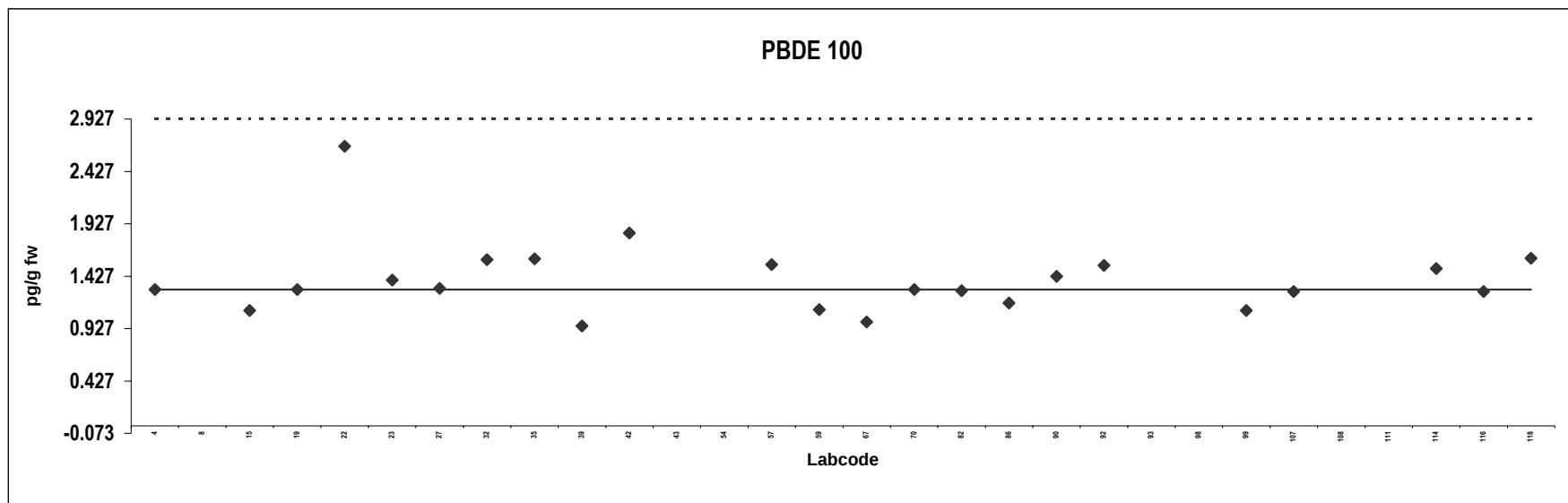
Consensus statistics	
Consensus median, pg/g	5.4
Median all values pg/g	5.6
Consensus mean, pg/g	5.8
Standard deviation, pg/g	1.4
Relative standard deviation, %	24
No. of values reported	30
No. of values removed	6
No. of reported non-detects	0



Beef
Congener: PBDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	1.3				
8	142	Outlier			
15	1.1				
19	1.3				
22	2.7				
23	1.4				
27	1.3				
32	1.6				
35	1.6				
39	0.95				
42	1.8				
43	3.2	Outlier			
54	4.6	Outlier			
57	1.5				
59	1.1				
67	0.99				
70	1.3				
82	1.3				
86	1.2				
90	1.4				
92	1.5				
93	3.8	Outlier			
98	3.0	Outlier			
99	1.1				
107	1.3				
108	22	Outlier			
111	4.0	Outlier,ND			
114	1.5				
116	1.3				
118	1.6				

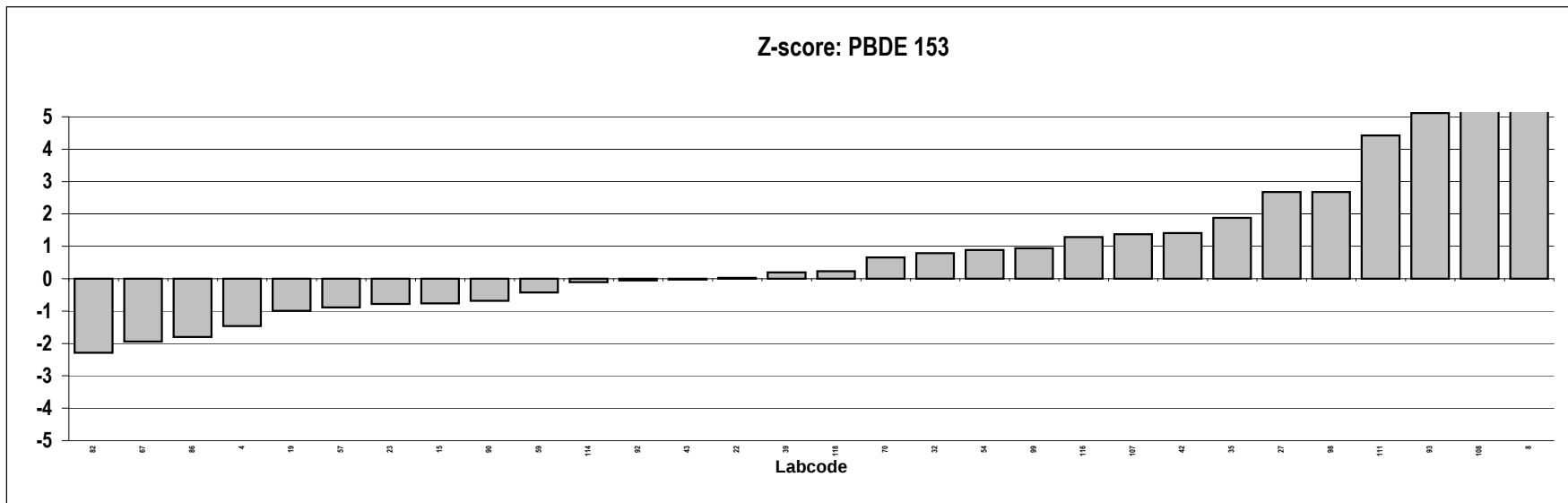
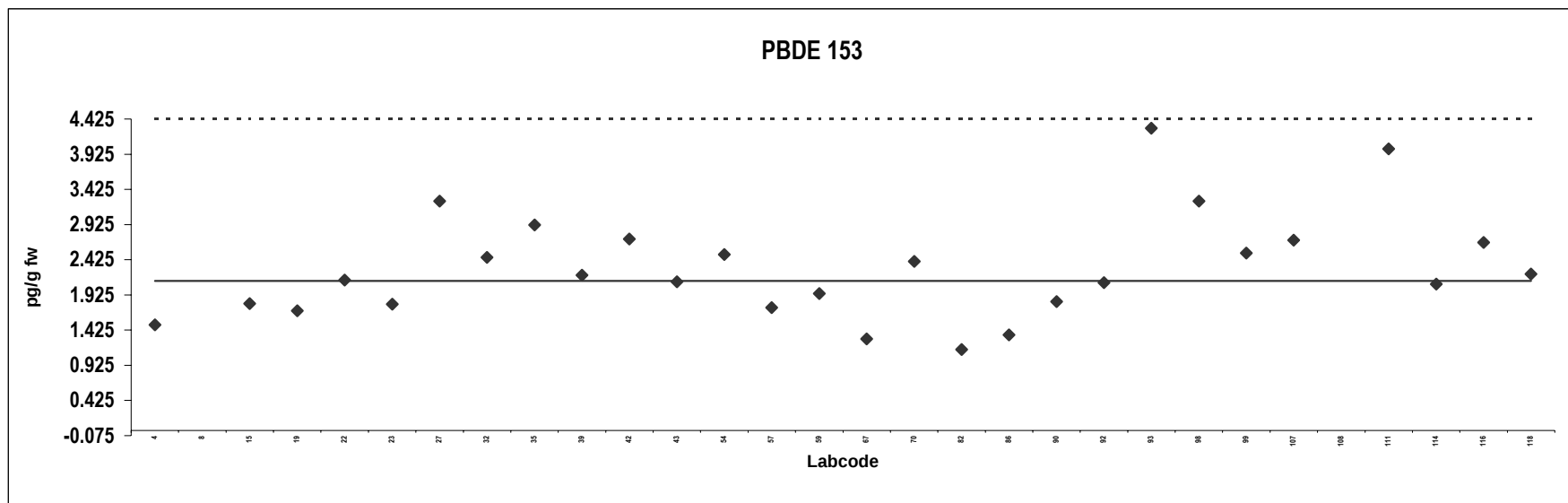
Consensus statistics	
Consensus median, pg/g	1.3
Median all values pg/g	1.5
Consensus mean, pg/g	1.4
Standard deviation, pg/g	0.35
Relative standard deviation, %	25
No. of values reported	30
No. of values removed	7
No. of reported non-detects	1



Beef
Congener: PBDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	1.5				
8	42	Outlier			
15	1.8				
19	1.7				
22	2.1				
23	1.8				
27	3.3				
32	2.5				
35	2.9				
39	2.2				
42	2.7				
43	2.1				
54	2.5	ND			
57	1.7				
59	1.9				
67	1.3				
70	2.4				
82	1.2				
86	1.4				
90	1.8				
92	2.1				
93	4.3				
98	3.3				
99	2.5				
107	2.7				
108	12	Outlier			
111	4.0	ND			
114	2.1				
116	2.7				
118	2.2				

Consensus statistics	
Consensus median, pg/g	2.1
Median all values pg/g	2.2
Consensus mean, pg/g	2.3
Standard deviation, pg/g	0.75
Relative standard deviation, %	33
No. of values reported	30
No. of values removed	2
No. of reported non-detects	2

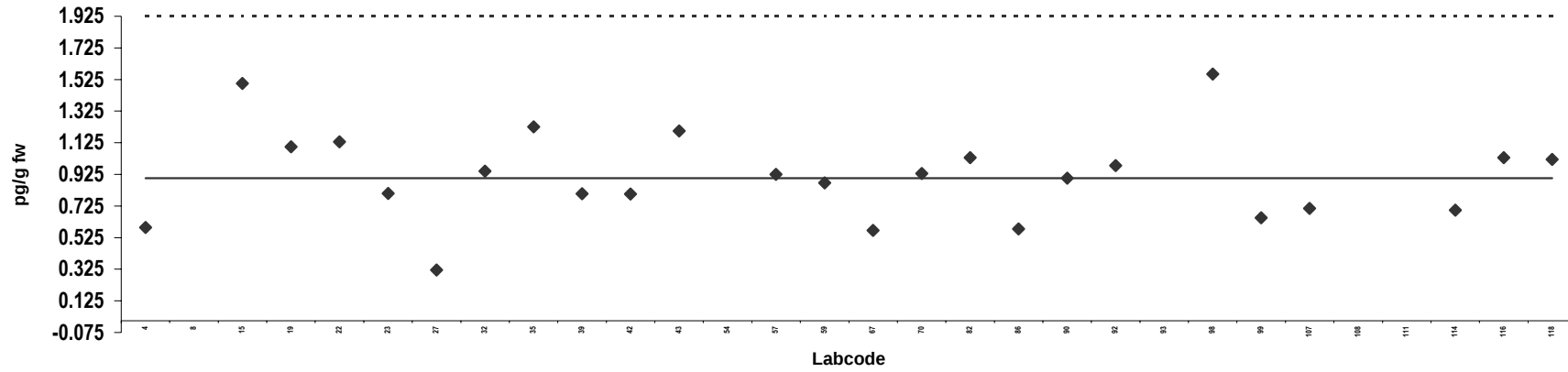


Beef
Congener: PBDE 154

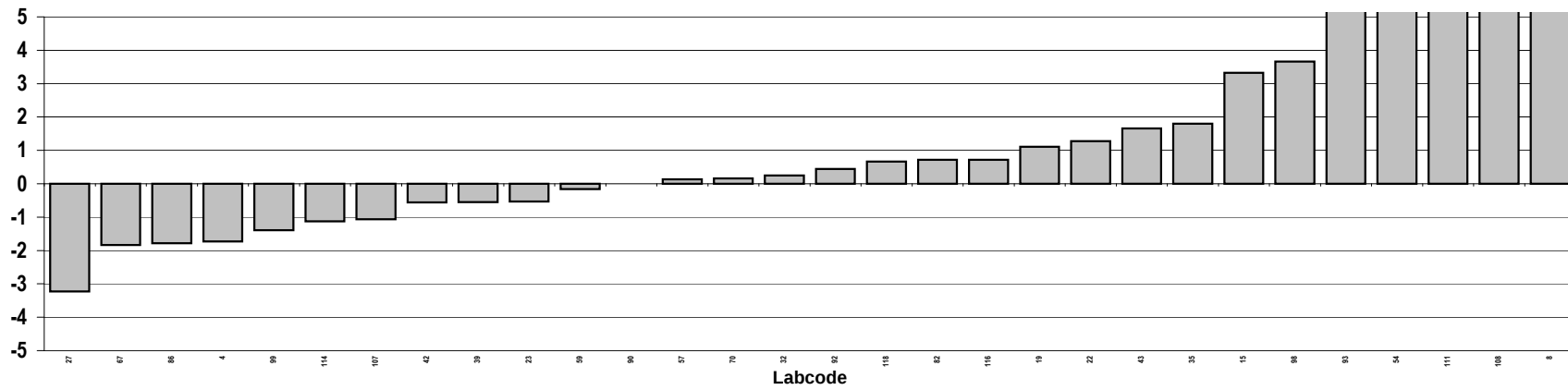
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	0.59				
8	128	Outlier			
15	1.5	ND			
19	1.1	ND			
22	1.1				
23	0.80				
27	0.32				
32	0.94				
35	1.2				
39	0.80				
42	0.80				
43	1.2				
54	2.5	Outlier,ND			
57	0.92				
59	0.87				
67	0.57				
70	0.93				
82	1.0				
86	0.58				
90	0.90				
92	0.98				
93	2.5	Outlier			
98	1.6				
99	0.65				
107	0.71				
108	10	Outlier			
111	4.0	Outlier,ND			
114	0.70				
116	1.0				
118	1.0				

Consensus statistics	
Consensus median, pg/g	0.90
Median all values pg/g	0.96
Consensus mean, pg/g	0.91
Standard deviation, pg/g	0.29
Relative standard deviation, %	31
No. of values reported	30
No. of values removed	5
No. of reported non-detects	4

PBDE 154



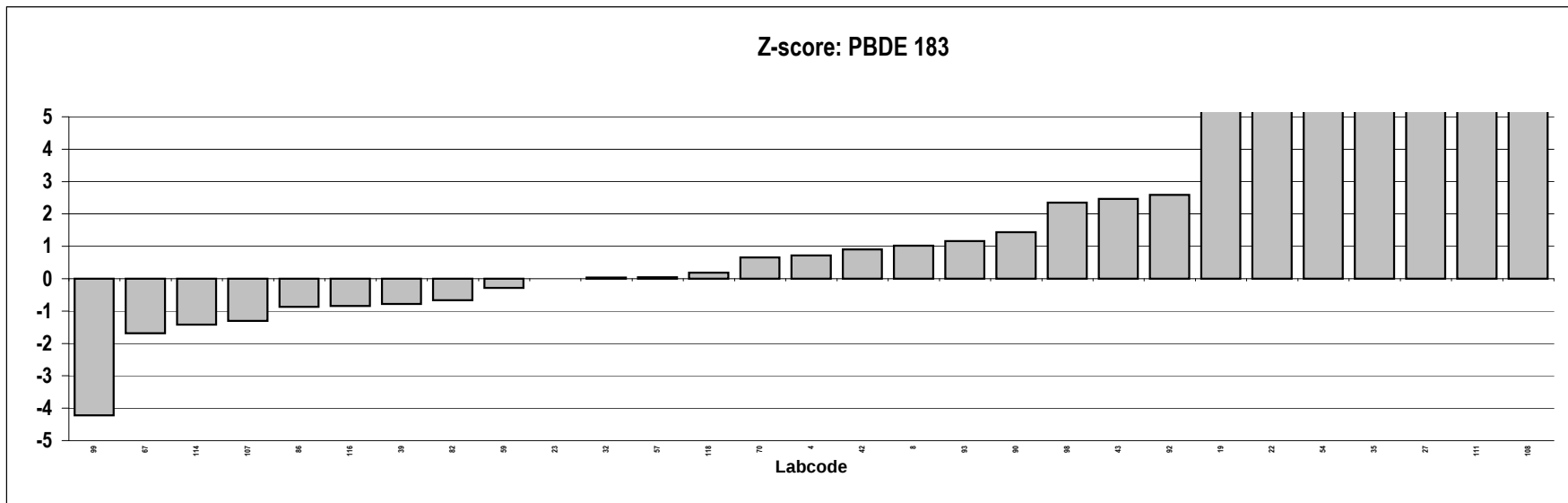
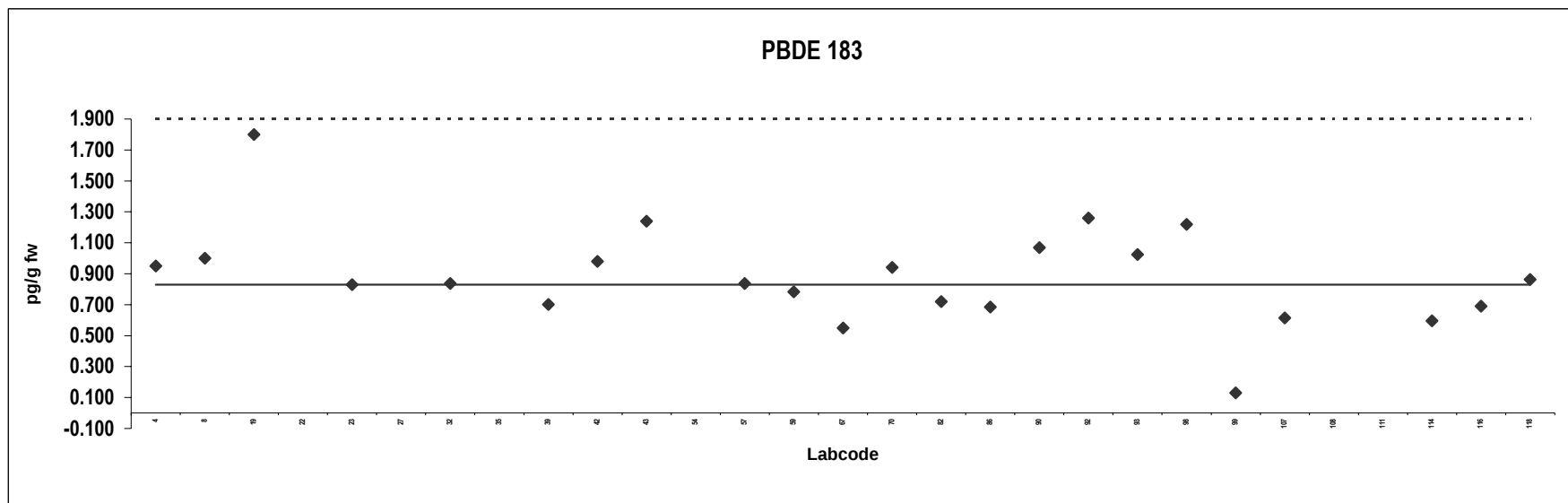
Z-score: PBDE 154



Beef
Congener: PBDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	0.95	ND			
8	1.0	ND			
19	1.8	ND			
22	2.4	Outlier			
23	0.83				
27	2.9	Outlier			
32	0.84				
35	2.9	Outlier			
39	0.70				
42	0.98				
43	1.2				
54	2.5	Outlier,ND			
57	0.84				
59	0.78				
67	0.55				
70	0.94				
82	0.72				
86	0.69				
90	1.1				
92	1.3				
93	1.0				
98	1.2	ND			
99	0.13				
107	0.61				
108	7.3	Outlier,ND			
111	4.0	Outlier,ND			
114	0.60				
116	0.69				
118	0.86				

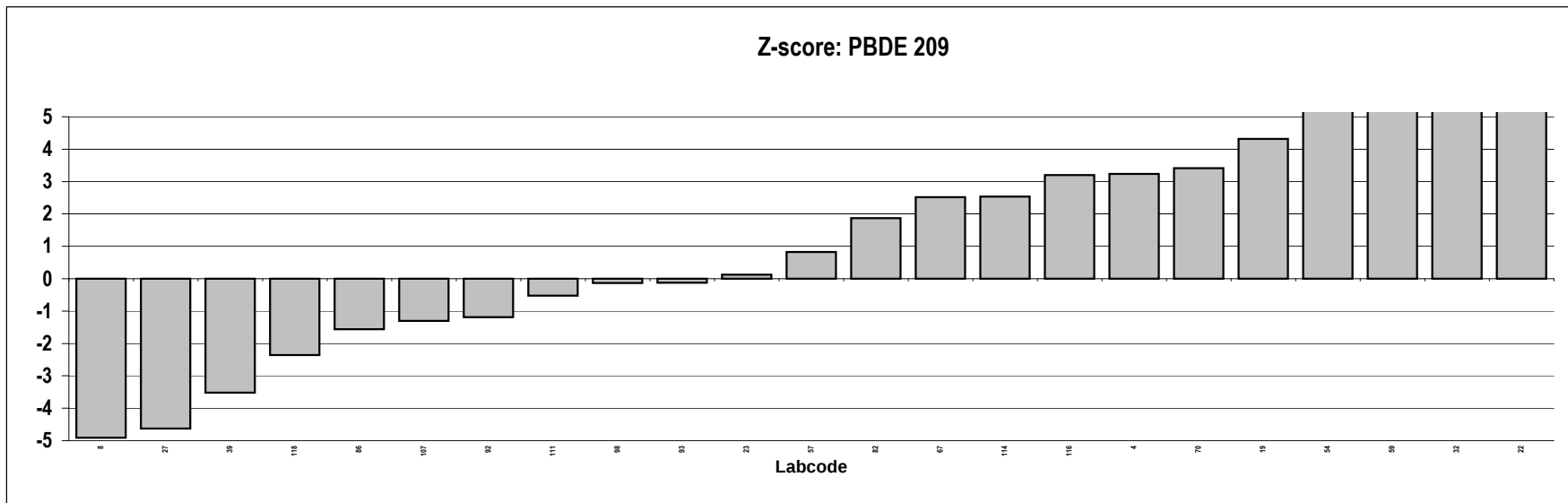
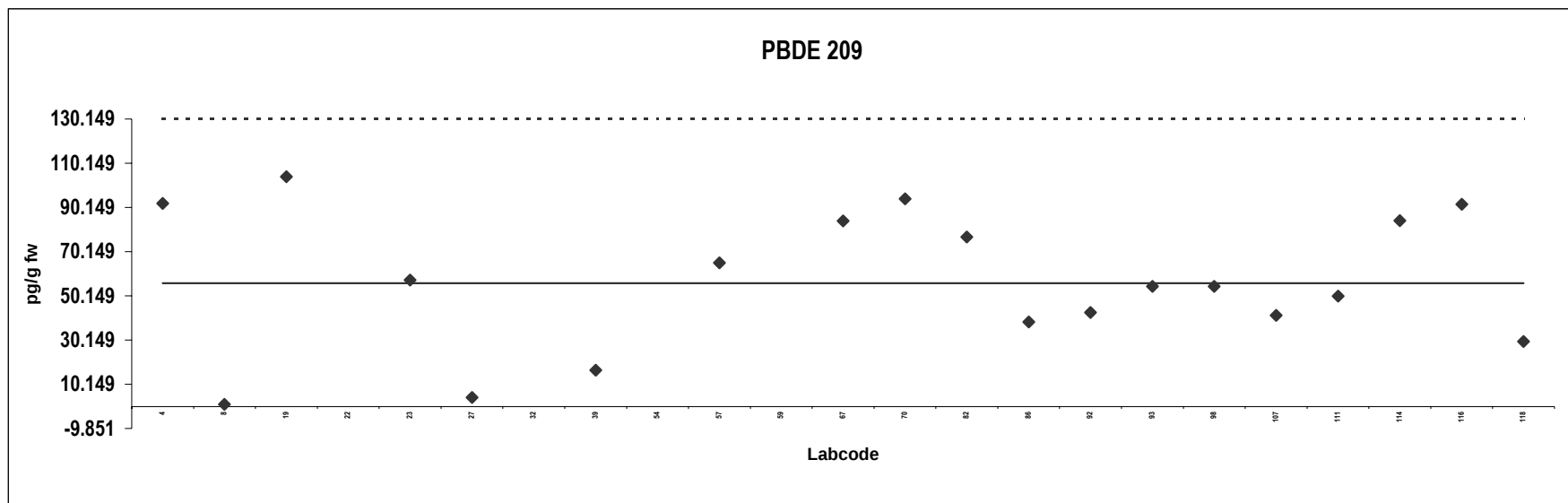
Consensus statistics	
Consensus median, pg/g	0.83
Median all values pg/g	0.95
Consensus mean, pg/g	0.88
Standard deviation, pg/g	0.32
Relative standard deviation, %	37
No. of values reported	29
No. of values removed	6
No. of reported non-detects	7



Beef
Congener: PBDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	92	ND			
8	1.0	ND			
19	104				
22	2179	Outlier			
23	57				
27	4.2				
32	235	Outlier			
39	17				
54	148	Outlier			
57	65				
59	152	Outlier			
67	84				
70	94				
82	77				
86	38				
92	43				
93	54				
98	54	ND			
107	41				
111	50				
114	84				
116	92				
118	30				

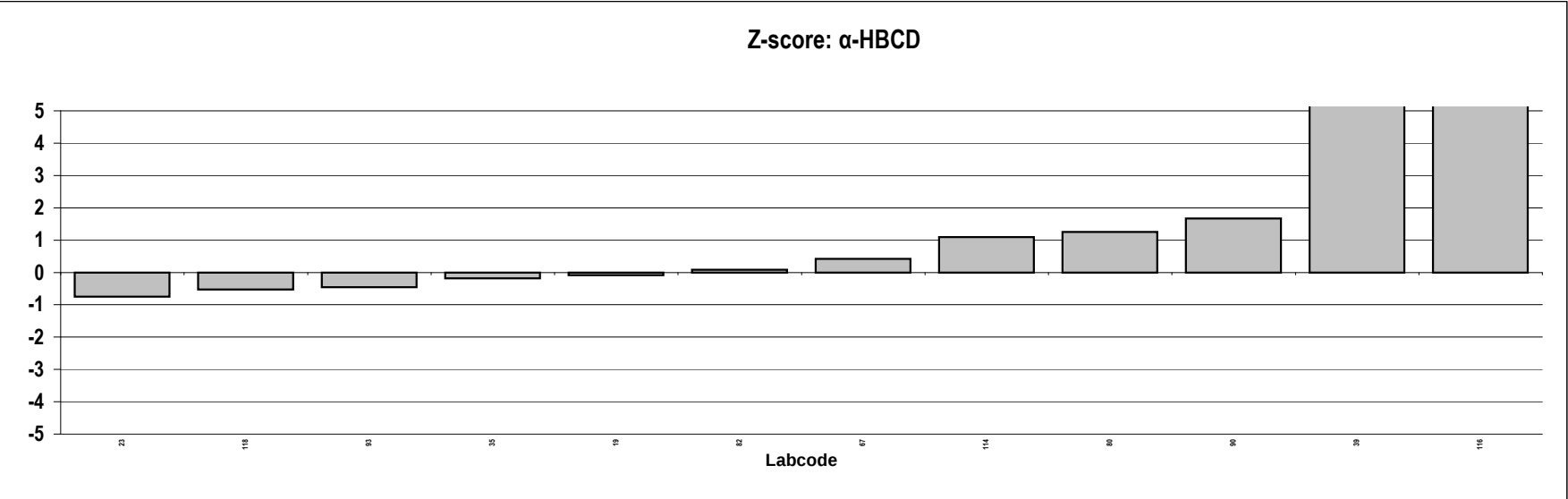
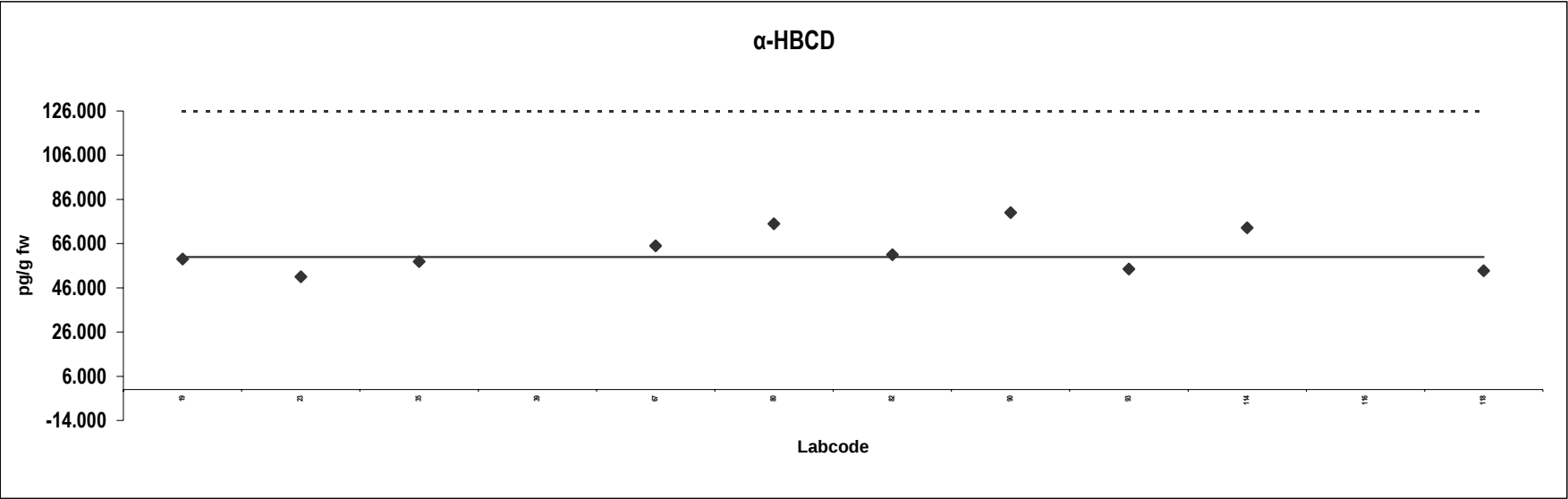
Consensus statistics	
Consensus median, pg/g	56
Median all values pg/g	65
Consensus mean, pg/g	57
Standard deviation, pg/g	31
Relative standard deviation, %	54
No. of values reported	23
No. of values removed	4
No. of reported non-detects	3



Beef
Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
19	59	Outlier			
23	51				
35	58				
39	147				
67	65				
80	75				
82	61				
90	80	Outlier			
93	54				
114	73				
116	181				
118	54				

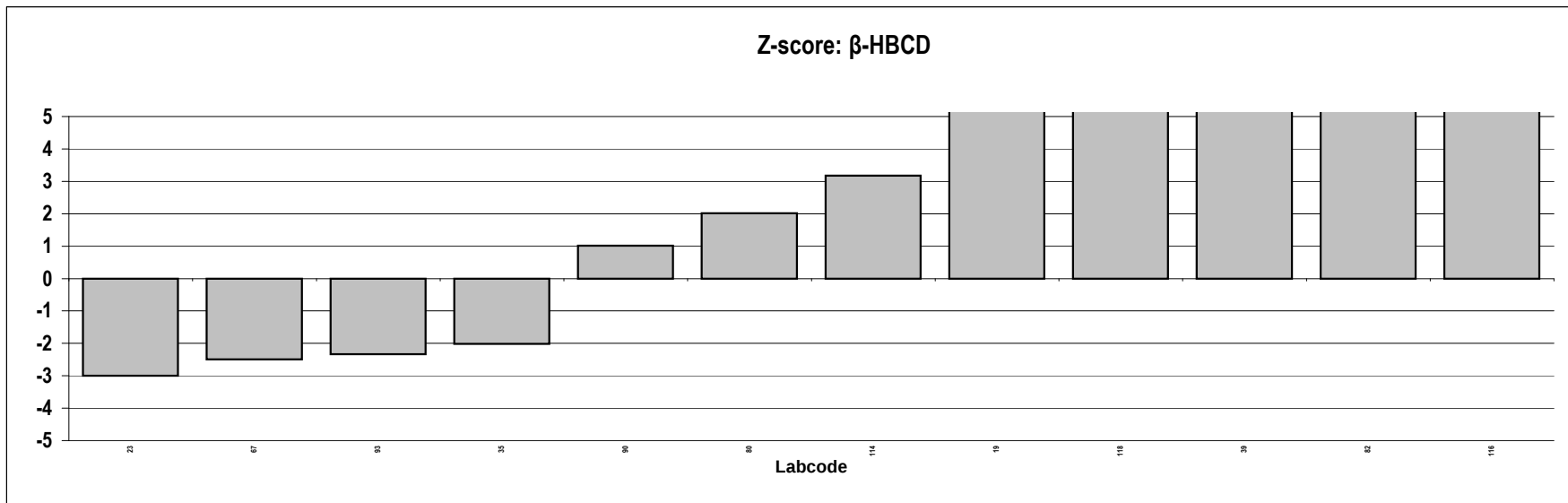
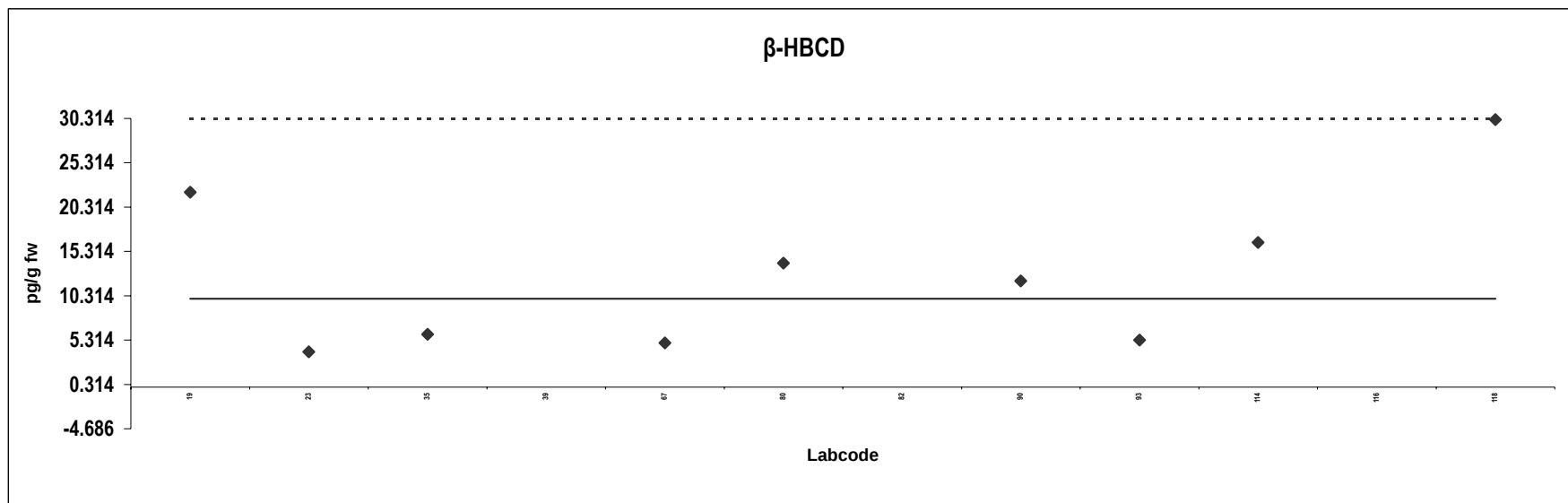
Consensus statistics	
Consensus median, pg/g	60
Median all values pg/g	63
Consensus mean, pg/g	63
Standard deviation, pg/g	9.9
Relative standard deviation, %	16
No. of values reported	12
No. of values removed	2
No. of reported non-detects	0



Beef
Congener: β -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
19	22	ND			
23	4.0	ND			
35	6.0				
39	30	Outlier			
67	5.0	ND			
80	14				
82	36	Outlier			
90	12	ND			
93	5.3				
114	16				
116	76	Outlier			
118	30	ND			

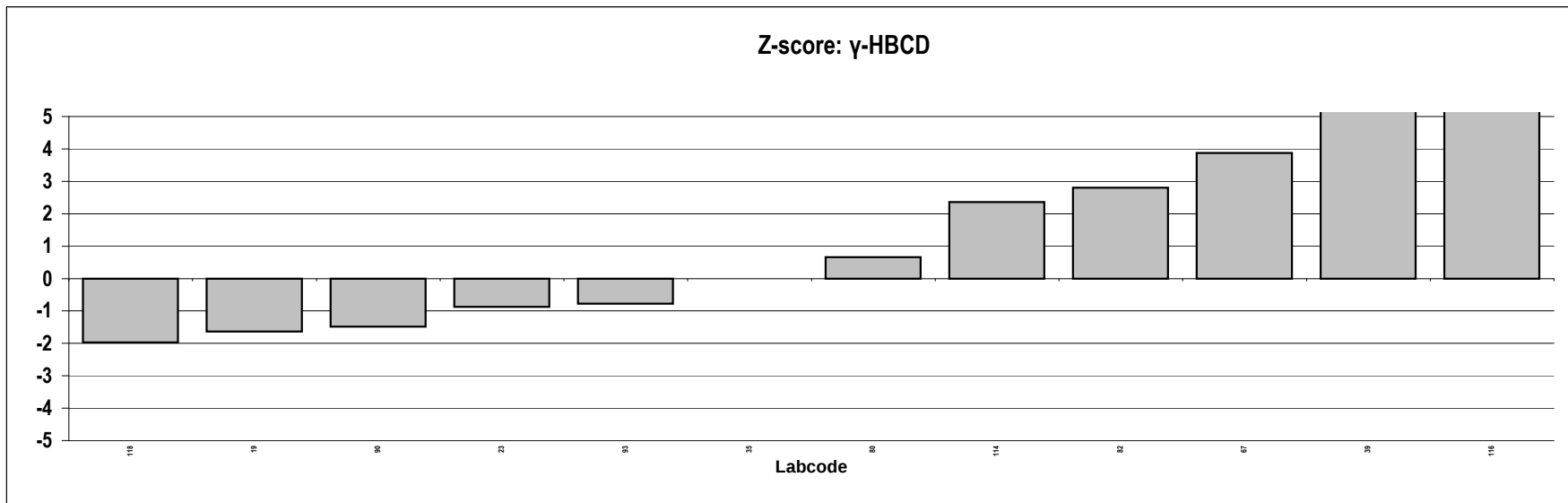
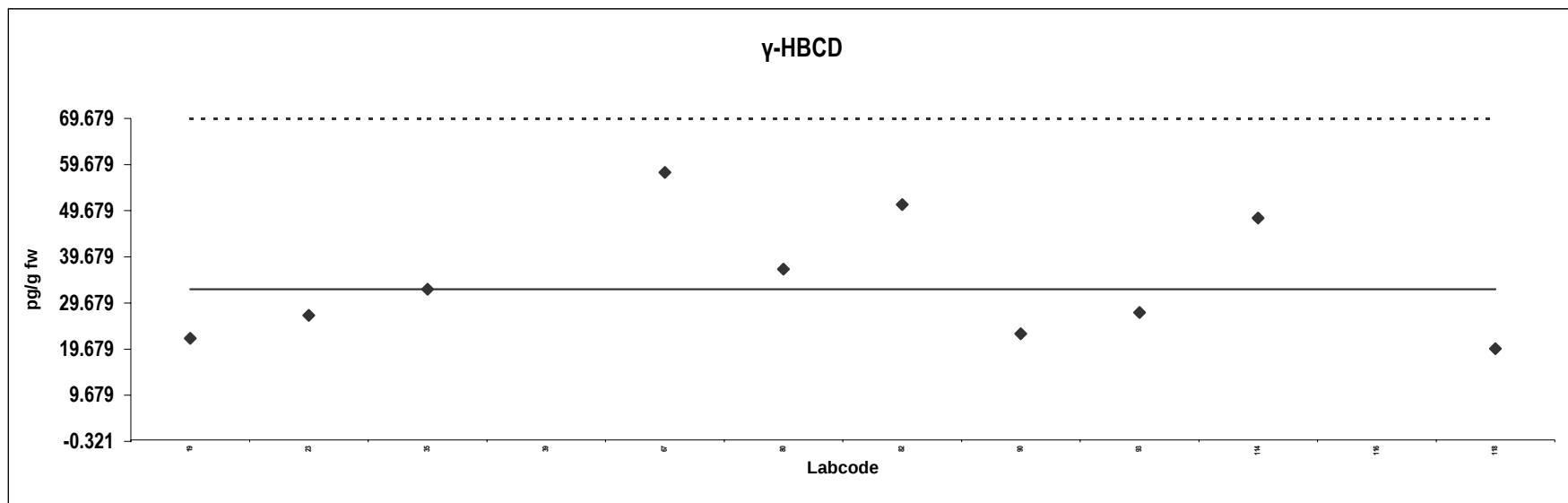
Consensus statistics	
Consensus median, pg/g	10
Median all values pg/g	15
Consensus mean, pg/g	13
Standard deviation, pg/g	9
Relative standard deviation, %	70
No. of values reported	12
No. of values removed	3
No. of reported non-detects	5



Beef
Congener: γ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
19	22	ND			
23	27				
35	33				
39	159	Outlier			
67	58				
80	37				
82	51				
90	23				
93	28				
114	48				
116	2155	Outlier			
118	20				

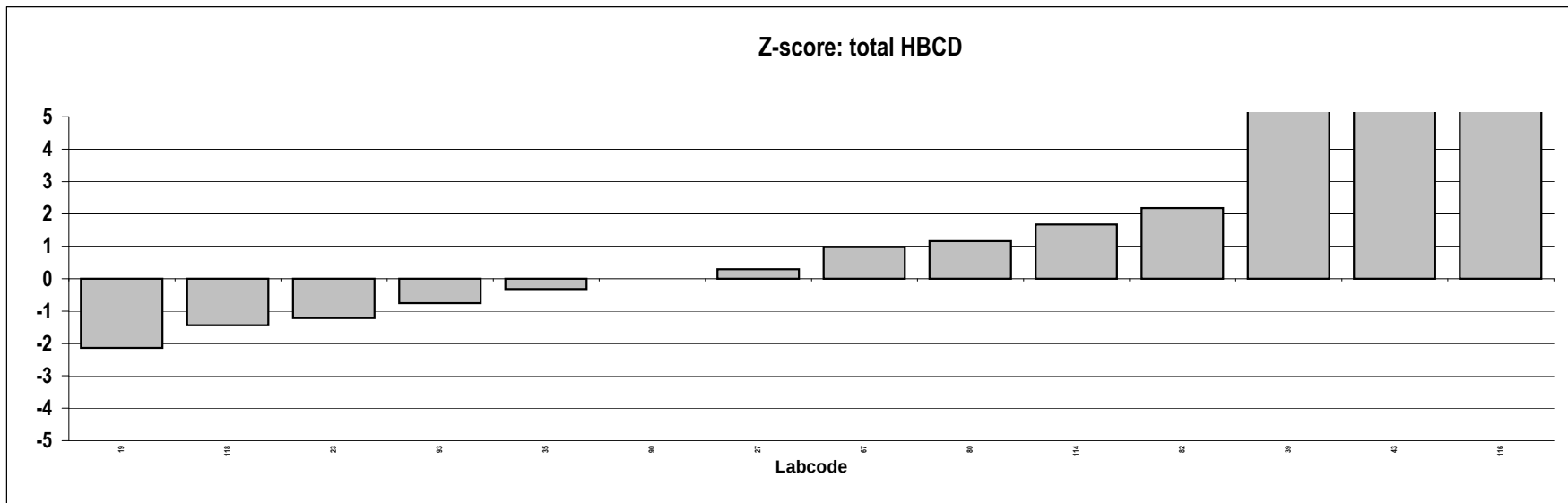
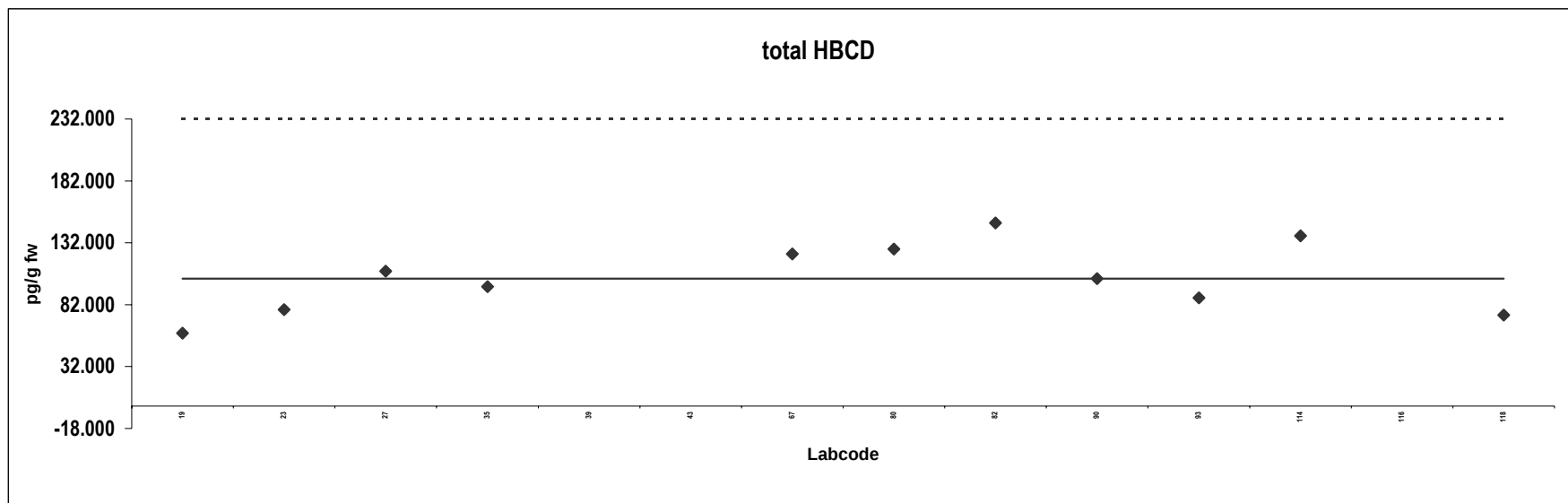
Consensus statistics	
Consensus median, pg/g	33
Median all values pg/g	35
Consensus mean, pg/g	35
Standard deviation, pg/g	13
Relative standard deviation, %	39
No. of values reported	12
No. of values removed	2
No. of reported non-detects	1



Beef
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
19	59				
23	78				
27	109				
35	96				
39	337	Outlier			
43	850	Outlier			
67	123				
80	127				
82	148				
90	103				
93	87				
114	138				
116	2412	Outlier			
118	74				

Consensus statistics	
Consensus median, pg/g	103
Median all values pg/g	116
Consensus mean, pg/g	104
Standard deviation, pg/g	28
Relative standard deviation, %	27
No. of values reported	14
No. of values removed	3
No. of reported non-detects	0



Appendix 3:

Presentation of results
for salmon-2015

Appendix 3: Presentation of results: Salmon-2015

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:

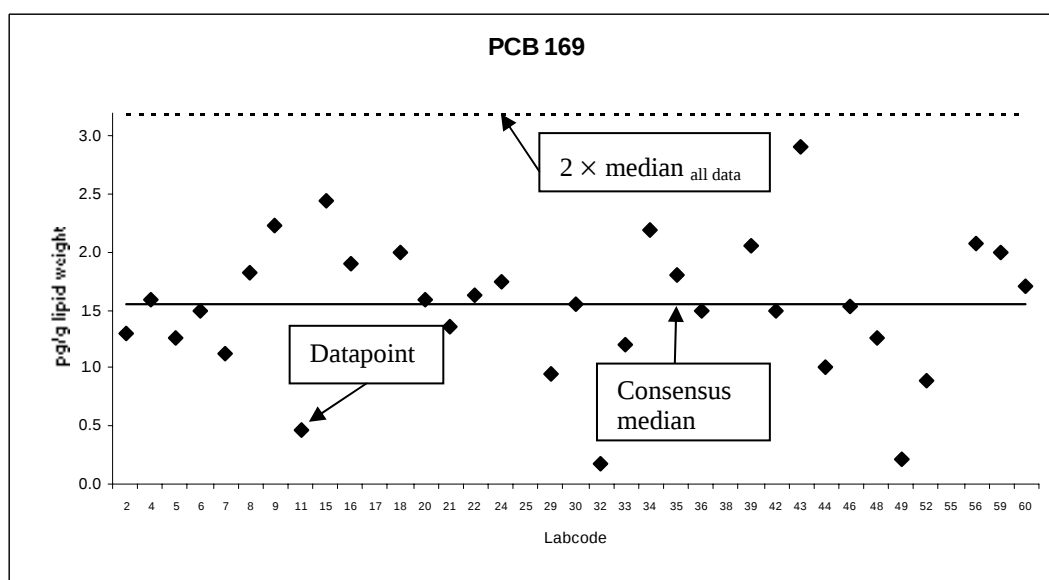
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding $2 \times$ this median were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

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

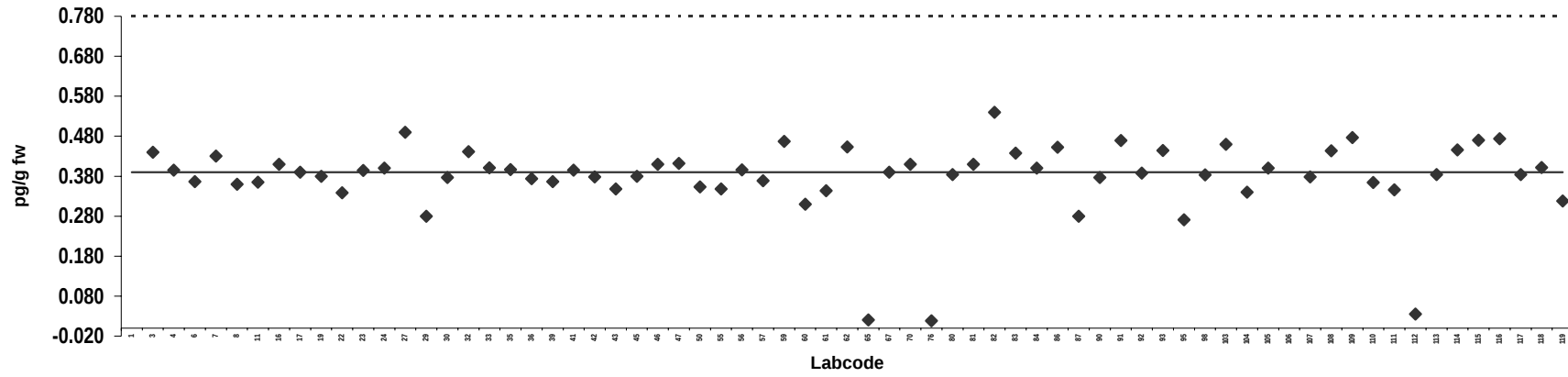
where x = reported value; X = assigned value (consensus); σ = target value for standard deviation. A σ of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of $\pm 20\%$ from the consensus value.

Salmon
Congener: 2,3,7,8 TCDD

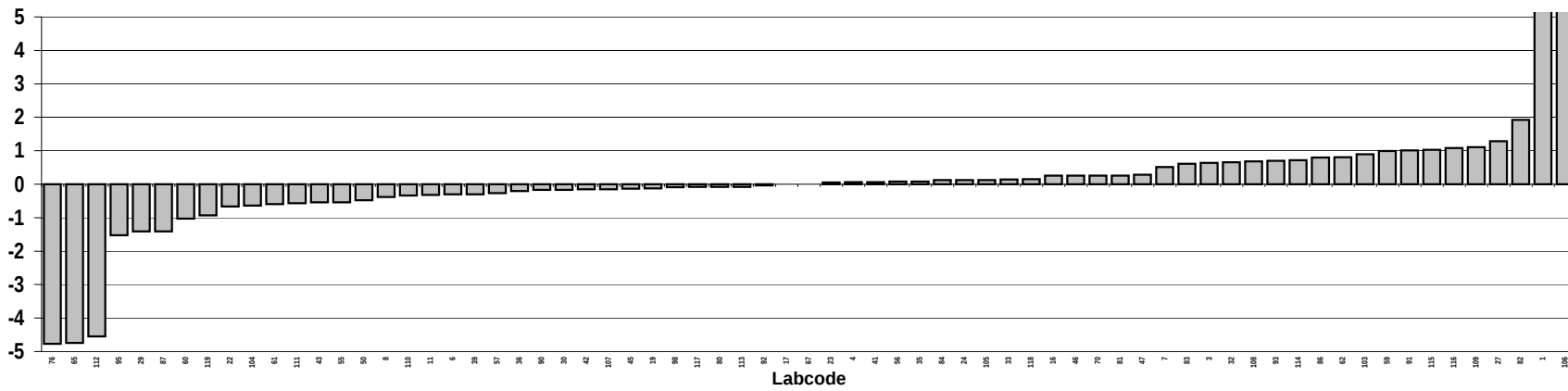
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.1	Outlier	87	0.28	Outlier
3	0.44		90	0.38	
4	0.40		91	0.47	
6	0.37		92	0.39	
7	0.43		93	0.44	
8	0.36		95	0.27	
11	0.37		98	0.38	
16	0.41		103	0.46	
17	0.39		104	0.34	
19	0.38		105	0.40	
22	0.34		106	4.1	
23	0.39		107	0.38	
24	0.40		108	0.44	
27	0.49		109	0.48	
29	0.28		110	0.36	
30	0.38		111	0.35	
32	0.44		112	0.035	ND
33	0.40		113	0.38	
35	0.40		114	0.45	
36	0.37		115	0.47	
39	0.37		116	0.47	
41	0.40		117	0.38	
42	0.38		118	0.40	
43	0.35		119	0.32	
45	0.38				
46	0.41				
47	0.41				
50	0.35				
55	0.35				
56	0.40				
57	0.37				
59	0.47				
60	0.31				
61	0.34				
62	0.45				
65	0.020	ND			
67	0.39				
70	0.41				
76	0.018				
80	0.38				
81	0.41				
82	0.54				
83	0.44				
84	0.40				
86	0.45				

Consensus statistics	
Consensus median, pg/g	0.39
Median all values pg/g	0.39
Consensus mean, pg/g	0.38
Standard deviation, pg/g	0.092
Relative standard deviation, %	24
No. of values reported	69
No. of values removed	2
No. of reported non-detects	2

2,3,7,8 TCDD



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

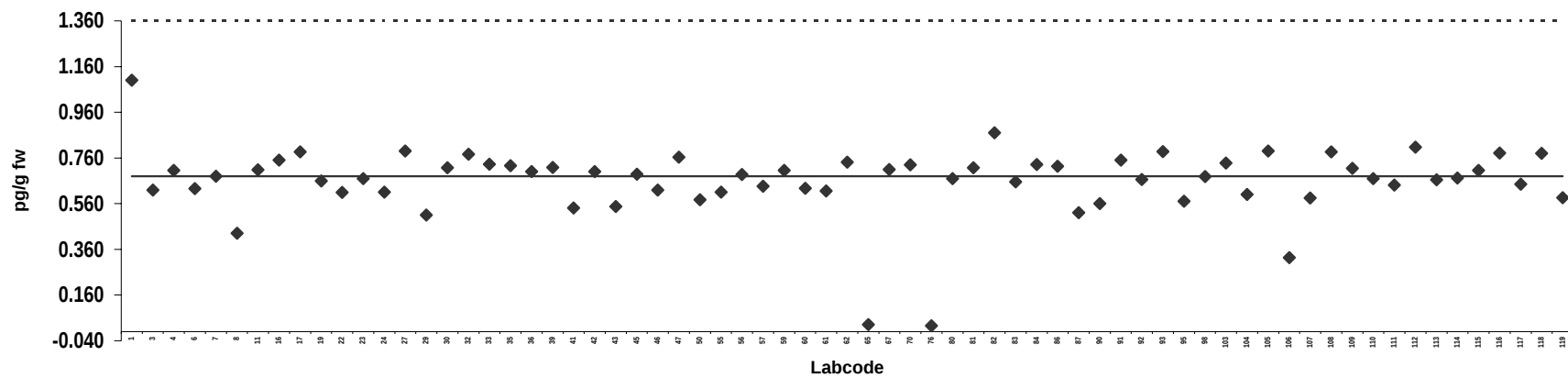


Salmon
Congener: 1,2,3,7,8 PeCDD

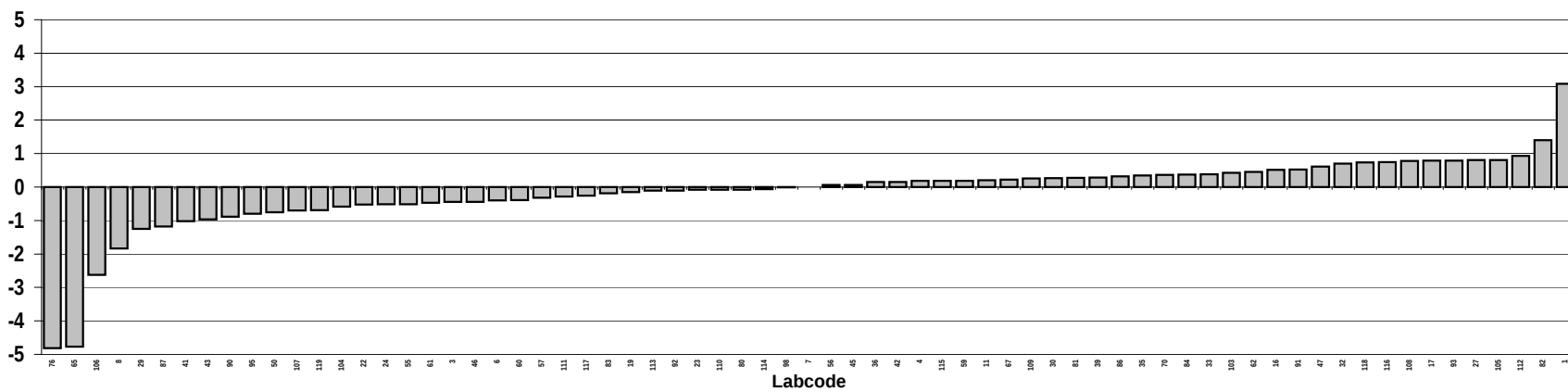
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.1	ND	87	0.52	
3	0.62		90	0.56	
4	0.71		91	0.75	
6	0.63		92	0.67	
7	0.68		93	0.79	
8	0.43		95	0.57	
11	0.71		98	0.68	
16	0.75		103	0.74	
17	0.79		104	0.60	
19	0.66		105	0.79	
22	0.61		106	0.32	
23	0.67		107	0.59	
24	0.61		108	0.79	
27	0.79		109	0.72	
29	0.51		110	0.67	
30	0.72		111	0.64	
32	0.78		112	0.81	
33	0.73		113	0.67	
35	0.73		114	0.67	
36	0.70		115	0.71	
39	0.72		116	0.78	
41	0.54		117	0.64	
42	0.70		118	0.78	
43	0.55		119	0.59	
45	0.69				
46	0.62				
47	0.76				
50	0.58				
55	0.61				
56	0.69				
57	0.64				
59	0.71				
60	0.63				
61	0.62				
62	0.74				
65	0.031				
67	0.71				
70	0.73				
76	0.025				
80	0.67				
81	0.72				
82	0.87				
83	0.66				
84	0.73				
86	0.72				

Consensus statistics	
Consensus median, pg/g	0.68
Median all values pg/g	0.68
Consensus mean, pg/g	0.66
Standard deviation, pg/g	0.15
Relative standard deviation, %	23
No. of values reported	69
No. of values removed	0
No. of reported non-detects	1

1,2,3,7,8 PeCDD



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

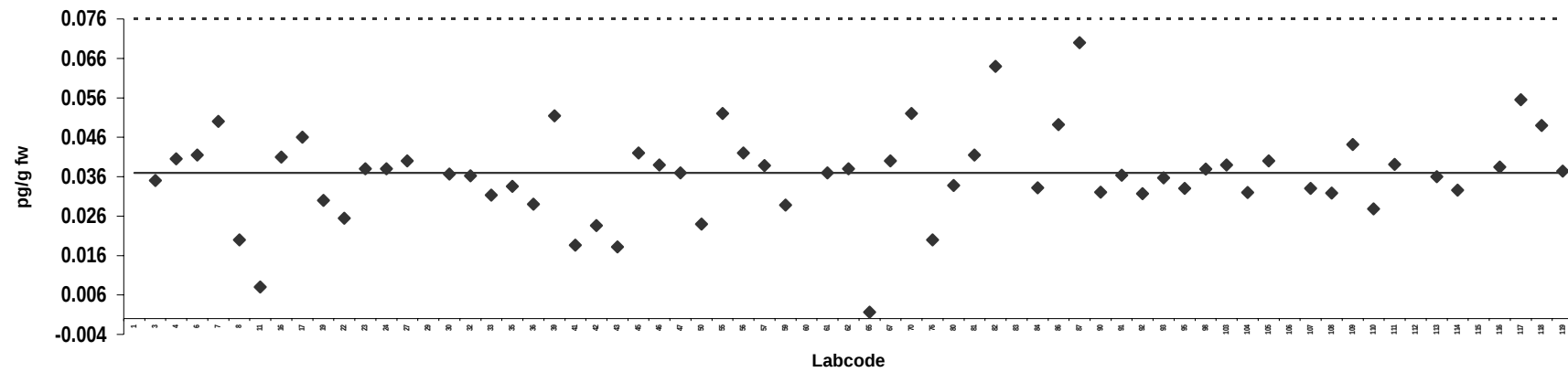


Salmon
Congener: 1,2,3,4,7,8 HxCDD

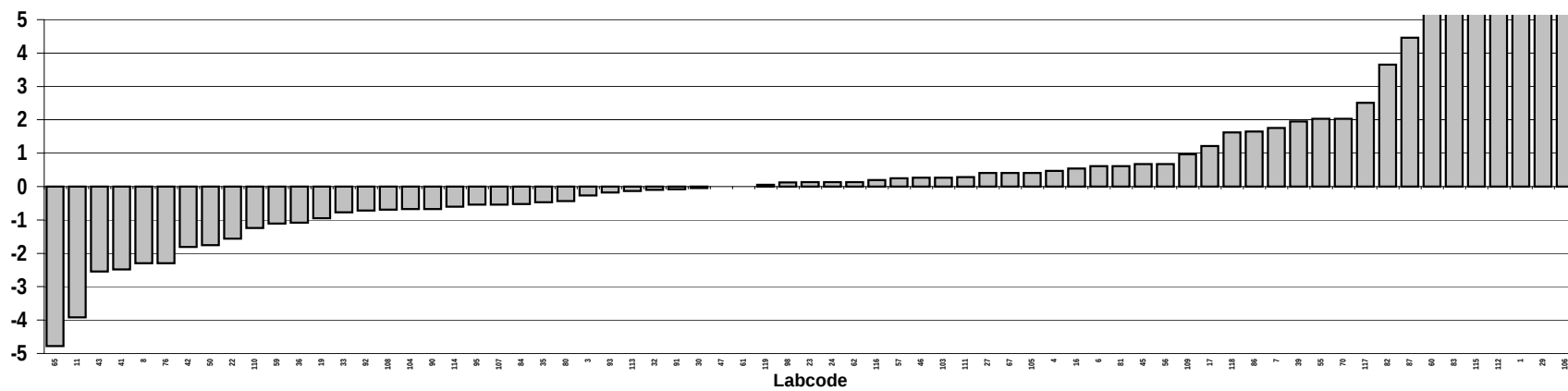
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.30	Outlier,ND	87	0.070	
3	0.035		90	0.032	
4	0.041		91	0.036	
6	0.042		92	0.032	
7	0.050		93	0.036	
8	0.020	ND	95	0.033	ND
11	0.0080	ND	98	0.038	
16	0.041		103	0.039	
17	0.046		104	0.032	
19	0.030		105	0.040	
22	0.025		106	0.50	Outlier
23	0.038		107	0.033	
24	0.038		108	0.032	
27	0.040		109	0.044	
29	0.49	Outlier,ND	110	0.028	
30	0.037		111	0.039	
32	0.036		112	0.15	Outlier
33	0.031		113	0.036	
35	0.034		114	0.033	
36	0.029		115	0.11	Outlier
39	0.051		116	0.038	
41	0.019	ND	117	0.056	ND
42	0.024		118	0.049	
43	0.018		119	0.037	
45	0.042				
46	0.039				
47	0.037				
50	0.024				
55	0.052				
56	0.042				
57	0.039				
59	0.029				
60	0.079	Outlier			
61	0.037				
62	0.038				
65	0.0017	ND			
67	0.040				
70	0.052				
76	0.020	ND			
80	0.034				
81	0.042				
82	0.064				
83	0.099	Outlier			
84	0.033				
86	0.049				

Consensus statistics	
Consensus median, pg/g	0.037
Median all values pg/g	0.038
Consensus mean, pg/g	0.036
Standard deviation, pg/g	0.011
Relative standard deviation, %	31
No. of values reported	69
No. of values removed	7
No. of reported non-detects	9

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



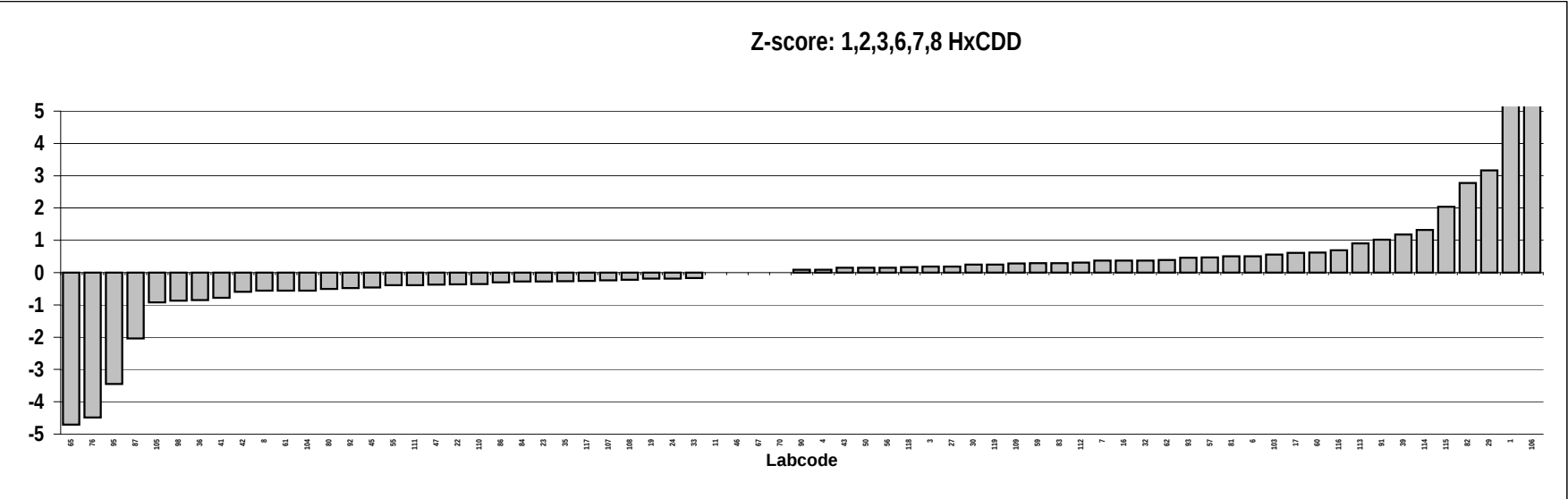
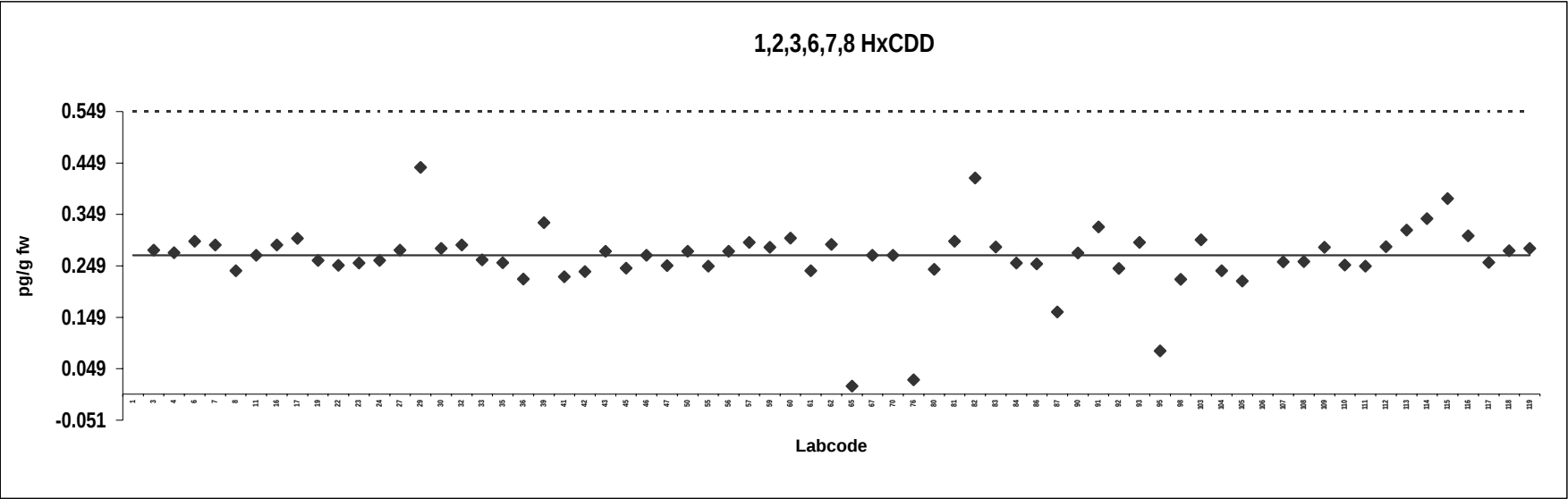
Z-score: 1,2,3,4,7,8 HxCDD



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.78	Outlier	87	0.16	
3	0.28		90	0.27	
4	0.28		91	0.33	
6	0.30		92	0.24	
7	0.29		93	0.30	
8	0.24		95	0.084	
11	0.27		98	0.22	
16	0.29		103	0.30	
17	0.30		104	0.24	
19	0.26		105	0.22	
22	0.25	ND	106	3.0	Outlier
23	0.26		107	0.26	
24	0.26		108	0.26	
27	0.28		109	0.29	
29	0.44		110	0.25	
30	0.28		111	0.25	
32	0.29		112	0.29	
33	0.26		113	0.32	
35	0.26		114	0.34	
36	0.22		115	0.38	
39	0.33		116	0.31	
41	0.23		117	0.26	
42	0.24		118	0.28	
43	0.28		119	0.28	
45	0.25				
46	0.27				
47	0.25				
50	0.28				
55	0.25				
56	0.28				
57	0.30	ND			
59	0.29				
60	0.30				
61	0.24				
62	0.29				
65	0.016				
67	0.27				
70	0.27				
76	0.028				
80	0.24				
81	0.30				
82	0.42				
83	0.29				
84	0.25				
86	0.25				

Consensus statistics	
Consensus median, pg/g	0.27
Median all values pg/g	0.27
Consensus mean, pg/g	0.27
Standard deviation, pg/g	0.065
Relative standard deviation, %	24
No. of values reported	69
No. of values removed	2
No. of reported non-detects	2

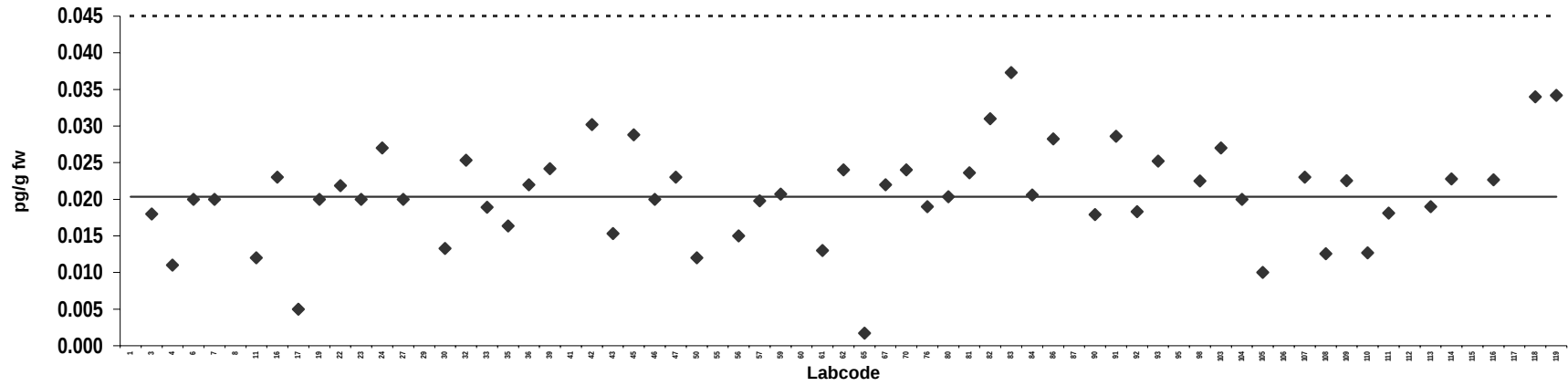


Salmon
Congener: 1,2,3,7,8,9 HxCDD

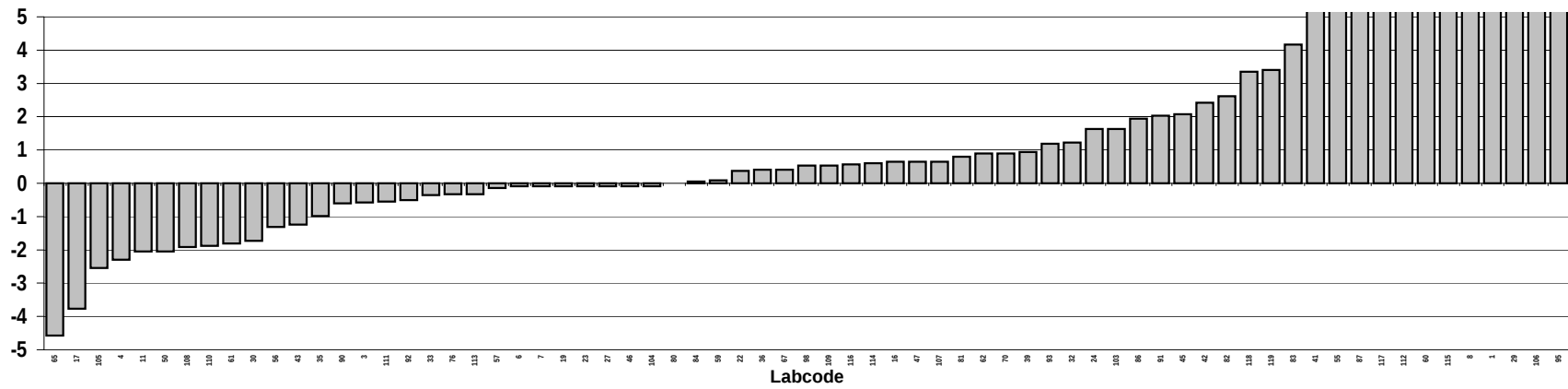
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.30	Outlier,ND	87	0.060	Outlier
3	0.018		90	0.018	
4	0.011		91	0.029	
6	0.020	ND	92	0.018	
7	0.020		93	0.025	
8	0.26	Outlier	95	4.1	Outlier
11	0.012	ND	98	0.023	
16	0.023		103	0.027	
17	0.0050	ND	104	0.020	
19	0.020		105	0.010	
22	0.022		106	0.46	Outlier
23	0.020		107	0.023	
24	0.027		108	0.013	
27	0.020		109	0.023	
29	0.46	Outlier,ND	110	0.013	
30	0.013	ND	111	0.018	
32	0.025		112	0.071	Outlier,ND
33	0.019		113	0.019	
35	0.016		114	0.023	
36	0.022		115	0.11	Outlier
39	0.024		116	0.023	
41	0.052	Outlier	117	0.064	Outlier,ND
42	0.030		118	0.034	
43	0.015		119	0.034	
45	0.029				
46	0.020				
47	0.023				
50	0.012				
55	0.059	Outlier			
56	0.015				
57	0.020				
59	0.021				
60	0.084	Outlier			
61	0.013				
62	0.024				
65	0.0017	ND			
67	0.022				
70	0.024				
76	0.019	ND			
80	0.020				
81	0.024				
82	0.031				
83	0.037				
84	0.021				
86	0.028				

Consensus statistics	
Consensus median, pg/g	0.020
Median all values pg/g	0.023
Consensus mean, pg/g	0.021
Standard deviation, pg/g	0.0067
Relative standard deviation, %	33
No. of values reported	69
No. of values removed	12
No. of reported non-detects	10

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



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

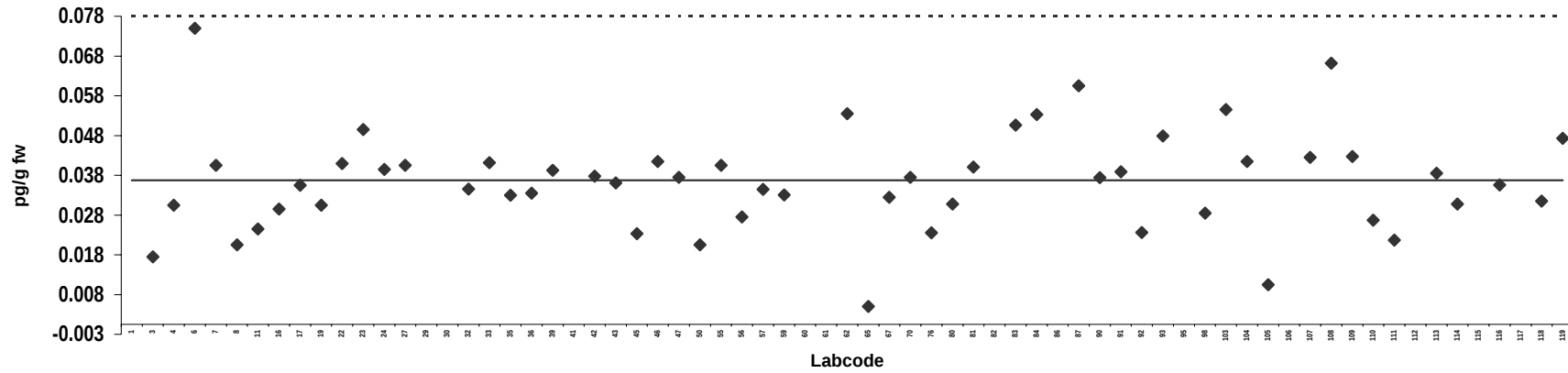


Salmon
Congener: 1,2,3,4,6,7,8 HpCDD

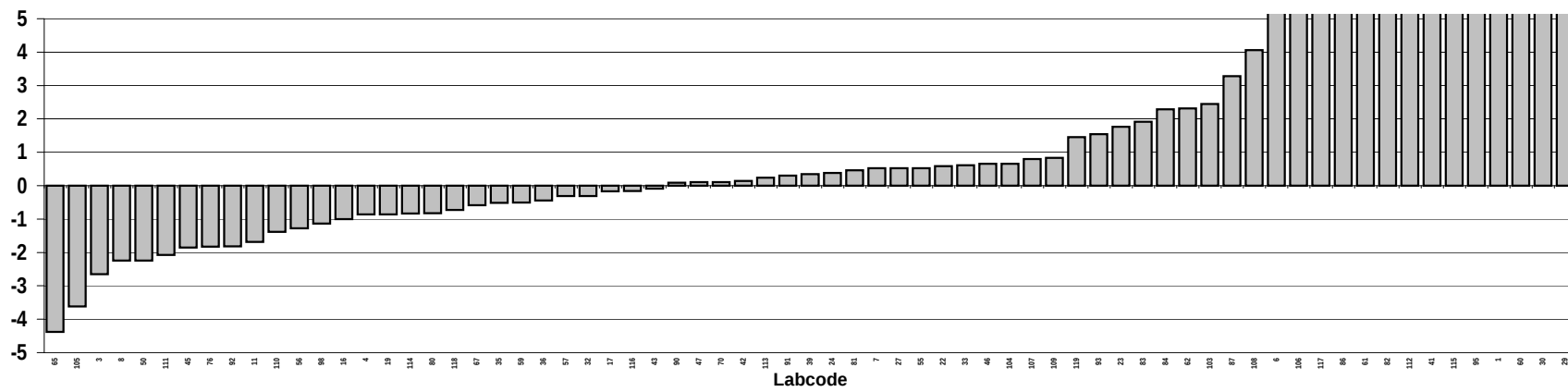
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.40	Outlier,ND	87	0.060	
3	0.017		90	0.037	
4	0.030		91	0.038	
6	0.075		92	0.023	
7	0.040		93	0.047	
8	0.020	ND	95	0.27	Outlier
11	0.024		98	0.028	
16	0.029		103	0.054	
17	0.035		104	0.041	
19	0.030		105	0.010	
22	0.040		106	0.087	Outlier
23	0.049		107	0.042	
24	0.039	ND	108	0.066	
27	0.040		109	0.042	
29	1.0	Outlier,ND	110	0.026	
30	0.93	Outlier	111	0.021	
32	0.034		112	0.20	Outlier,ND
33	0.041		113	0.038	
35	0.032		114	0.030	
36	0.033		115	0.21	Outlier
39	0.039		116	0.035	
41	0.21	Outlier	117	0.090	Outlier,ND
42	0.037		118	0.031	
43	0.036		119	0.047	
45	0.023				
46	0.041				
47	0.037				
50	0.020				
55	0.040	ND			
56	0.027				
57	0.034				
59	0.033				
60	0.46	Outlier			
61	0.14	Outlier			
62	0.053				
65	0.0045				
67	0.032				
70	0.037				
76	0.023	ND			
80	0.030				
81	0.040				
82	0.15	Outlier			
83	0.050				
84	0.053				
86	0.093	Outlier			

Consensus statistics	
Consensus median, pg/g	0.036
Median all values pg/g	0.039
Consensus mean, pg/g	0.036
Standard deviation, pg/g	0.013
Relative standard deviation, %	35
No. of values reported	69
No. of values removed	13
No. of reported non-detects	8

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



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



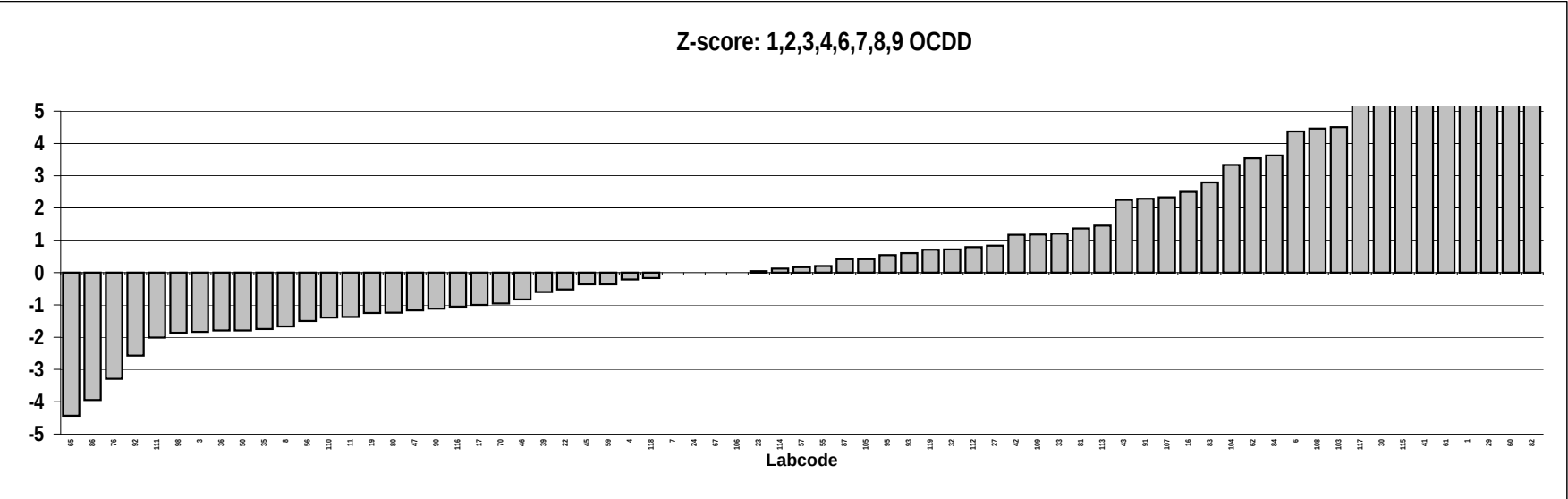
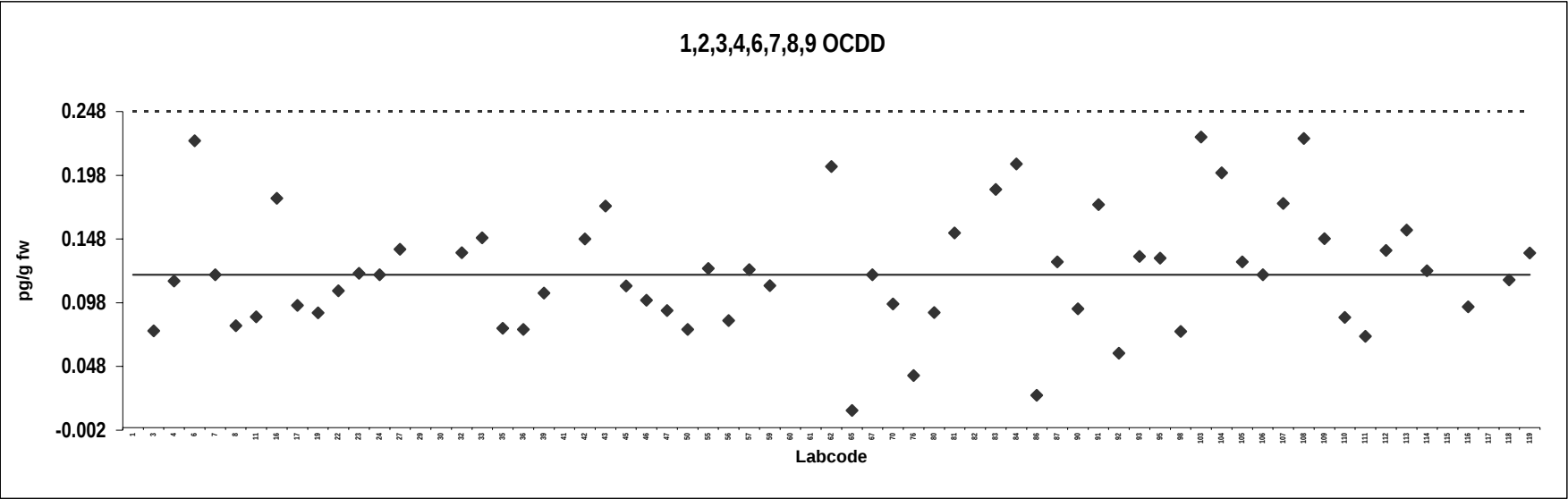
Salmon

Congener: 1,2,3,4,6,7,8,9 OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.2	Outlier,ND	87	0.13	
3	0.076		90	0.093	
4	0.12		91	0.18	
6	0.23		92	0.058	
7	0.12		93	0.13	
8	0.080		95	0.13	ND
11	0.087		98	0.075	
16	0.18		103	0.23	
17	0.096		104	0.20	
19	0.090		105	0.13	
22	0.11		106	0.12	
23	0.12		107	0.18	
24	0.12	ND	108	0.23	
27	0.14		109	0.15	
29	2.5	Outlier,ND	110	0.087	
30	0.37	Outlier	111	0.072	
32	0.14		112	0.14	ND
33	0.15		113	0.16	
35	0.078		114	0.12	
36	0.077		115	0.75	Outlier
39	0.11		116	0.095	
41	0.85	Outlier	117	0.35	Outlier,ND
42	0.15		118	0.12	
43	0.17		119	0.14	
45	0.11				
46	0.10				
47	0.092				
50	0.077				
55	0.13				
56	0.084				
57	0.12				
59	0.11				
60	4.6	Outlier			
61	0.89	Outlier			
62	0.21				
65	0.014				
67	0.12				
70	0.097				
76	0.041	ND			
80	0.090				
81	0.15				
82	5.8	Outlier			
83	0.19				
84	0.21				
86	0.025	ND			

Consensus statistics

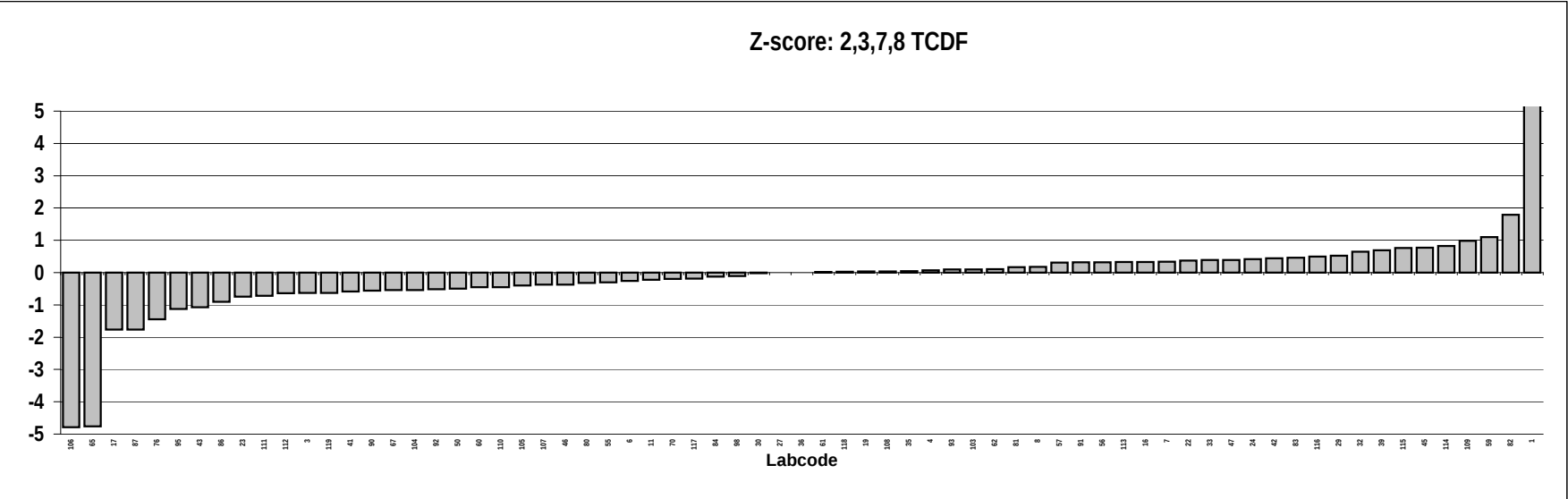
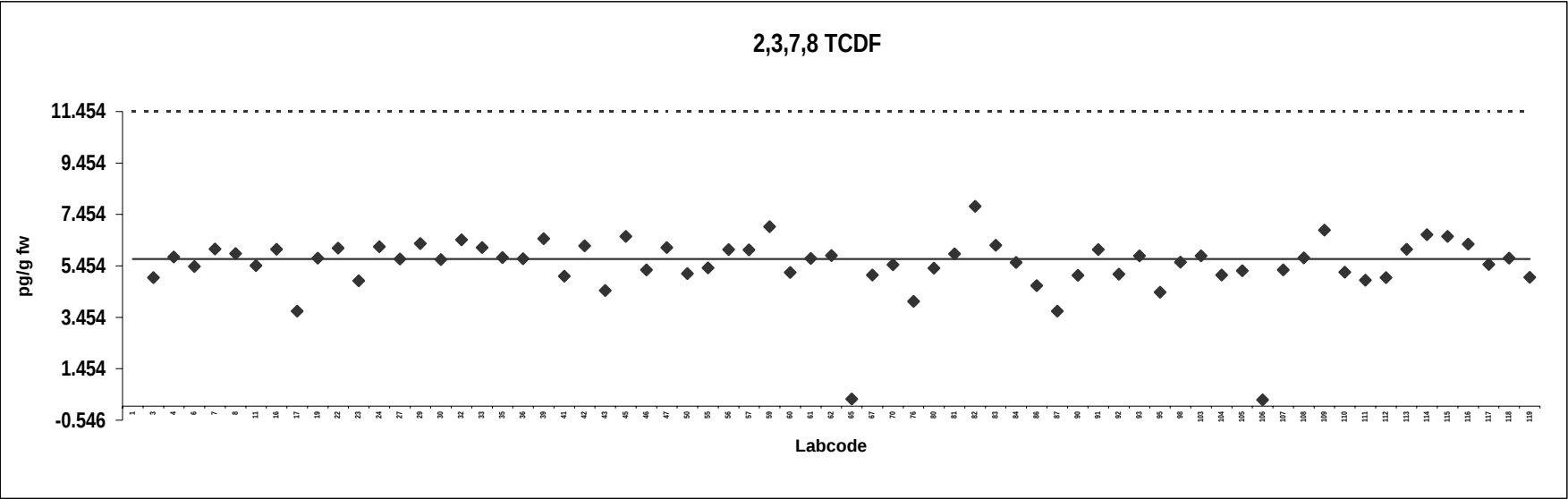
Consensus median, pg/g	0.12
Median all values pg/g	0.12
Consensus mean, pg/g	0.12
Standard deviation, pg/g	0.047
Relative standard deviation, %	39
No. of values reported	69
No. of values removed	9
No. of reported non-detects	8



Salmon
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	25	Outlier	87	3.7	
3	5.0		90	5.1	
4	5.8		91	6.1	
6	5.4		92	5.1	
7	6.1		93	5.8	
8	5.9		95	4.4	
11	5.5		98	5.6	
16	6.1		103	5.8	
17	3.7		104	5.1	
19	5.8		105	5.3	
22	6.1		106	0.24	
23	4.9		107	5.3	
24	6.2		108	5.8	
27	5.7		109	6.8	
29	6.3		110	5.2	
30	5.7		111	4.9	
32	6.5		112	5.0	
33	6.2		113	6.1	
35	5.8		114	6.7	
36	5.7		115	6.6	
39	6.5		116	6.3	
41	5.1		117	5.5	
42	6.2		118	5.8	
43	4.5		119	5.0	
45	6.6				
46	5.3				
47	6.2				
50	5.2				
55	5.4				
56	6.1				
57	6.1				
59	7.0				
60	5.2				
61	5.7				
62	5.9				
65	0.28				
67	5.1				
70	5.5				
76	4.1				
80	5.4				
81	5.9				
82	7.8				
83	6.3				
84	5.6				
86	4.7				

Consensus statistics	
Consensus median, pg/g	5.7
Median all values pg/g	5.7
Consensus mean, pg/g	5.5
Standard deviation, pg/g	1.2
Relative standard deviation, %	21
No. of values reported	69
No. of values removed	1
No. of reported non-detects	0

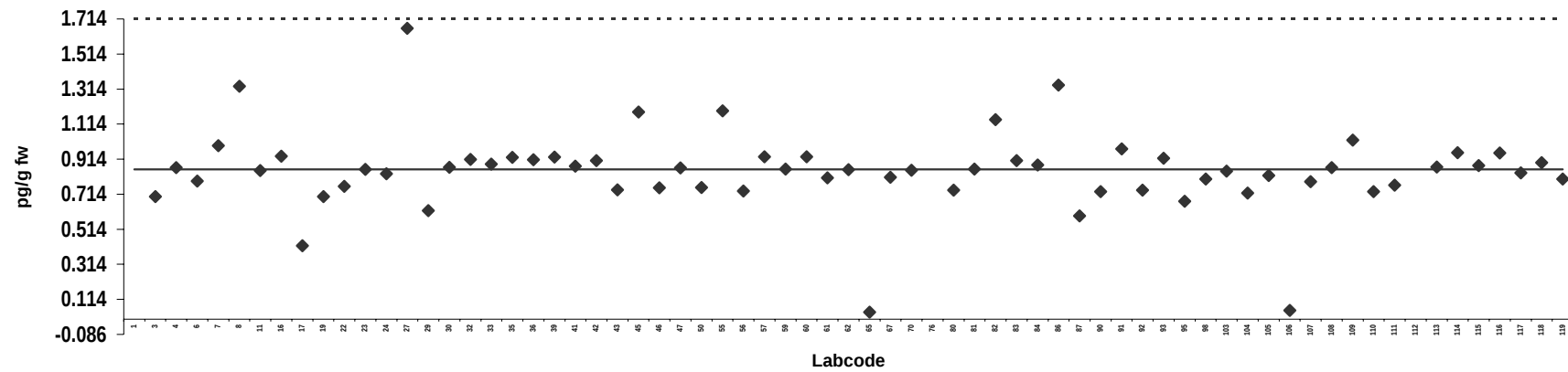


Salmon
Congener: 1,2,3,7,8 PeCDF

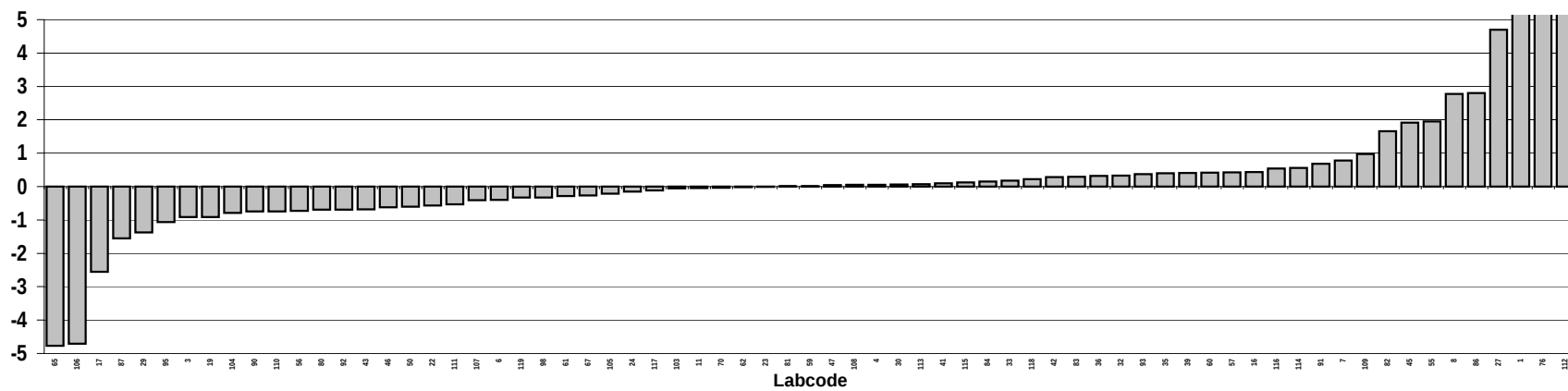
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.2	Outlier	87	0.59	ND
3	0.70		90	0.73	
4	0.87		91	0.97	
6	0.79		92	0.74	
7	0.99		93	0.92	
8	1.3		95	0.67	
11	0.85		98	0.80	
16	0.93		103	0.85	
17	0.42		104	0.72	
19	0.70		105	0.82	
22	0.76		106	0.050	Outlier
23	0.86		107	0.79	
24	0.83		108	0.86	
27	1.7		109	1.0	
29	0.62		110	0.73	
30	0.87		111	0.77	
32	0.91		112	5.9	
33	0.89		113	0.87	
35	0.92		114	0.95	
36	0.91		115	0.88	
39	0.93		116	0.95	
41	0.87		117	0.84	
42	0.91		118	0.89	
43	0.74		119	0.80	
45	1.2				
46	0.75				
47	0.86				
50	0.75				
55	1.2				
56	0.73				
57	0.93	Outlier			
59	0.86				
60	0.93				
61	0.81				
62	0.85				
65	0.040				
67	0.81				
70	0.85				
76	5.0				
80	0.74				
81	0.86				
82	1.1				
83	0.91				
84	0.88				
86	1.3				

Consensus statistics	
Consensus median, pg/g	0.86
Median all values pg/g	0.86
Consensus mean, pg/g	0.85
Standard deviation, pg/g	0.23
Relative standard deviation, %	27
No. of values reported	69
No. of values removed	3
No. of reported non-detects	1

1,2,3,7,8 PeCDF



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

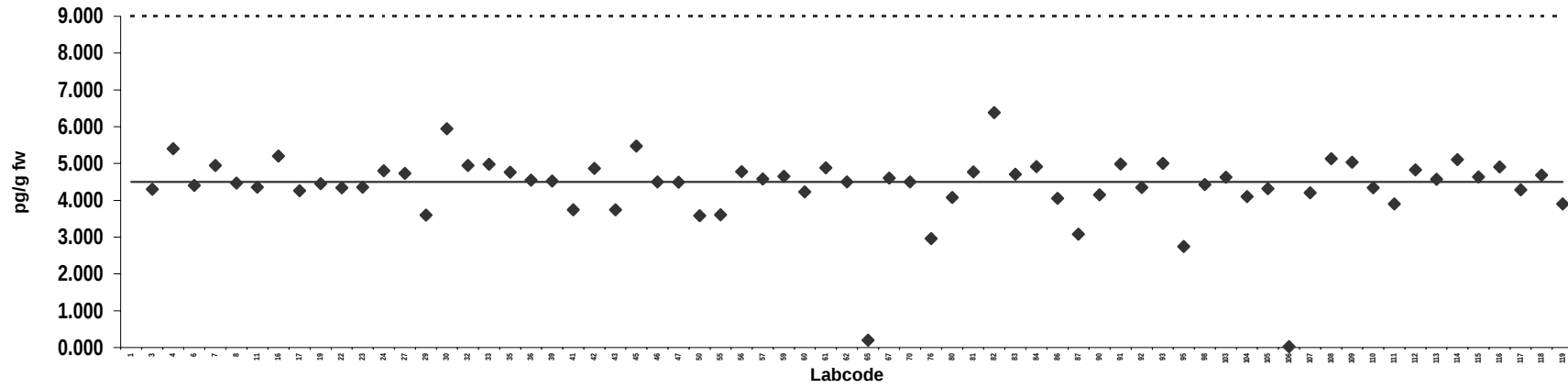


Salmon
Congener: 2,3,4,7,8 PeCDF

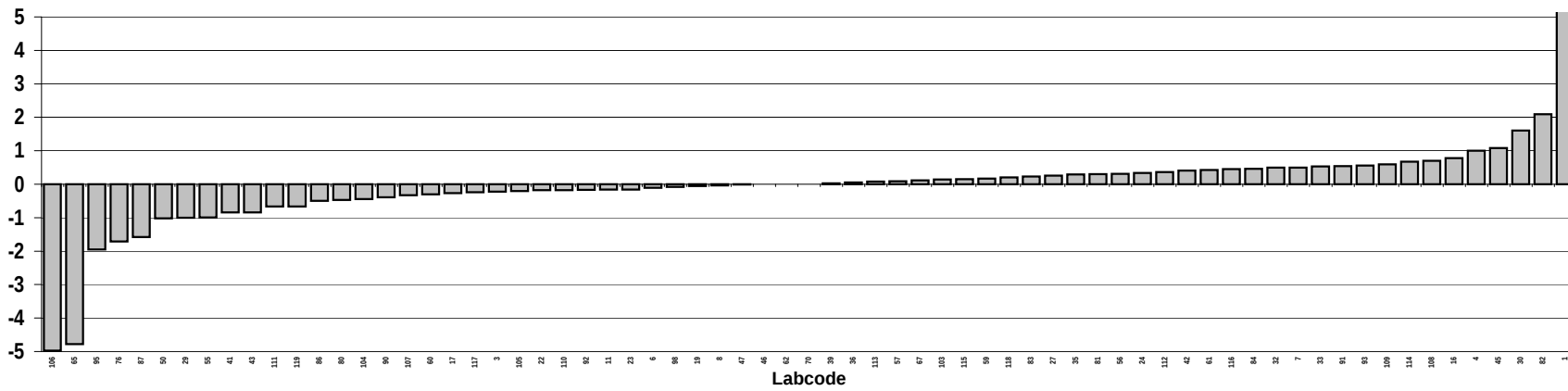
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	20	Outlier	87	3.1	
3	4.3		90	4.2	
4	5.4		91	5.0	
6	4.4		92	4.4	
7	5.0		93	5.0	
8	4.5		95	2.7	
11	4.4		98	4.4	
16	5.2		103	4.6	
17	4.3		104	4.1	
19	4.5		105	4.3	
22	4.3		106	0.020	
23	4.4		107	4.2	
24	4.8		108	5.1	
27	4.7		109	5.0	
29	3.6		110	4.3	
30	5.9		111	3.9	
32	4.9		112	4.8	
33	5.0		113	4.6	
35	4.8		114	5.1	
36	4.5		115	4.6	
39	4.5		116	4.9	
41	3.7		117	4.3	
42	4.9		118	4.7	
43	3.7		119	3.9	
45	5.5				
46	4.5				
47	4.5				
50	3.6				
55	3.6				
56	4.8				
57	4.6				
59	4.7				
60	4.2				
61	4.9				
62	4.5				
65	0.20				
67	4.6				
70	4.5				
76	3.0				
80	4.1				
81	4.8				
82	6.4				
83	4.7				
84	4.9				
86	4.1				

Consensus statistics	
Consensus median, pg/g	4.5
Median all values pg/g	4.5
Consensus mean, pg/g	4.4
Standard deviation, pg/g	0.96
Relative standard deviation, %	22
No. of values reported	69
No. of values removed	1
No. of reported non-detects	0

2,3,4,7,8 PeCDF



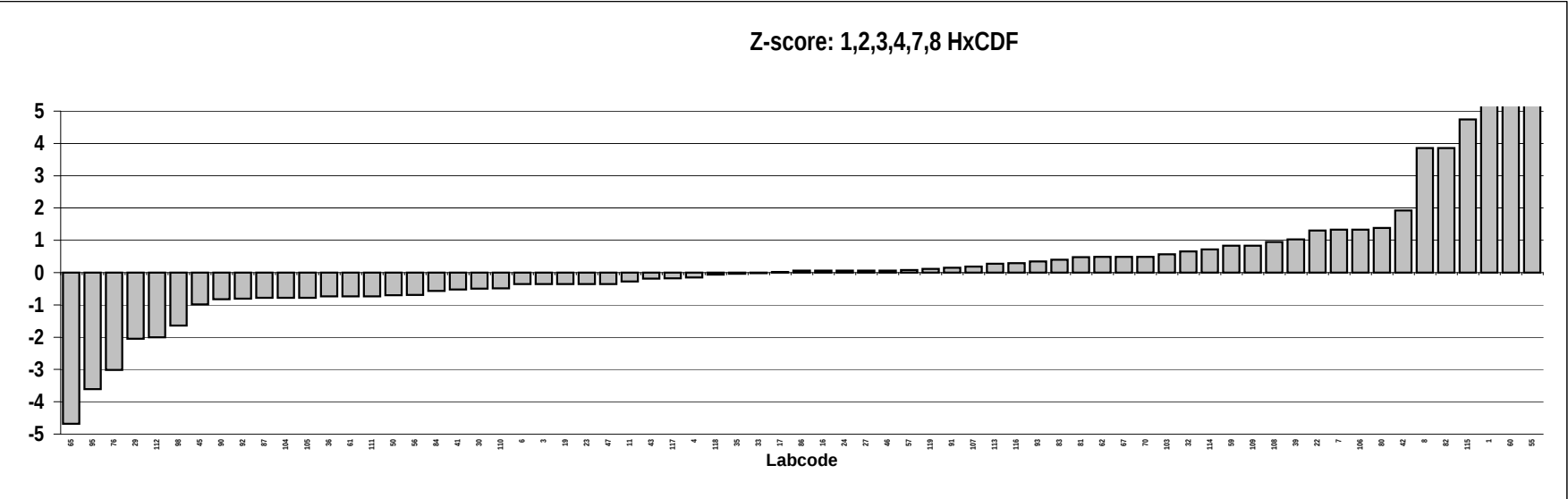
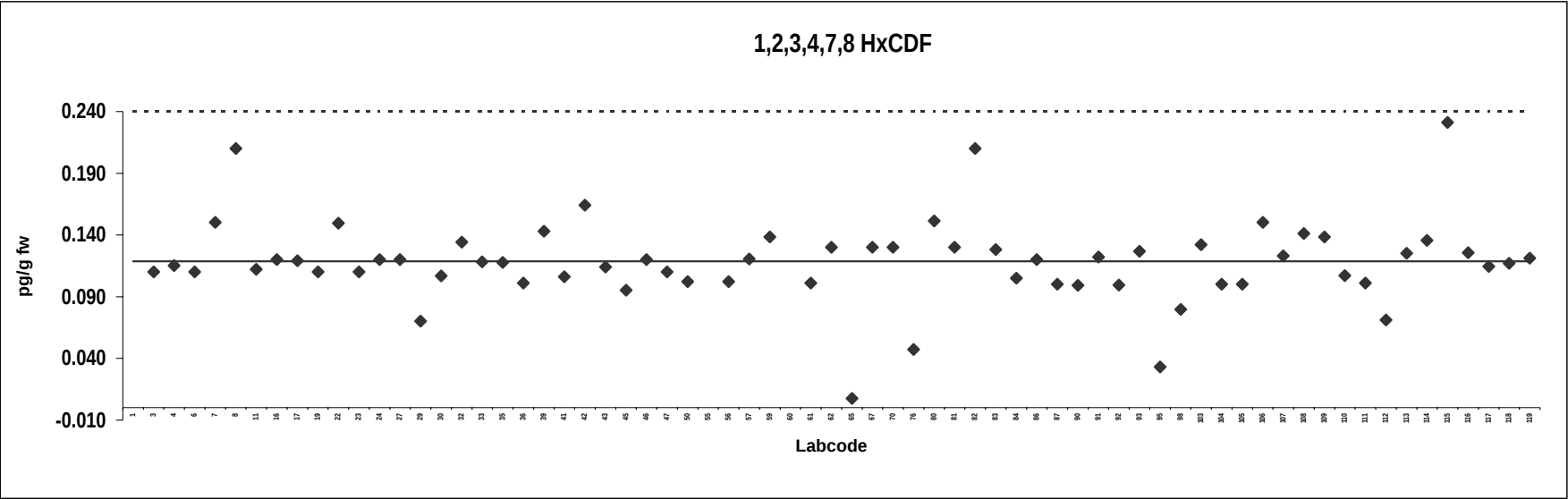
Z-score: 2,3,4,7,8 PeCDF



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.73	Outlier	87	0.10	ND
3	0.11		90	0.099	
4	0.12		91	0.12	
6	0.11		92	0.099	
7	0.15		93	0.13	
8	0.21		95	0.033	
11	0.11		98	0.080	
16	0.12		103	0.13	
17	0.12		104	0.10	
19	0.11		105	0.10	
22	0.15		106	0.15	ND
23	0.11		107	0.12	
24	0.12		108	0.14	
27	0.12		109	0.14	
29	0.070		110	0.11	
30	0.11		111	0.10	
32	0.13		112	0.071	
33	0.12		113	0.13	
35	0.12		114	0.14	
36	0.10		115	0.23	
39	0.14		116	0.13	
41	0.11		117	0.11	
42	0.16		118	0.12	
43	0.11		119	0.12	
45	0.095				
46	0.12				
47	0.11				
50	0.10				
55	2.0				
56	0.10				
57	0.12	Outlier			
59	0.14				
60	1.1				
61	0.10				
62	0.13				
65	0.0075				
67	0.13				
70	0.13				
76	0.047				
80	0.15				
81	0.13				
82	0.21				
83	0.13				
84	0.10				
86	0.12				

Consensus statistics	
Consensus median, pg/g	0.12
Median all values pg/g	0.12
Consensus mean, pg/g	0.12
Standard deviation, pg/g	0.034
Relative standard deviation, %	29
No. of values reported	69
No. of values removed	3
No. of reported non-detects	2

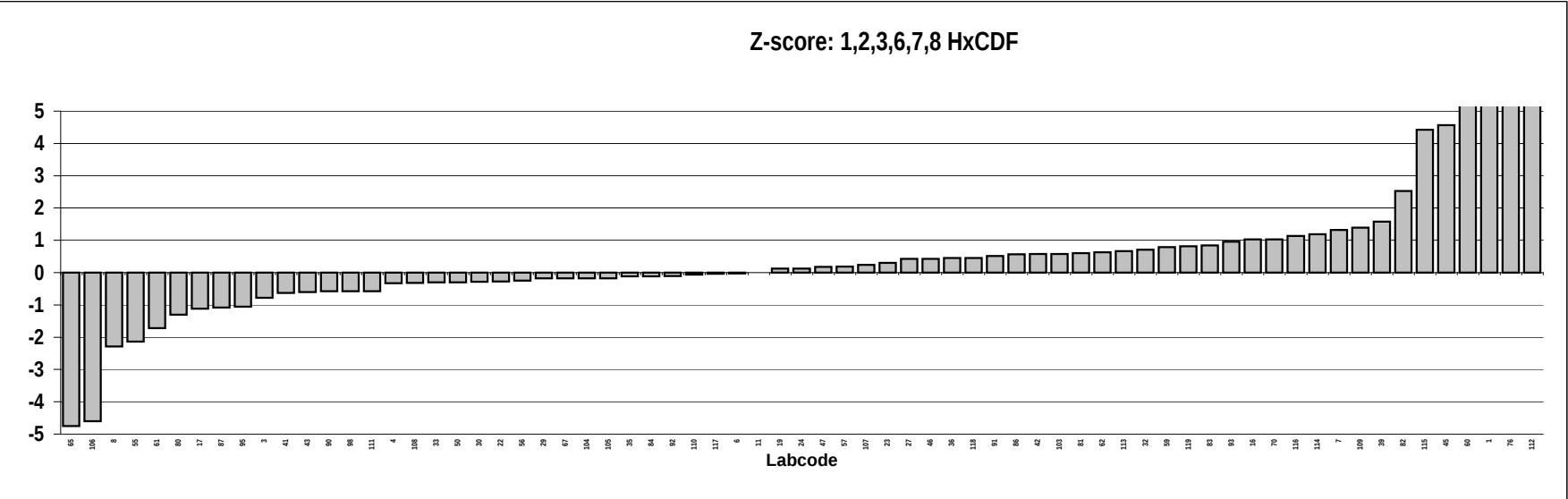
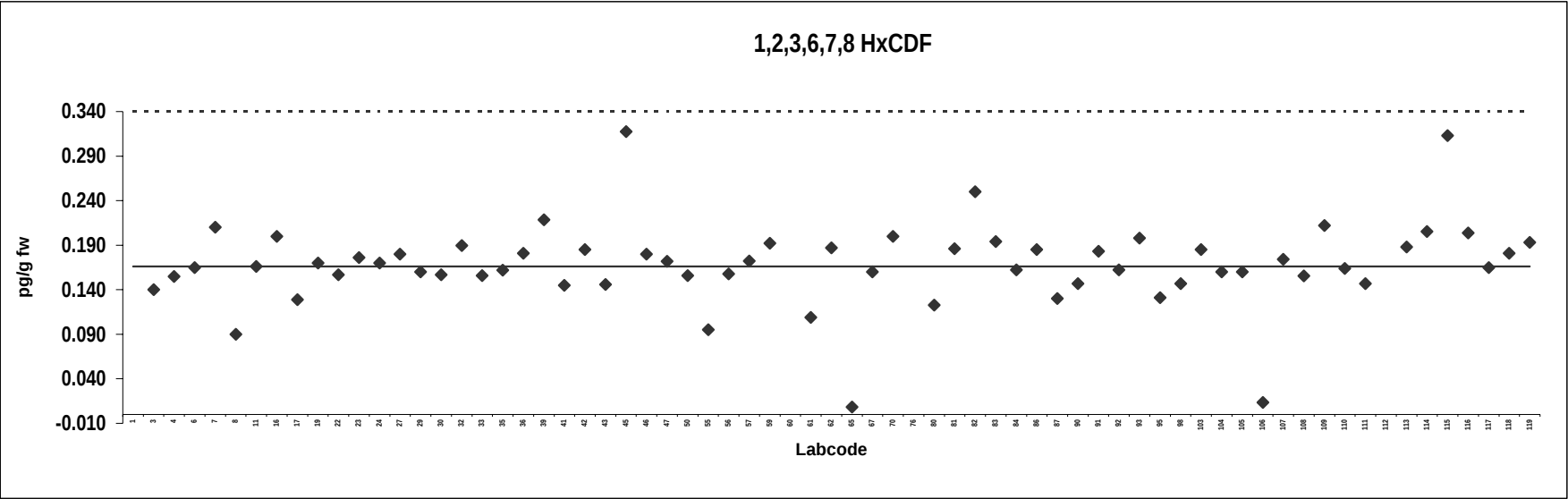


Salmon

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.55	Outlier	87	0.13	Outlier
3	0.14		90	0.15	
4	0.16		91	0.18	
6	0.17		92	0.16	
7	0.21		93	0.20	
8	0.090		95	0.13	
11	0.17		98	0.15	
16	0.20		103	0.19	
17	0.13		104	0.16	
19	0.17		105	0.16	
22	0.16		106	0.013	
23	0.18		107	0.17	
24	0.17		108	0.16	
27	0.18		109	0.21	
29	0.16		110	0.16	
30	0.16		111	0.15	
32	0.19		112	4.9	
33	0.16		113	0.19	
35	0.16		114	0.21	
36	0.18		115	0.31	
39	0.22		116	0.20	
41	0.15	Outlier	117	0.16	
42	0.19		118	0.18	
43	0.15		119	0.19	
45	0.32				
46	0.18				
47	0.17				
50	0.16				
55	0.095				
56	0.16				
57	0.17				
59	0.19	Outlier			
60	0.50				
61	0.11				
62	0.19				
65	0.0083				
67	0.16	Outlier			
70	0.20				
76	0.78				
80	0.12				
81	0.19				
82	0.25				
83	0.19				
84	0.16				
86	0.18				

Consensus statistics	
Consensus median, pg/g	0.17
Median all values pg/g	0.17
Consensus mean, pg/g	0.17
Standard deviation, pg/g	0.047
Relative standard deviation, %	28
No. of values reported	69
No. of values removed	4
No. of reported non-detects	0



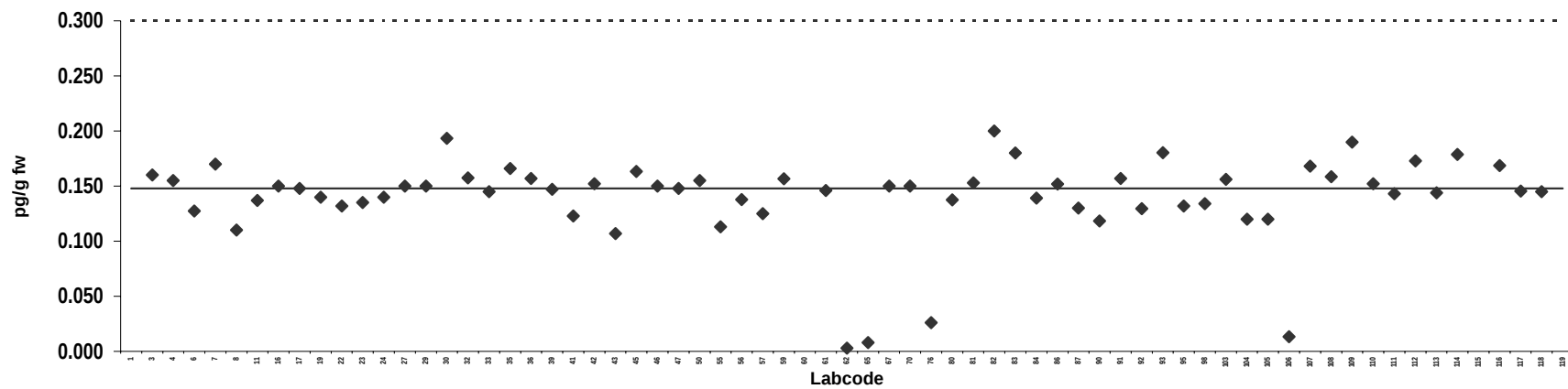
Salmon

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

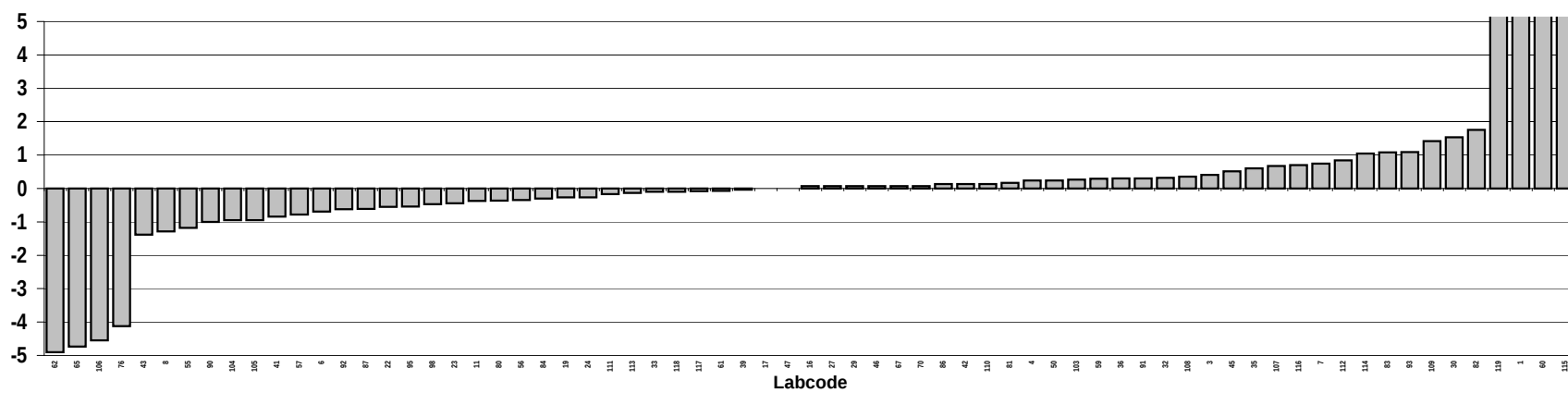
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.35	Outlier,ND	87	0.13	
3	0.16		90	0.12	
4	0.16		91	0.16	
6	0.13		92	0.13	
7	0.17		93	0.18	
8	0.11		95	0.13	
11	0.14		98	0.13	
16	0.15		103	0.16	
17	0.15		104	0.12	
19	0.14		105	0.12	
22	0.13		106	0.013	
23	0.14		107	0.17	
24	0.14		108	0.16	
27	0.15		109	0.19	
29	0.15		110	0.15	
30	0.19		111	0.14	
32	0.16		112	0.17	
33	0.15		113	0.14	
35	0.17		114	0.18	
36	0.16		115	0.39	Outlier
39	0.15		116	0.17	
41	0.12		117	0.15	
42	0.15		118	0.15	Outlier
43	0.11		119	0.34	
45	0.16				
46	0.15				
47	0.15				
50	0.16				
55	0.11				
56	0.14				
57	0.12				
59	0.16				
60	0.36	Outlier			
61	0.15	ND			
62	0.0030				
65	0.0079				
67	0.15	ND			
70	0.15				
76	0.026				
80	0.14				
81	0.15				
82	0.20				
83	0.18				
84	0.14				
86	0.15				

Consensus statistics	
Consensus median, pg/g	0.15
Median all values pg/g	0.15
Consensus mean, pg/g	0.14
Standard deviation, pg/g	0.038
Relative standard deviation, %	27
No. of values reported	69
No. of values removed	4
No. of reported non-detects	3

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



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



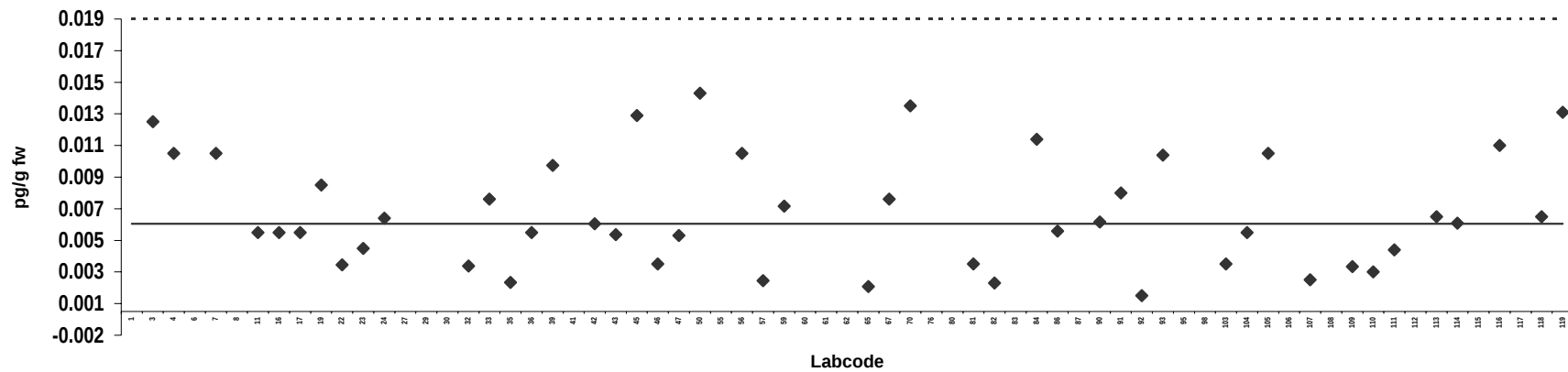
Salmon

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

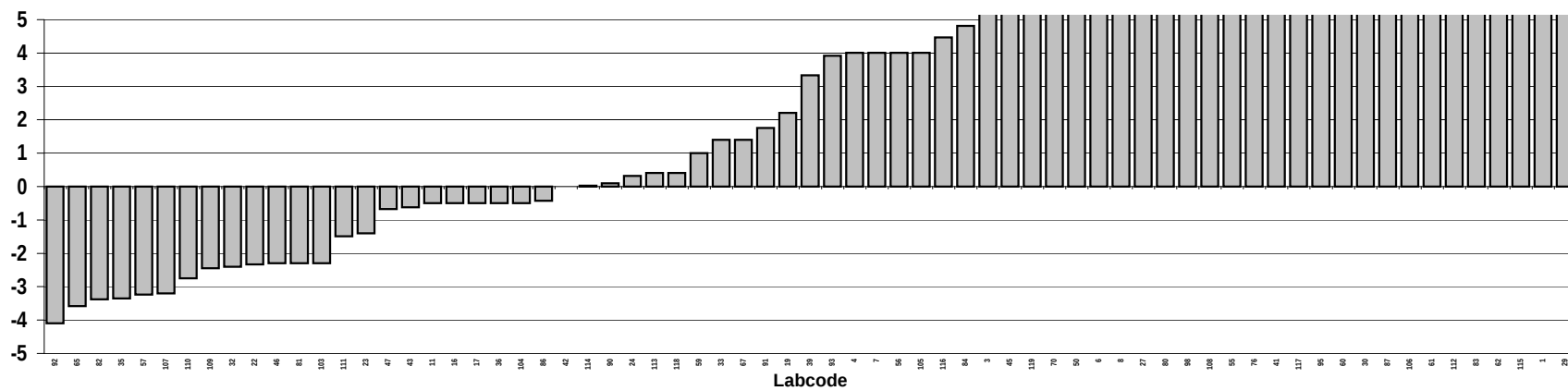
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.35	Outlier,ND	87	0.040	Outlier
3	0.012		90	0.0057	
4	0.010	ND	91	0.0075	ND
6	0.020	Outlier,ND	92	0.0010	ND
7	0.010	ND	93	0.0099	
8	0.020	Outlier	95	0.033	Outlier,ND
11	0.0050	ND	98	0.023	Outlier
16	0.0050	ND	103	0.0030	ND
17	0.0050	ND	104	0.0050	ND
19	0.0080	ND	105	0.010	ND
22	0.0030		106	0.050	Outlier,ND
23	0.0040		107	0.0020	
24	0.0059	ND	108	0.025	Outlier
27	0.020	Outlier,ND	109	0.0028	ND
29	0.65	Outlier,ND	110	0.0025	ND
30	0.040	Outlier	111	0.0039	ND
32	0.0029		112	0.071	Outlier,ND
33	0.0071	ND	113	0.0060	ND
35	0.0018		114	0.0056	
36	0.0050	ND	115	0.21	Outlier
39	0.0093		116	0.011	
41	0.032	Outlier	117	0.032	Outlier,ND
42	0.0056		118	0.0060	
43	0.0049		119	0.013	
45	0.012				
46	0.0030				
47	0.0048	ND			
50	0.014	ND			
55	0.030	Outlier,ND			
56	0.010	ND			
57	0.0020				
59	0.0067	ND			
60	0.036	Outlier			
61	0.063	Outlier			
62	0.16	Outlier			
65	0.0016	ND			
67	0.0071				
70	0.013	ND			
76	0.030	Outlier,ND			
80	0.022	Outlier			
81	0.0030	ND			
82	0.0018	ND			
83	0.084	Outlier			
84	0.011				
86	0.0051	ND			

Consensus statistics	
Consensus median, pg/g	0.0056
Median all values pg/g	0.0093
Consensus mean, pg/g	0.0062
Standard deviation, pg/g	0.0035
Relative standard deviation, %	56
No. of values reported	69
No. of values removed	22
No. of reported non-detects	37

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



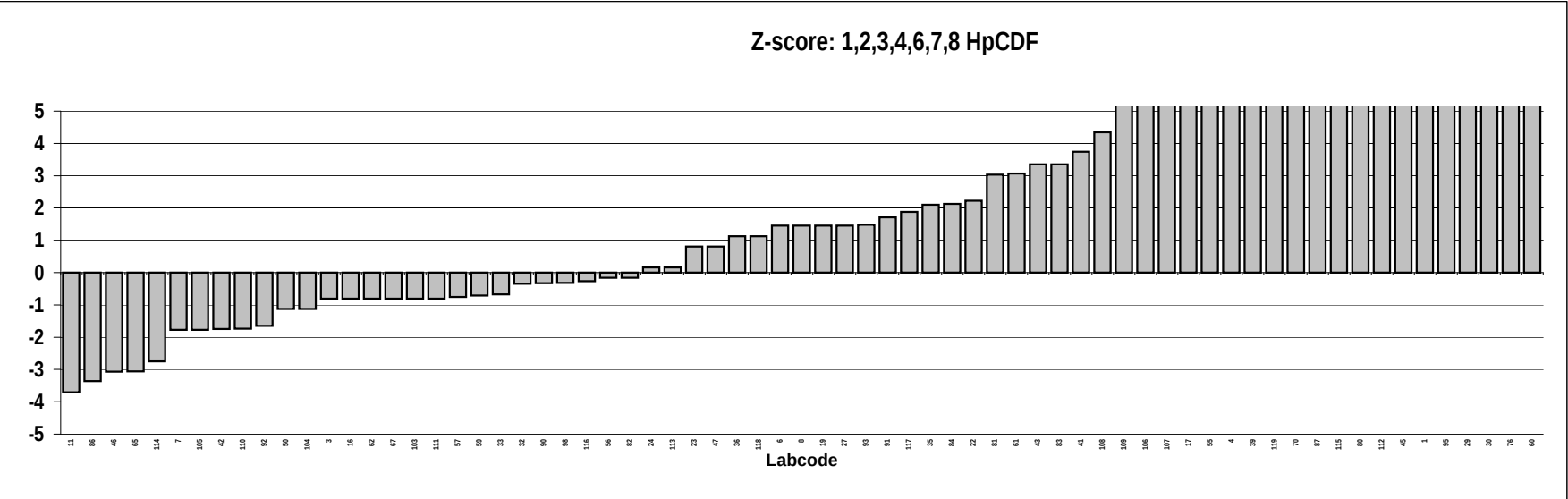
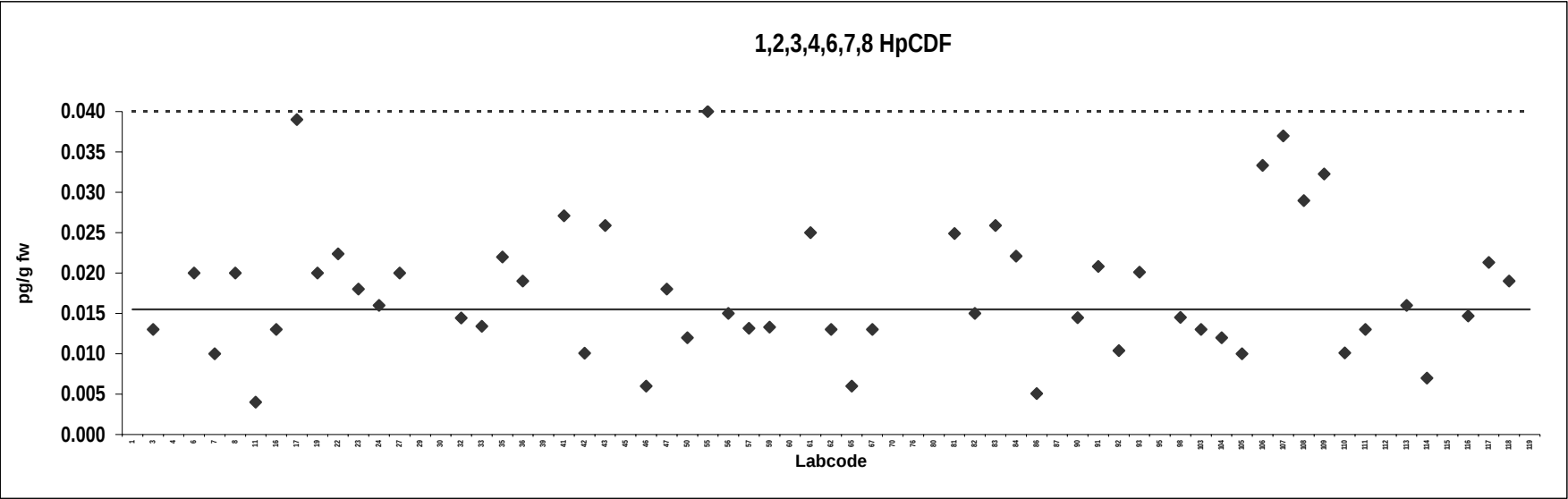
Z-score: 1,2,3,7,8,9 HxCDF



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.26	Outlier,ND	87	0.070	Outlier
3	0.013		90	0.014	
4	0.042	Outlier	91	0.021	
6	0.020	ND	92	0.010	
7	0.010		93	0.020	
8	0.020	ND	95	0.27	Outlier
11	0.0040	ND	98	0.015	
16	0.013		103	0.013	
17	0.039		104	0.012	ND
19	0.020	ND	105	0.010	ND
22	0.022		106	0.033	
23	0.018		107	0.037	
24	0.016	ND	108	0.029	
27	0.020		109	0.032	
29	0.44	Outlier,ND	110	0.010	
30	0.45	Outlier	111	0.013	
32	0.014		112	0.20	Outlier,ND
33	0.013		113	0.016	
35	0.022		114	0.0070	
36	0.019		115	0.15	Outlier
39	0.048	Outlier	116	0.015	
41	0.027	ND	117	0.021	ND
42	0.010		118	0.019	
43	0.026		119	0.049	Outlier
45	0.23	Outlier			
46	0.0060				
47	0.018				
50	0.012				
55	0.040	ND			
56	0.015	ND			
57	0.013				
59	0.013				
60	5.2	Outlier			
61	0.025	ND			
62	0.013				
65	0.0060				
67	0.013				
70	0.051	Outlier			
76	0.47	Outlier			
80	0.17	Outlier			
81	0.025				
82	0.015				
83	0.026				
84	0.022				
86	0.0051	ND			

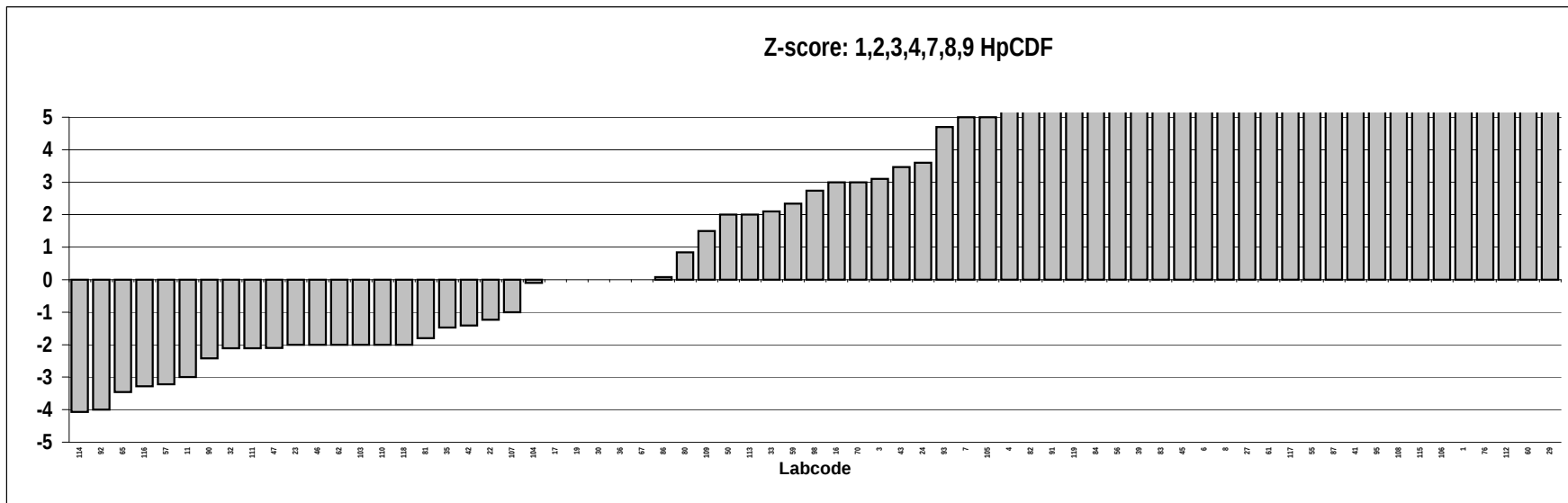
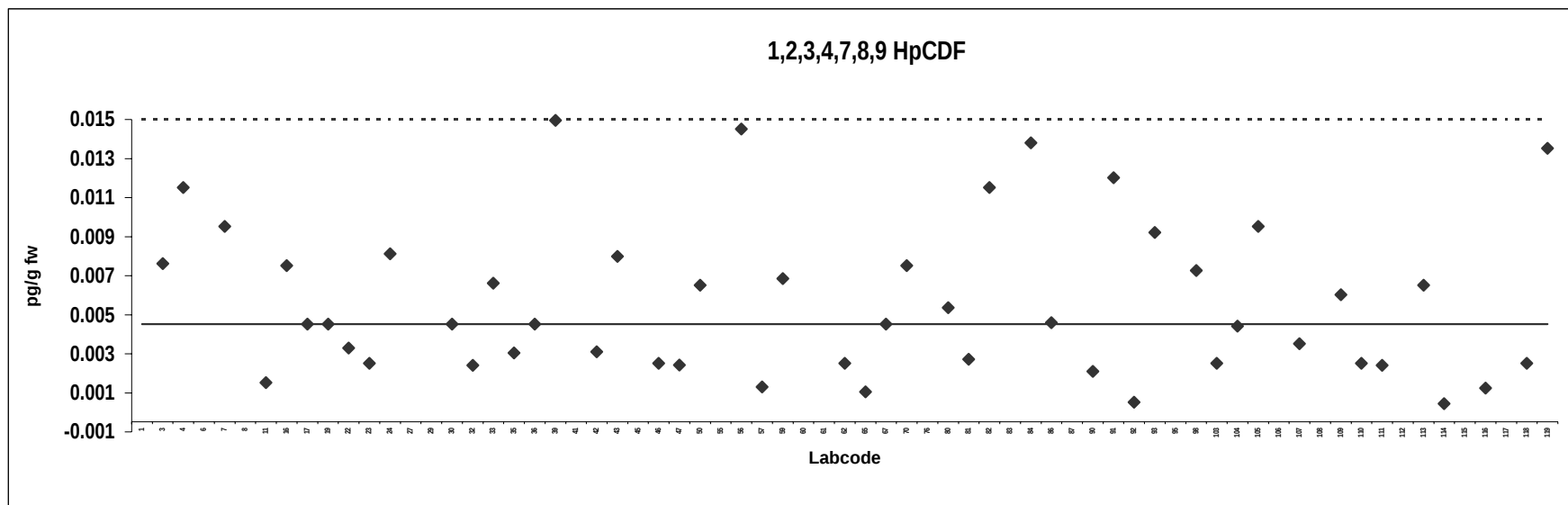
Consensus statistics	
Consensus median, pg/g	0.016
Median all values pg/g	0.020
Consensus mean, pg/g	0.018
Standard deviation, pg/g	0.0083
Relative standard deviation, %	47
No. of values reported	69
No. of values removed	15
No. of reported non-detects	16



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.13	Outlier,ND	87	0.050	Outlier
3	0.0081	ND	90	0.0026	
4	0.012	ND	91	0.013	ND
6	0.020	Outlier,ND	92	0.0010	ND
7	0.010	ND	93	0.0097	
8	0.020	Outlier,ND	95	0.067	Outlier,ND
11	0.0020	ND	98	0.0077	
16	0.0080	ND	103	0.0030	ND
17	0.0050	ND	104	0.0049	
19	0.0050	ND	105	0.010	ND
22	0.0038		106	0.10	Outlier,ND
23	0.0030		107	0.0040	
24	0.0086	ND	108	0.072	Outlier
27	0.020	Outlier,ND	109	0.0065	
29	0.83	Outlier,ND	110	0.0030	ND
30	0.0050		111	0.0029	ND
32	0.0029		112	0.20	Outlier,ND
33	0.0071	ND	113	0.0070	ND
35	0.0035		114	0.00093	ND
36	0.0050	ND	115	0.092	Outlier
39	0.015		116	0.0017	ND
41	0.062	Outlier	117	0.039	Outlier,ND
42	0.0036		118	0.0030	
43	0.0085		119	0.014	
45	0.020	Outlier			
46	0.0030				
47	0.0029	ND			
50	0.0070				
55	0.040	Outlier,ND			
56	0.015	ND			
57	0.0018				
59	0.0073	ND			
60	0.60	Outlier			
61	0.025	Outlier,ND			
62	0.0030	ND			
65	0.0015	ND			
67	0.0050	ND			
70	0.0080	ND			
76	0.13	Outlier			
80	0.0058	ND			
81	0.0032	ND			
82	0.012				
83	0.017	Outlier			
84	0.014				
86	0.0051	ND			

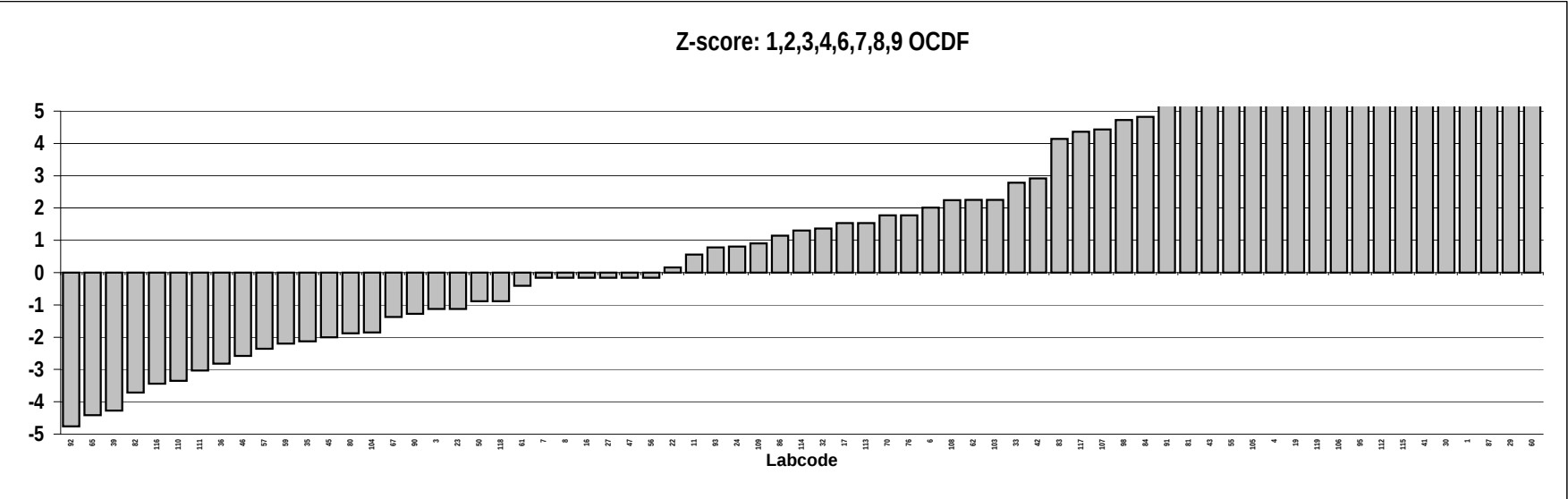
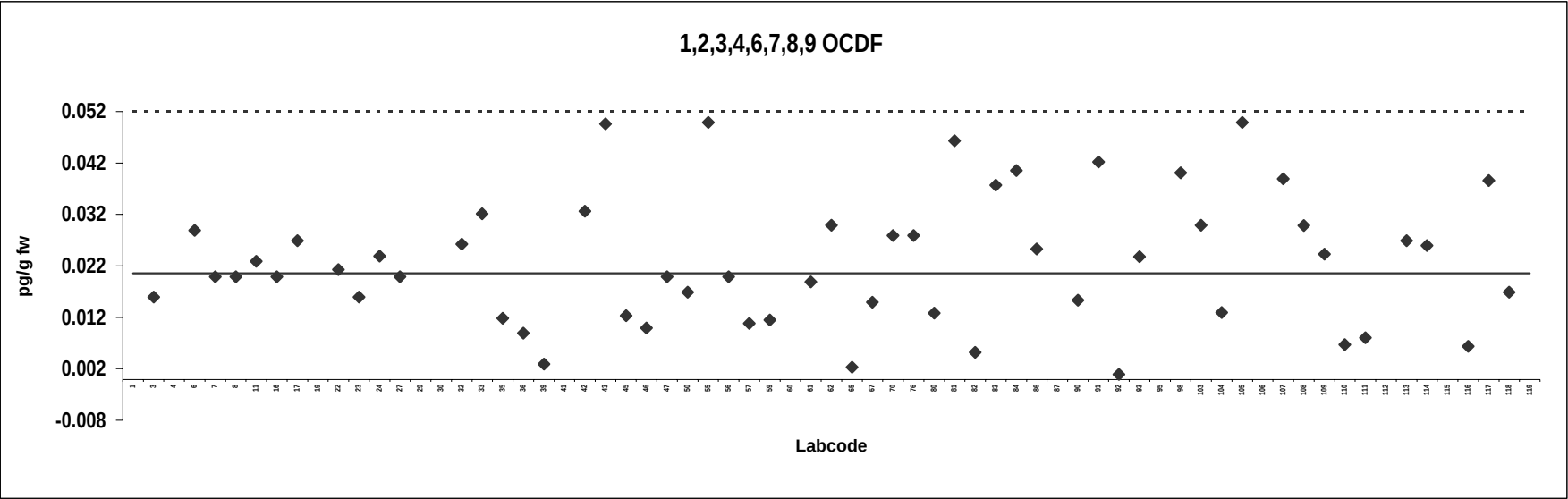
Consensus statistics	
Consensus median, pg/g	0.0050
Median all values pg/g	0.0077
Consensus mean, pg/g	0.0061
Standard deviation, pg/g	0.0039
Relative standard deviation, %	64
No. of values reported	69
No. of values removed	19
No. of reported non-detects	40



Salmon
Congener: 1,2,3,4,6,7,8,9 OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.30	Outlier,ND	87	0.37	Outlier
3	0.016	ND	90	0.015	
4	0.058	Outlier,ND	91	0.042	
6	0.029		92	0.0010	ND
7	0.020		93	0.024	
8	0.020	ND	95	0.13	Outlier,ND
11	0.023	ND	98	0.040	
16	0.020		103	0.030	
17	0.027		104	0.013	ND
19	0.060	Outlier,ND	105	0.050	ND
22	0.021		106	0.11	Outlier
23	0.016		107	0.039	
24	0.024		108	0.030	
27	0.020		109	0.024	
29	1.8	Outlier,ND	110	0.0068	
30	0.25	Outlier	111	0.0081	
32	0.026		112	0.14	Outlier,ND
33	0.032		113	0.027	
35	0.012		114	0.026	
36	0.0090		115	0.18	Outlier
39	0.0030	ND	116	0.0065	ND
41	0.19	Outlier	117	0.039	ND
42	0.033		118	0.017	
43	0.050		119	0.081	Outlier
45	0.012				
46	0.010				
47	0.020				
50	0.017				
55	0.050	ND			
56	0.020	ND			
57	0.011				
59	0.012				
60	10	Outlier			
61	0.019				
62	0.030				
65	0.0024	ND			
67	0.015				
70	0.028	ND			
76	0.028	ND			
80	0.013				
81	0.046				
82	0.0053	ND			
83	0.038				
84	0.041				
86	0.025	ND			

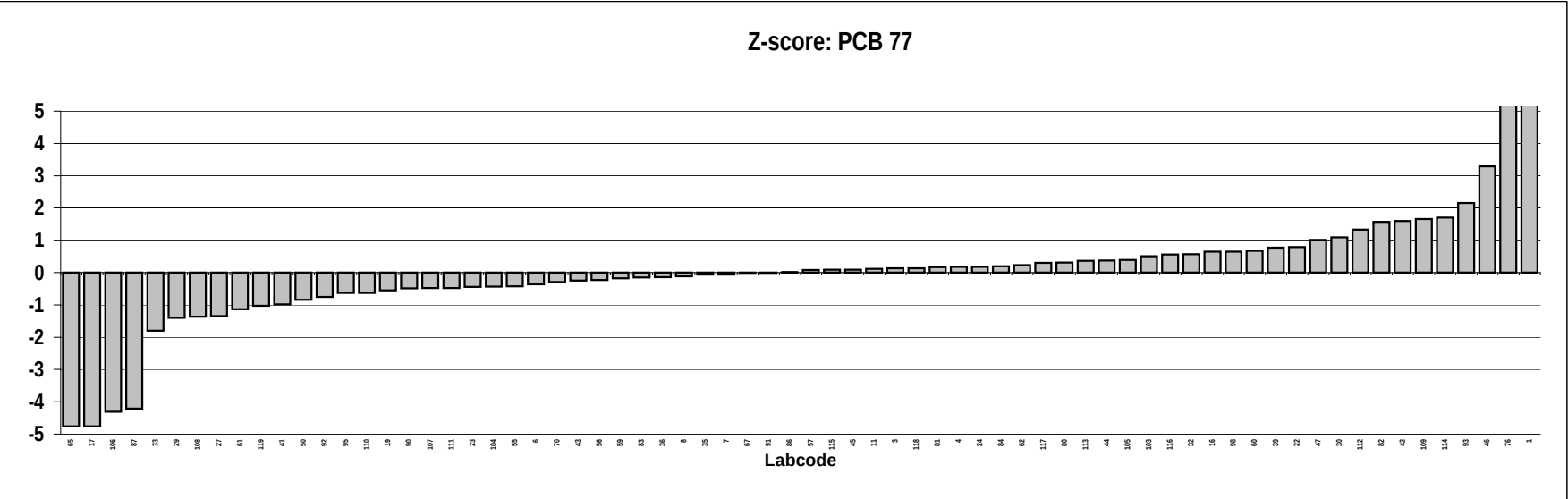
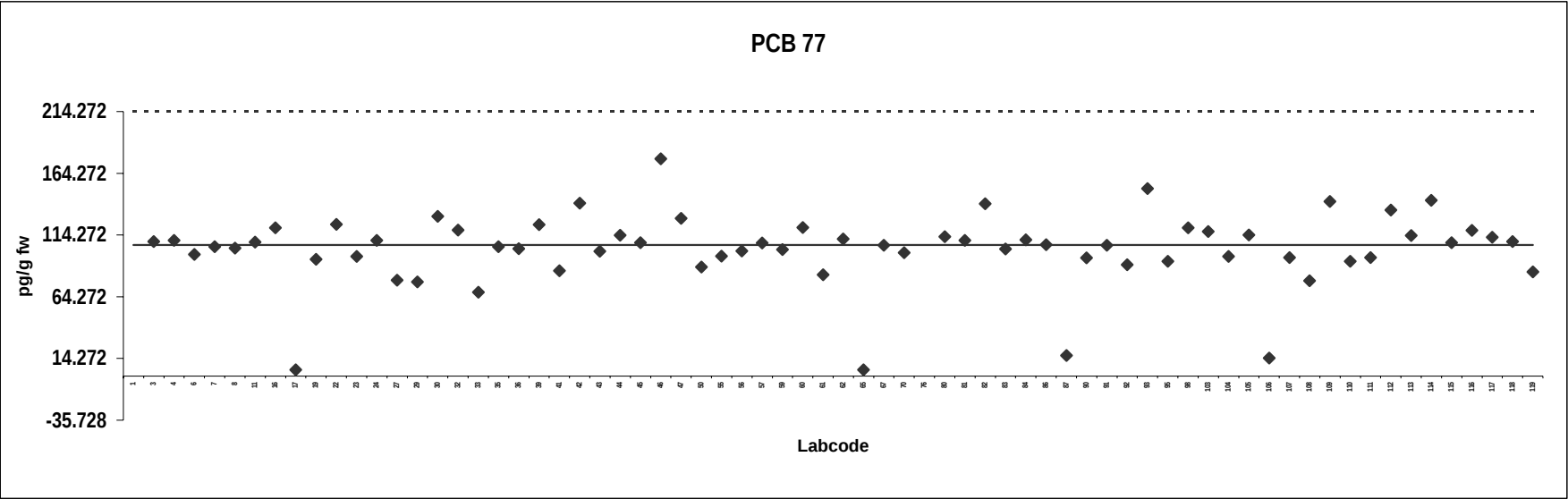
Consensus statistics	
Consensus median, pg/g	0.021
Median all values pg/g	0.026
Consensus mean, pg/g	0.023
Standard deviation, pg/g	0.013
Relative standard deviation, %	55
No. of values reported	69
No. of values removed	13
No. of reported non-detects	22



Salmon
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	358	Outlier	86	106	
3	109		87	17	
4	110		90	96	
6	99		91	106	
7	105		92	90	
8	104		93	152	
11	109		95	93	
16	120		98	120	
17	5.1		103	117	
19	95		104	97	
22	123		105	114	
23	97		106	15	
24	110		107	96	
27	78		108	77	
29	76		109	141	
30	129		110	93	
32	118		111	96	
33	68		112	134	
35	105		113	114	
36	103		114	142	
39	123		115	108	
41	85		116	118	
42	140		117	113	
43	101		118	109	
44	114		119	84	
45	108				
46	176				
47	128				
50	88				
55	97				
56	101				
57	108				
59	102				
60	120				
61	82				
62	111				
65	5.0				
67	106				
70	100				
76	327	Outlier			
80	113				
81	110				
82	140				
83	103				
84	110				

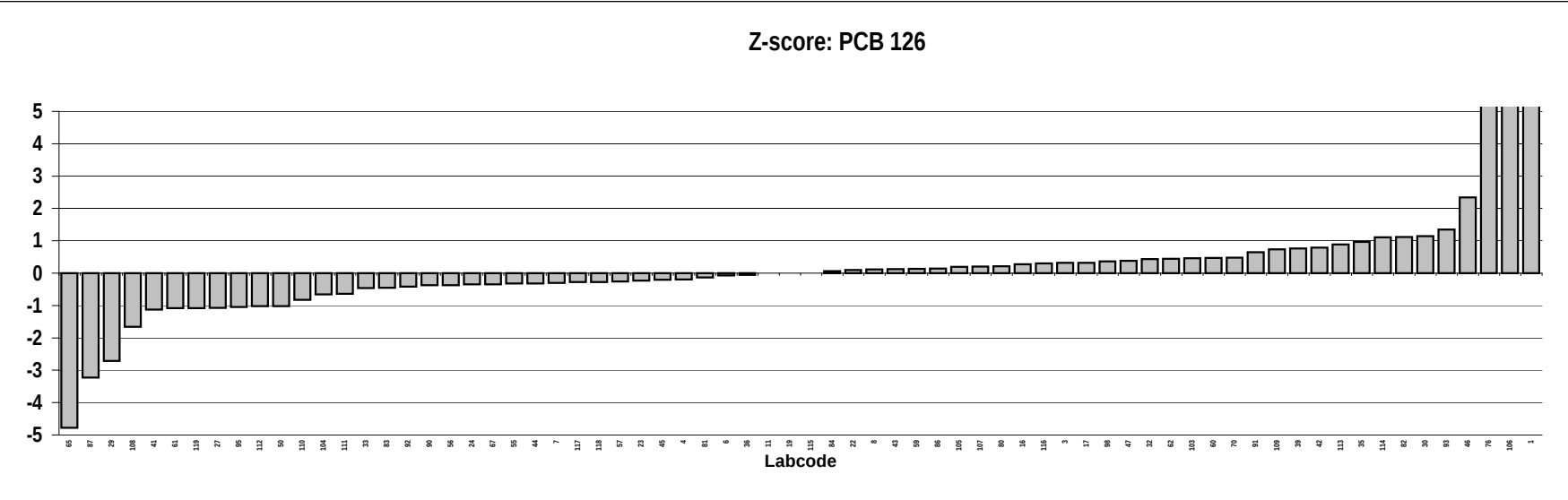
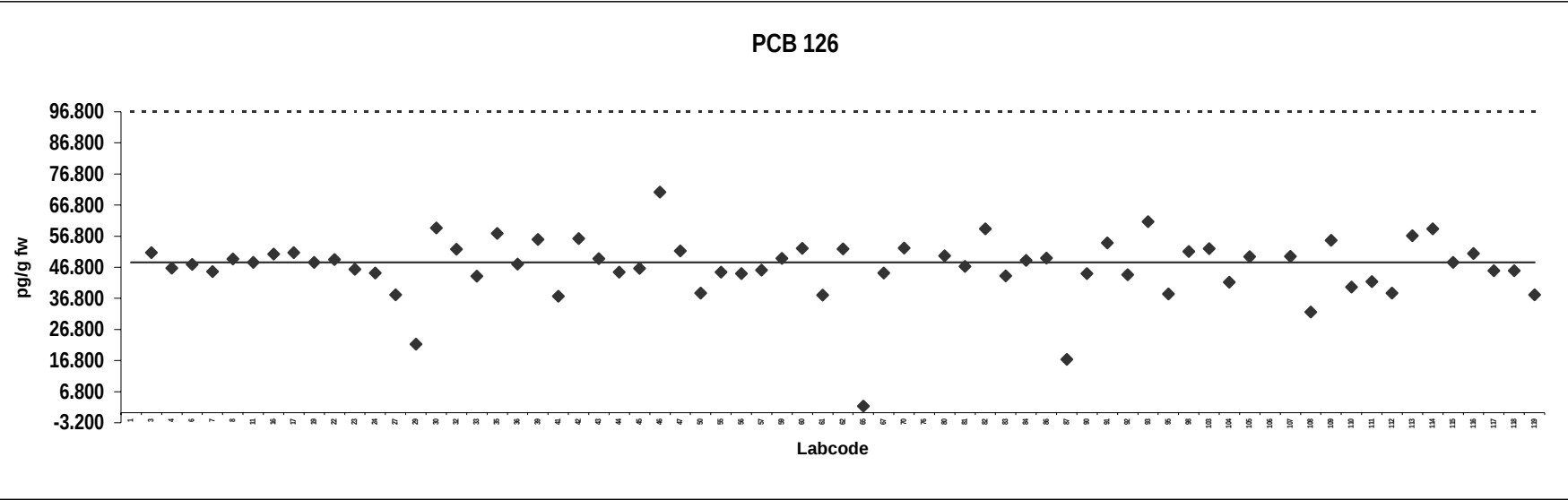
Consensus statistics	
Consensus median, pg/g	106
Median all values pg/g	107
Consensus mean, pg/g	103
Standard deviation, pg/g	30
Relative standard deviation, %	29
No. of values reported	70
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	144	Outlier	86	50	Outlier
3	52		87	17	
4	47		90	45	
6	48		91	55	
7	45		92	44	
8	49		93	61	
11	48		95	38	
16	51		98	52	
17	52		103	53	
19	48		104	42	
22	49		105	50	
23	46		106	143	
24	45		107	50	
27	38		108	32	
29	22		109	55	
30	59		110	40	
32	53		111	42	
33	44		112	38	
35	58		113	57	
36	48		114	59	
39	56		115	48	
41	38		116	51	
42	56		117	46	
43	50		118	46	
44	45		119	38	
45	46	Outlier			
46	71				
47	52				
50	39				
55	45				
56	45				
57	46				
59	50				
60	53				
61	38				
62	53				
65	2.1				
67	45				
70	53				
76	143				
80	50				
81	47				
82	59				
83	44				
84	49				

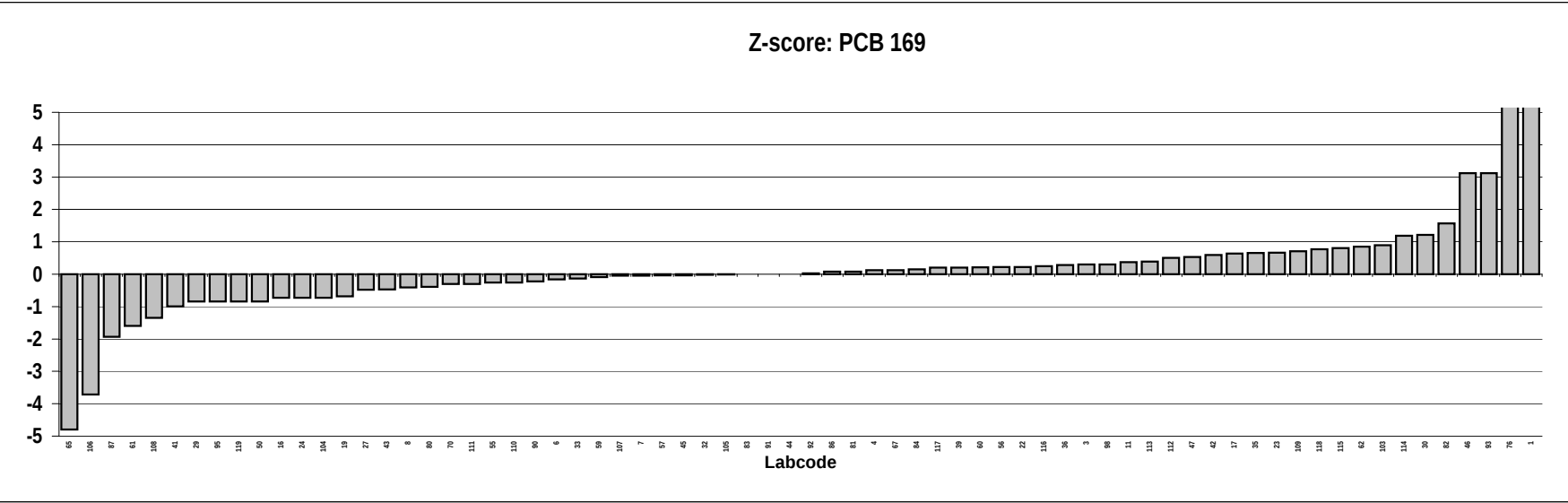
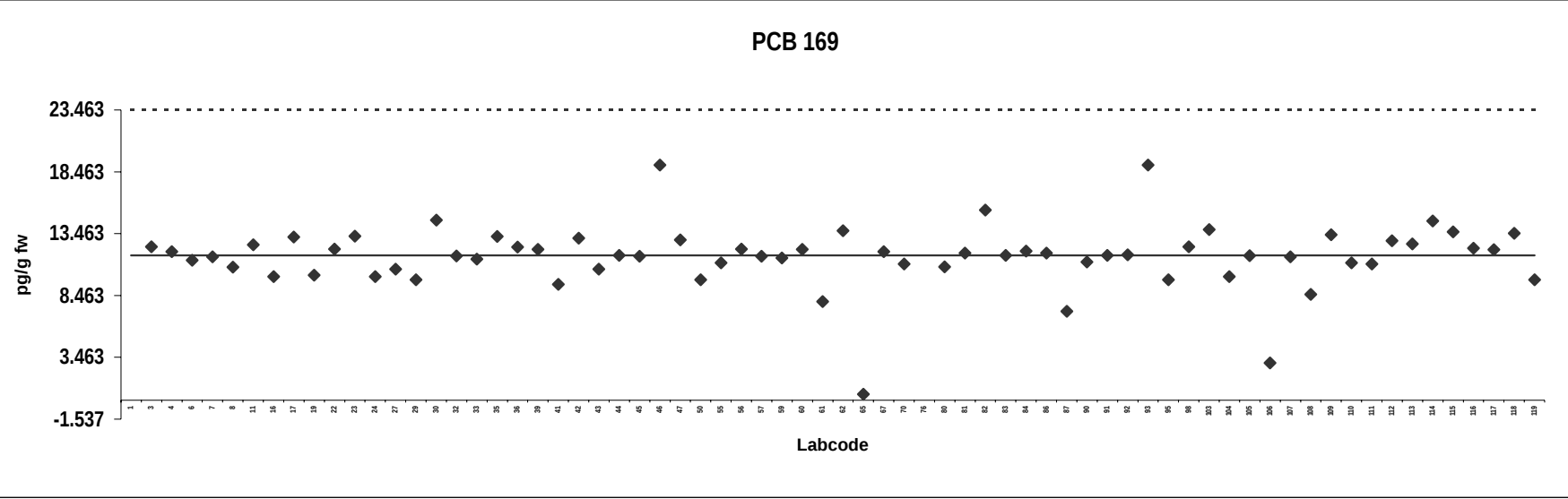
Consensus statistics	
Consensus median, pg/g	48
Median all values pg/g	48
Consensus mean, pg/g	47
Standard deviation, pg/g	10
Relative standard deviation, %	21
No. of values reported	70
No. of values removed	3
No. of reported non-detects	0



Salmon
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	40	Outlier	86	12	ND
3	12		87	7.2	
4	12		90	11	
6	11		91	12	
7	12		92	12	
8	11		93	19	
11	13		95	9.7	
16	10		98	12	
17	13		103	14	
19	10		104	10	
22	12		105	12	
23	13		106	3.0	
24	10		107	12	
27	11		108	8.6	
29	9.7		109	13	
30	15		110	11	
32	12		111	11	
33	11		112	13	
35	13		113	13	
36	12		114	14	
39	12		115	14	
41	9.4		116	12	
42	13		117	12	
43	11		118	14	
44	12		119	9.7	
45	12				
46	19				
47	13				
50	9.7				
55	11				
56	12				
57	12				
59	11				
60	12				
61	8.0				
62	14				
65	0.48				
67	12				
70	11				
76	37	Outlier			
80	11				
81	12				
82	15				
83	12				
84	12				

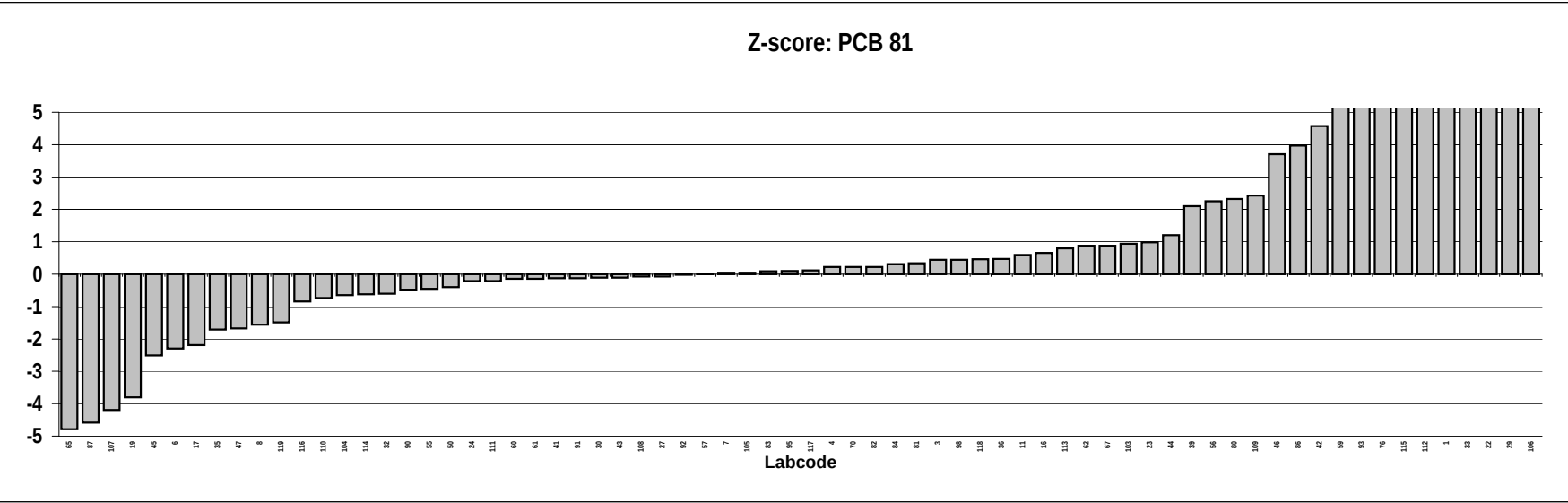
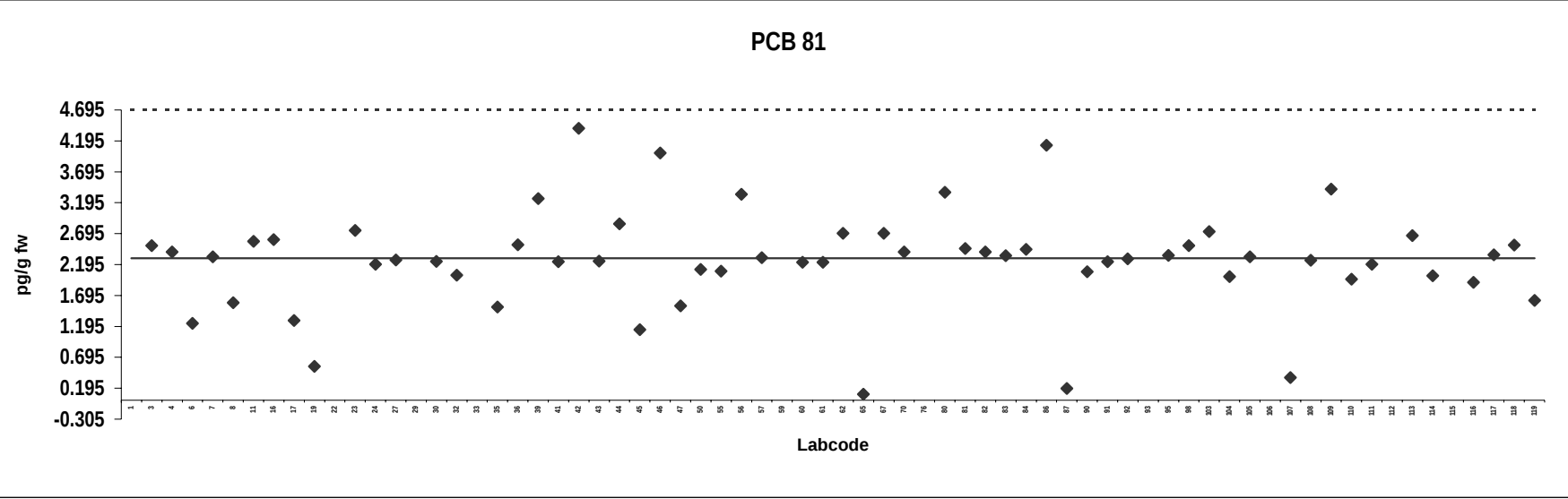
Consensus statistics	
Consensus median, pg/g	12
Median all values pg/g	12
Consensus mean, pg/g	12
Standard deviation, pg/g	2.6
Relative standard deviation, %	22
No. of values reported	70
No. of values removed	2
No. of reported non-detects	1



Salmon
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	6.0	Outlier,ND	86	4.1	Outlier,ND
3	2.5		87	0.19	
4	2.4		90	2.1	
6	1.2		91	2.2	
7	2.3		92	2.3	
8	1.6		93	4.7	
11	2.6		95	2.3	
16	2.6		98	2.5	
17	1.3		103	2.7	
19	0.55		104	2.0	
22	18	Outlier	105	2.3	Outlier
23	2.7		106	7144	
24	2.2		107	0.37	
27	2.3	Outlier	108	2.3	Outlier
29	28		109	3.4	
30	2.2		110	2.0	
32	2.0	Outlier	111	2.2	Outlier
33	6.6		112	5.6	
35	1.5		113	2.7	
36	2.5		114	2.0	Outlier
39	3.3		115	5.3	
41	2.2		116	1.9	
42	4.4		117	2.4	
43	2.3		118	2.5	
44	2.9		119	1.6	
45	1.1				
46	4.0				
47	1.5				
50	2.1				
55	2.1	Outlier,ND			
56	3.3				
57	2.3				
59	4.7				
60	2.2				
61	2.2				
62	2.7				
65	0.098				
67	2.7				
70	2.4				
76	5.1	Outlier			
80	3.4				
81	2.5				
82	2.4				
83	2.3				
84	2.4				

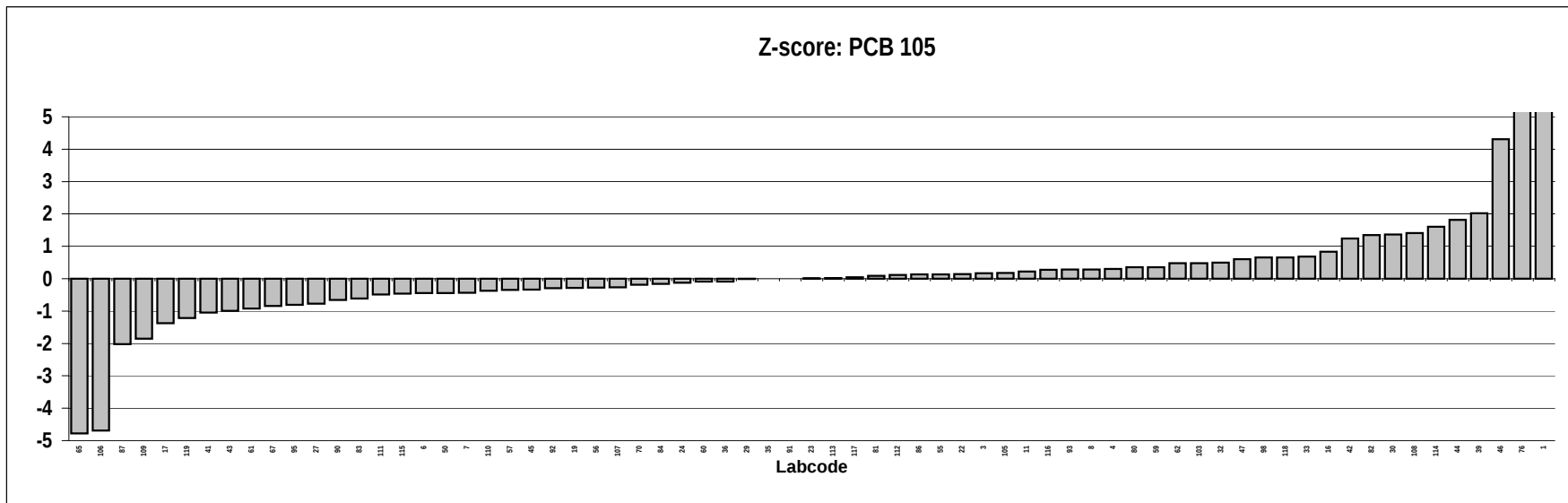
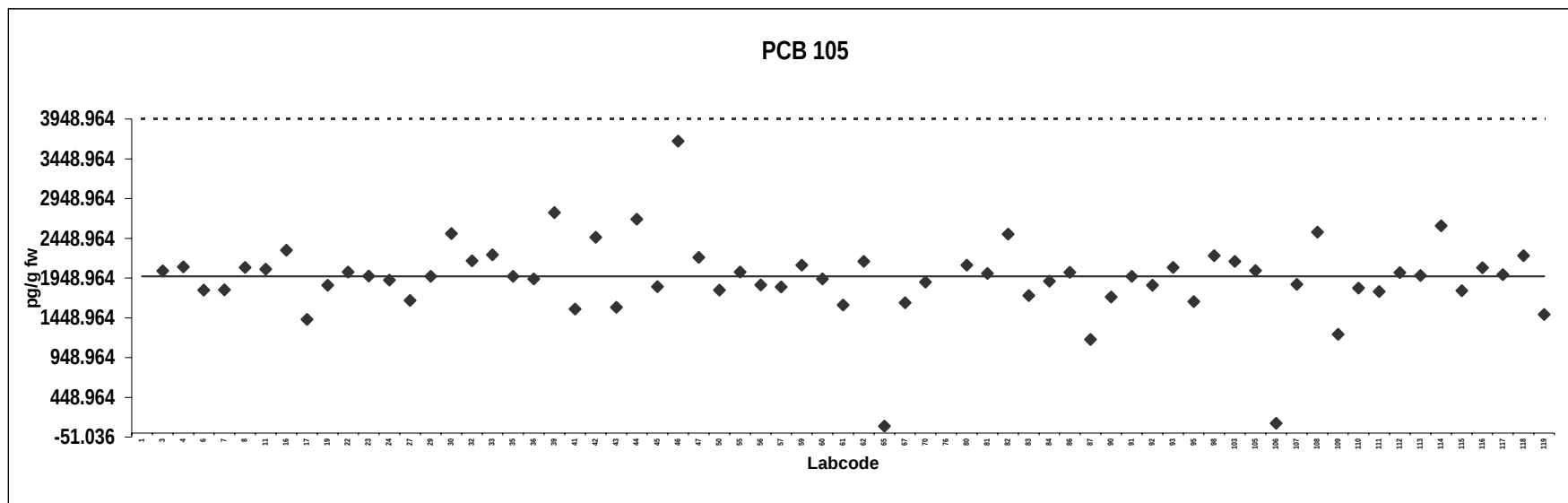
Consensus statistics	
Consensus median, pg/g	2.3
Median all values pg/g	2.3
Consensus mean, pg/g	2.3
Standard deviation, pg/g	0.81
Relative standard deviation, %	36
No. of values reported	70
No. of values removed	10
No. of reported non-detects	3



Salmon
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	9263	Outlier	86	2023	
3	2038		87	1176	
4	2090		90	1712	
6	1796		91	1972	
7	1800		92	1858	
8	2083		93	2082	
11	2060		95	1653	
16	2300		98	2230	
17	1430		103	2160	
19	1860		105	2042	
22	2027		106	123	
23	1974		107	1868	
24	1923		108	2528	
27	1667		109	1241	
29	1970		110	1824	
30	2510		111	1780	
32	2167		112	2019	
33	2242		113	1980	
35	1971		114	2605	
36	1939		115	1790	
39	2770		116	2080	
41	1560		117	1991	
42	2460		118	2230	
43	1580		119	1492	
44	2688				
45	1839				
46	3670				
47	2209				
50	1797				
55	2023				
56	1863				
57	1836				
59	2112				
60	1938				
61	1609				
62	2160				
65	88				
67	1640				
70	1900				
76	5802	Outlier			
80	2111				
81	2006				
82	2502				
83	1730				
84	1909				

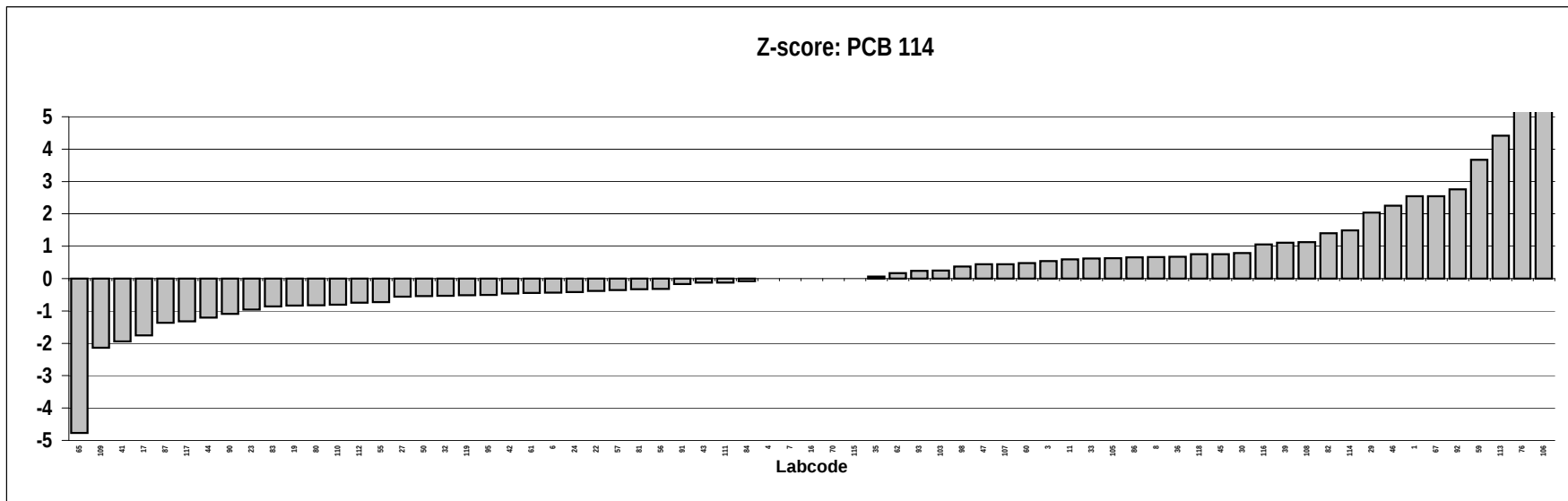
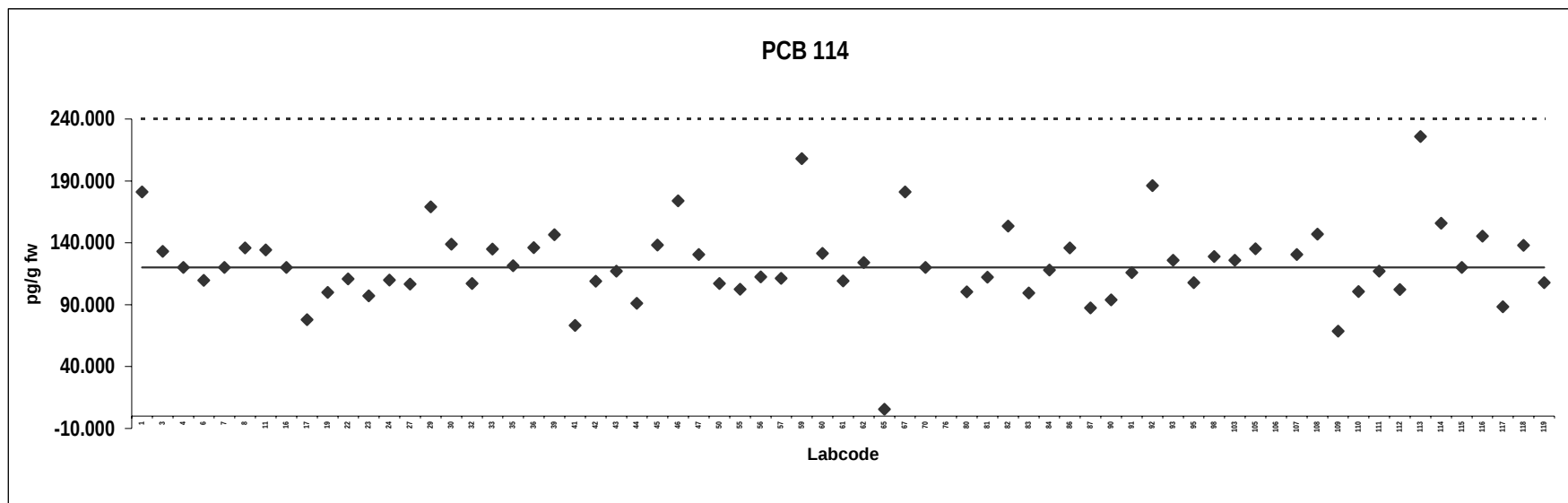
Consensus statistics	
Consensus median, pg/g	1972
Median all values pg/g	1974
Consensus mean, pg/g	1945
Standard deviation, pg/g	491
Relative standard deviation, %	25
No. of values reported	69
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	181		86	136	
3	133		87	87	
4	120		90	94	
6	110		91	116	
7	120		92	186	
8	136		93	126	
11	134		95	108	
16	120		98	129	
17	78		103	126	
19	100		105	135	
22	111		106	1990	Outlier
23	97		107	131	
24	110		108	147	
27	107		109	69	
29	169		110	101	
30	139		111	117	
32	107		112	102	
33	135		113	226	
35	122		114	156	
36	136		115	120	
39	147		116	145	
41	73		117	88	
42	109		118	138	
43	117		119	108	
44	91				
45	138				
46	174				
47	131				
50	107				
55	103				
56	112				
57	111				
59	208				
60	131				
61	109				
62	124				
65	5.6				
67	181				
70	120				
76	402	Outlier			
80	100				
81	112				
82	154				
83	99				
84	118				

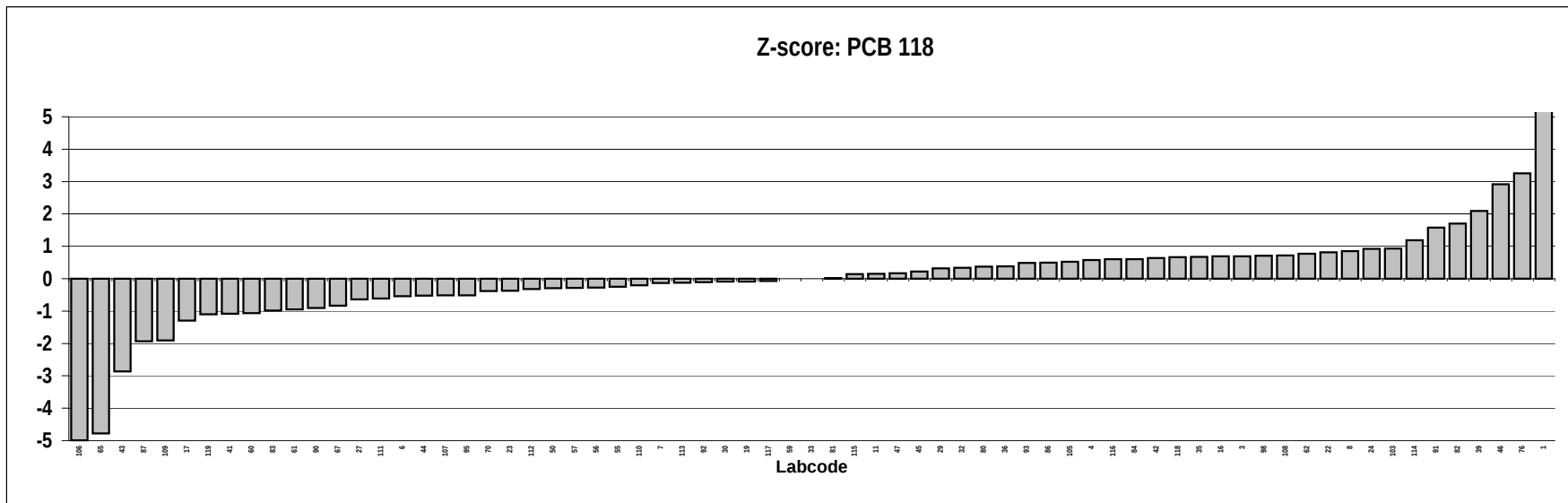
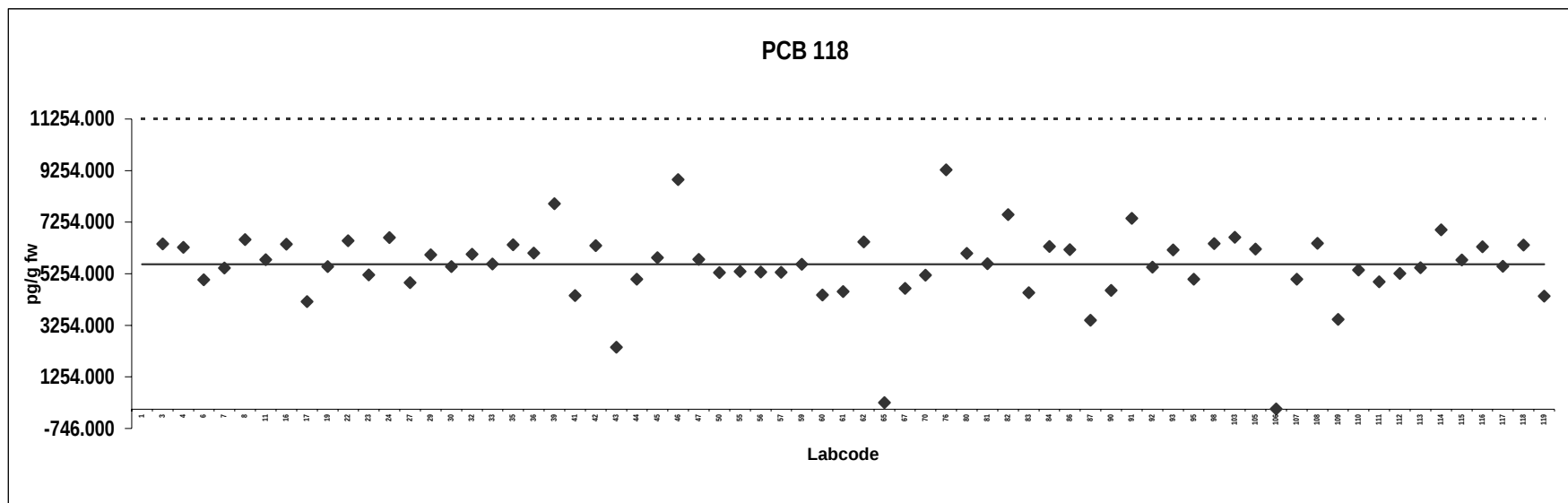
Consensus statistics	
Consensus median, pg/g	120
Median all values pg/g	120
Consensus mean, pg/g	123
Standard deviation, pg/g	33
Relative standard deviation, %	27
No. of values reported	69
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	20282	Outlier	86	6187	ND
3	6407		87	3448	
4	6275		90	4613	
6	5016		91	7402	
7	5480		92	5505	
8	6580		93	6177	
11	5800		95	5048	
16	6400		98	6420	
17	4170		103	6670	
19	5530		105	6212	
22	6539		106	8.0	
23	5206		107	5044	
24	6661		108	6434	
27	4911		109	3480	
29	5989		110	5398	
30	5530		111	4940	
32	6008		112	5262	
33	5627		113	5484	
35	6379		114	6958	
36	6059		115	5790	
39	7976		116	6300	
41	4410		117	5543	
42	6340		118	6370	
43	2400		119	4385	
44	5040				
45	5872				
46	8910				
47	5811				
50	5301				
55	5343				
56	5316				
57	5310				
59	5625				
60	4427				
61	4562				
62	6490				
65	252				
67	4690				
70	5200				
76	9288				
80	6043				
81	5641				
82	7544				
83	4520				
84	6306				

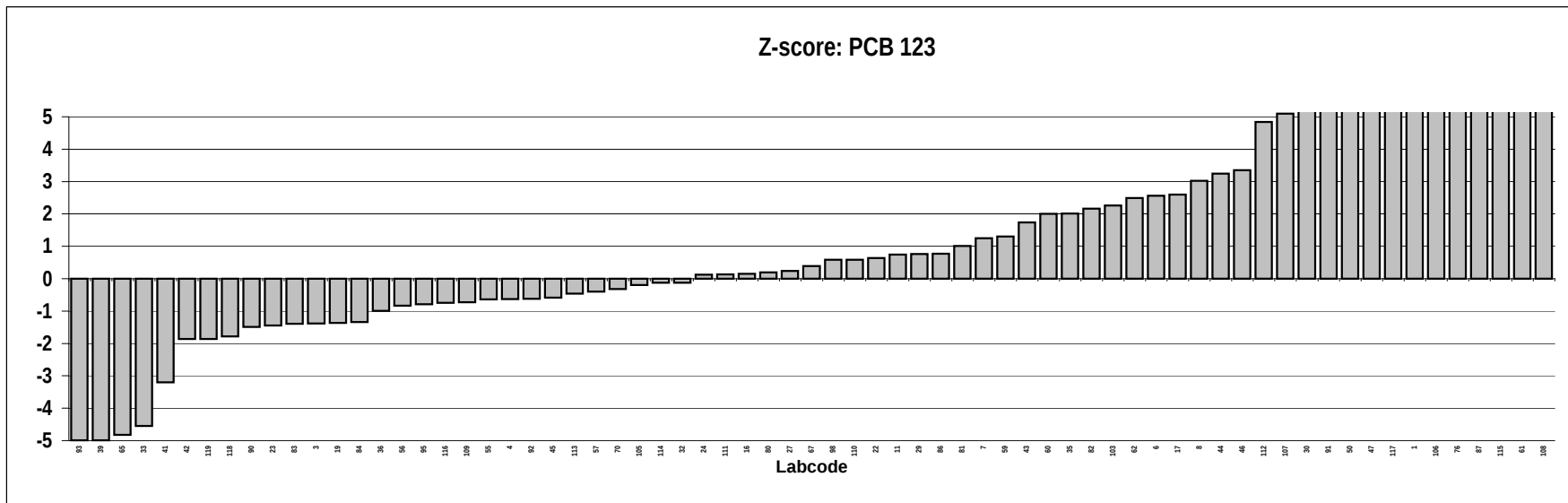
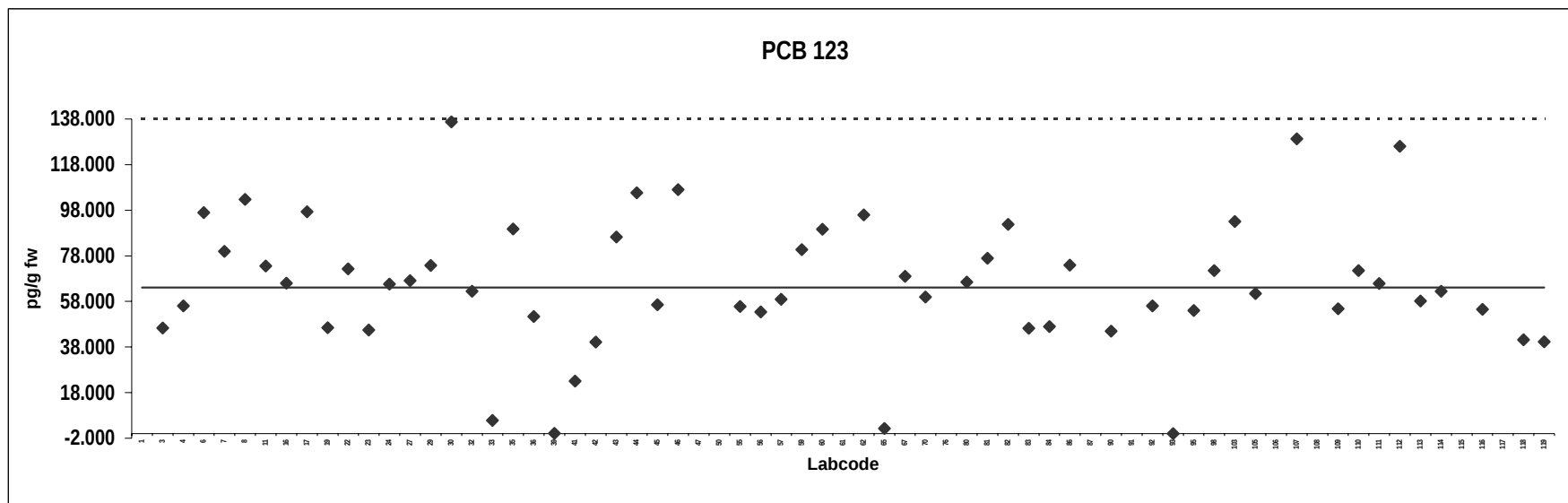
Consensus statistics	
Consensus median, pg/g	5626
Median all values pg/g	5627
Consensus mean, pg/g	5563
Standard deviation, pg/g	1468
Relative standard deviation, %	26
No. of values reported	69
No. of values removed	1
No. of reported non-detects	1



Salmon
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	228	Outlier	86	74	Outlier
3	46		87	584	
4	56		90	45	
6	97		91	139	Outlier
7	80		92	56	ND
8	103		93	0.066	
11	74		95	54	
16	66		98	72	Outlier
17	97		103	93	
19	47		105	62	
22	72	106	532	Outlier	
23	46	107	129	Outlier	
24	66	108	1029		
27	67	109	55		
29	74	110	72	ND	
30	137	111	66		
32	62	112	126		
33	5.8	113	58	Outlier	
35	90	114	62		
36	51	115	714		
39	0.16	ND	116	54	Outlier
41	23	ND	117	187	
42	40		118	41	
43	86		119	40	
44	106				
45	57				
46	107				
47	152	Outlier			
50	147	Outlier			
55	56				
56	53				
57	59				
59	81				
60	90				
61	735	Outlier			
62	96				
65	2.3				
67	69				
70	60				
76	558	Outlier			
80	66				
81	77				
82	92				
83	46				
84	47				

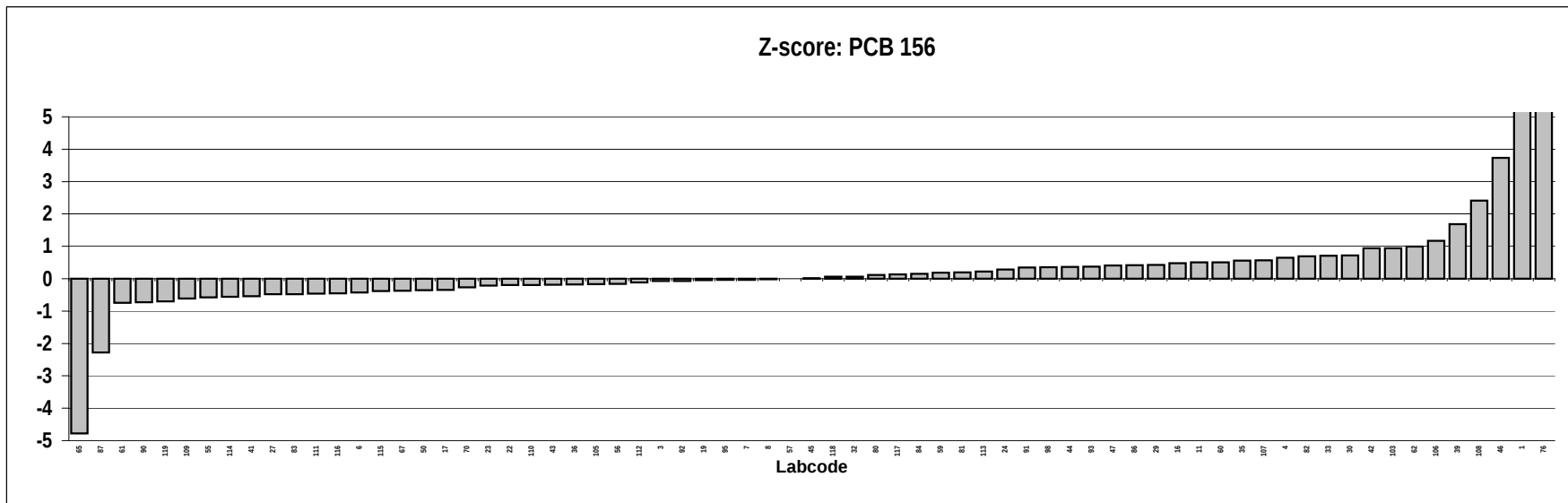
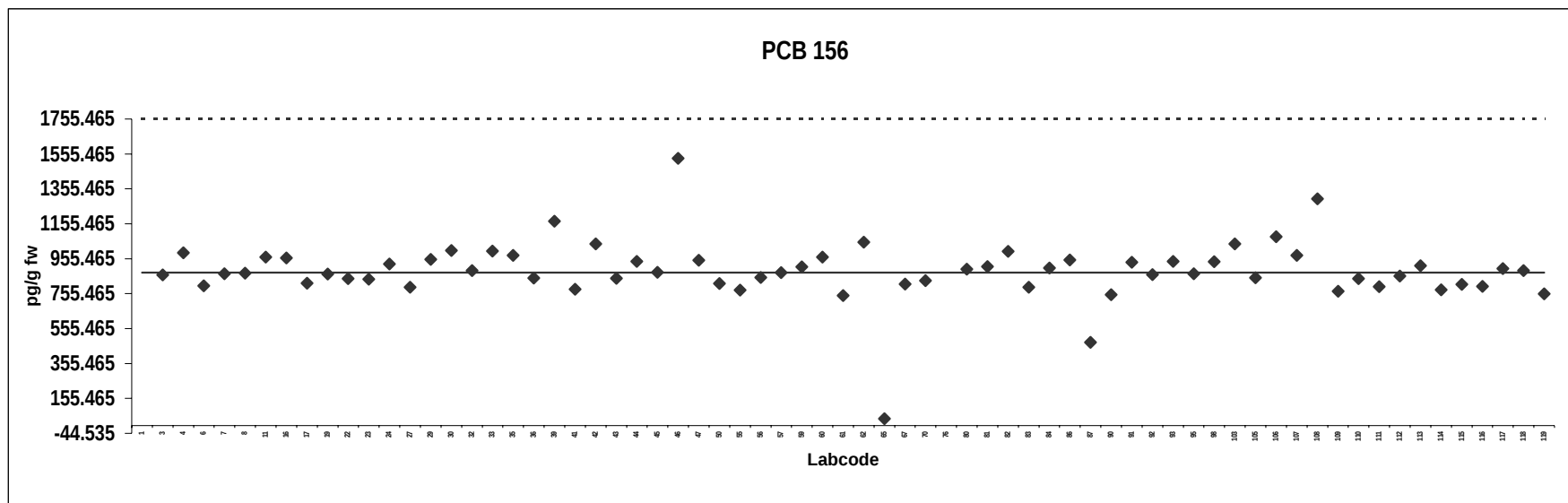
Consensus statistics	
Consensus median, pg/g	64
Median all values pg/g	69
Consensus mean, pg/g	66
Standard deviation, pg/g	29
Relative standard deviation, %	44
No. of values reported	69
No. of values removed	11
No. of reported non-detects	4



Salmon
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2618	Outlier	86	948	
3	863		87	477	
4	990		90	749	
6	801		91	936	
7	870		92	864	
8	872		93	940	
11	964		95	869	
16	960		98	938	
17	815		103	1040	
19	868		105	847	
22	842		106	1082	
23	838		107	975	
24	925		108	1299	
27	792		109	769	
29	951		110	842	
30	1002		111	795	
32	887		112	856	
33	1000		113	915	
35	974		114	778	
36	845		115	809	
39	1171		116	797	
41	781		117	899	
42	1040		118	887	
43	843		119	754	
44	940				
45	878				
46	1530				
47	947				
50	814				
55	775				
56	847				
57	876				
59	909				
60	964				
61	745				
62	1050				
65	39				
67	810				
70	830				
76	2897	Outlier			
80	895				
81	911				
82	997				
83	792				
84	903				

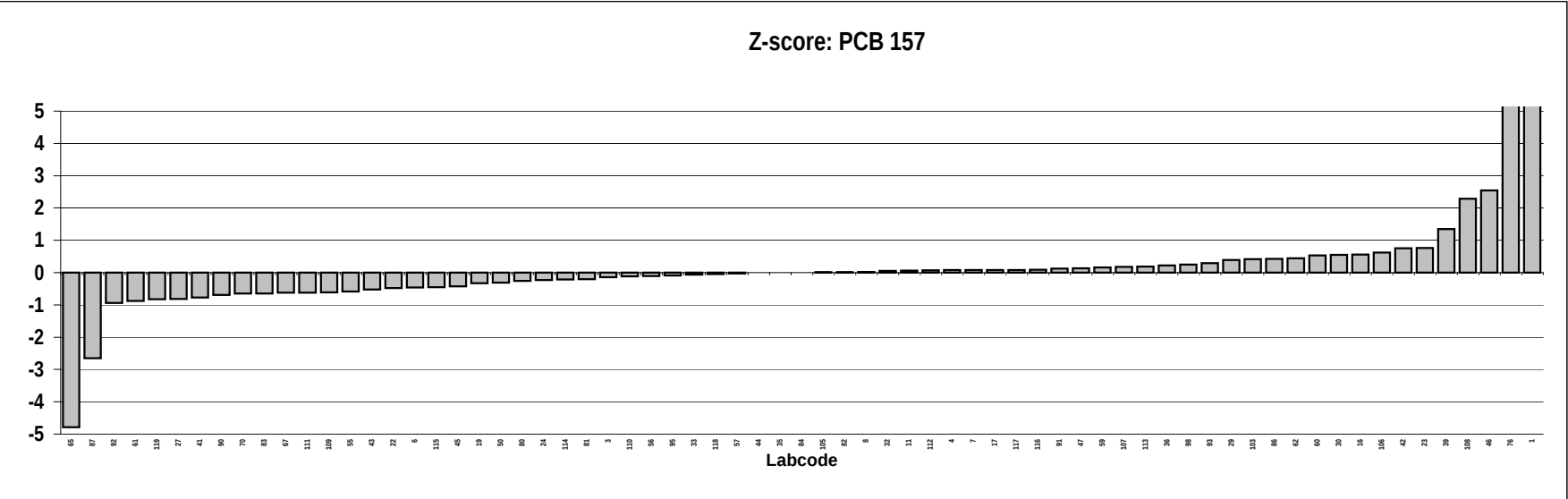
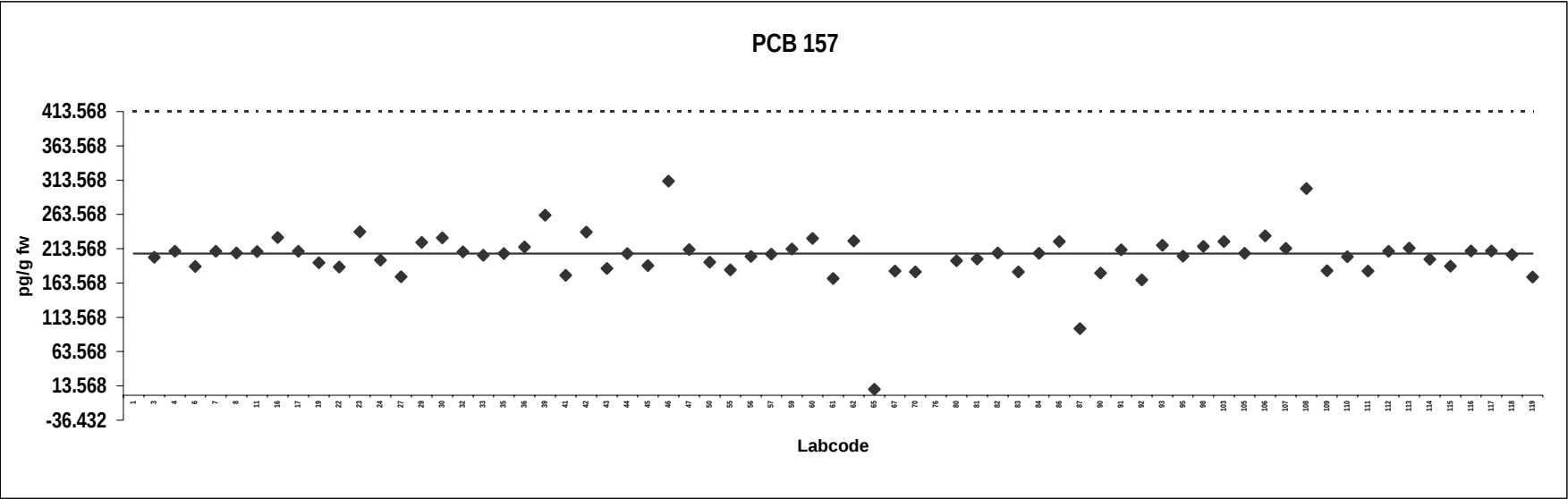
Consensus statistics	
Consensus median, pg/g	876
Median all values pg/g	878
Consensus mean, pg/g	887
Standard deviation, pg/g	172
Relative standard deviation, %	19
No. of values reported	69
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	741	Outlier	86	224	
3	201		87	97	
4	210		90	178	
6	188		91	212	
7	210		92	168	
8	207		93	219	
11	209		95	203	
16	230		98	217	
17	210		103	224	
19	193		105	207	
22	187		106	232	
23	238		107	214	
24	197		108	301	
27	173		109	181	
29	223		110	202	
30	230		111	181	
32	209		112	210	
33	204		113	214	
35	207		114	198	
36	216		115	188	
39	262		116	210	
41	175		117	210	
42	238		118	205	
43	185		119	172	
44	207				
45	189				
46	312				
47	212				
50	194				
55	183				
56	202				
57	206				
59	213				
60	229				
61	170				
62	225				
65	8.8				
67	181				
70	180				
76	601	Outlier			
80	196				
81	198				
82	207				
83	180				
84	207				

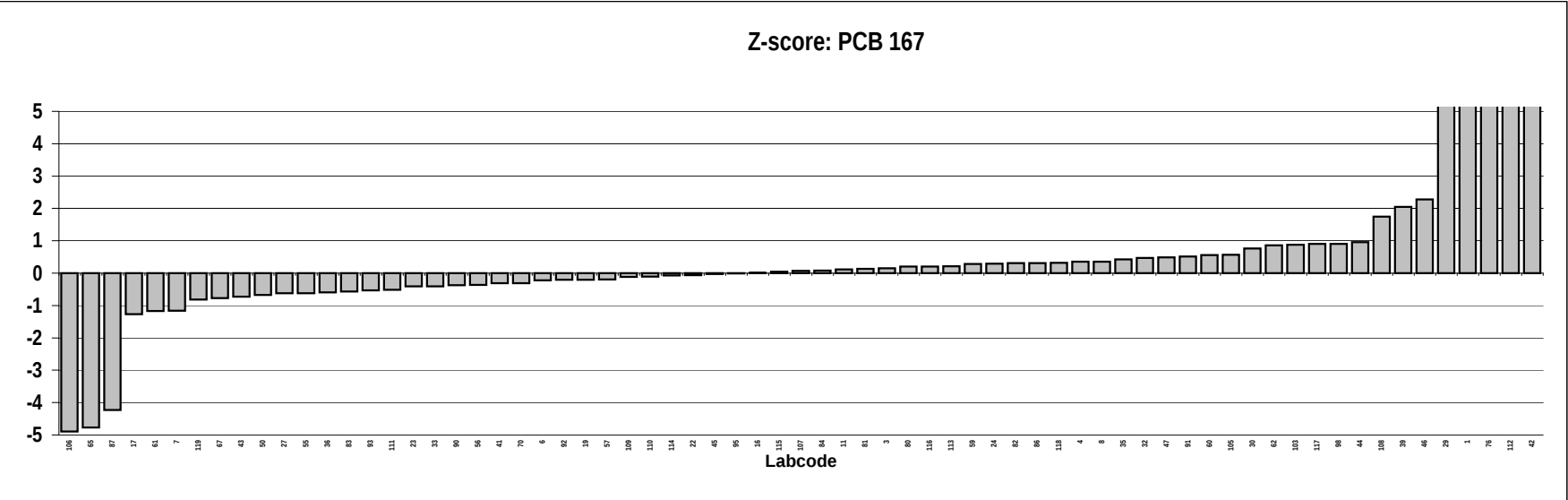
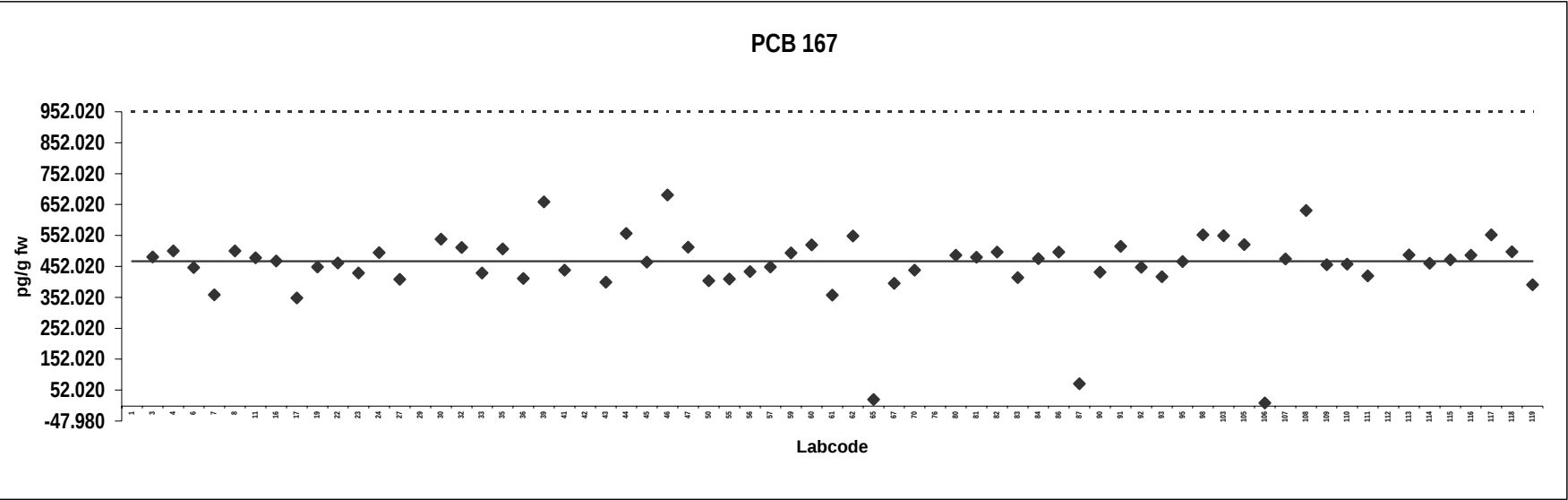
Consensus statistics	
Consensus median, pg/g	207
Median all values pg/g	207
Consensus mean, pg/g	203
Standard deviation, pg/g	37
Relative standard deviation, %	19
No. of values reported	69
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1518	Outlier	86	498	
3	483		87	73	
4	502		90	434	
6	448		91	517	
7	360		92	450	
8	503		93	419	
11	480		95	468	
16	470		98	554	
17	350		103	551	
19	450		105	522	
22	463		106	10	
23	431		107	476	
24	496		108	633	
27	411		109	458	
29	1109	Outlier	110	459	
30	540		111	421	
32	513		112	1819	Outlier
33	431		113	489	
35	509		114	462	
36	413		115	473	
39	661		116	488	
41	440		117	554	
42	2050	Outlier	118	499	
43	401		119	393	
44	559				
45	466				
46	683				
47	514				
50	406				
55	411				
56	435				
57	450				
59	495				
60	521				
61	359				
62	550				
65	22				
67	397				
70	440				
76	1566	Outlier			
80	488				
81	482				
82	498				
83	416				
84	477				

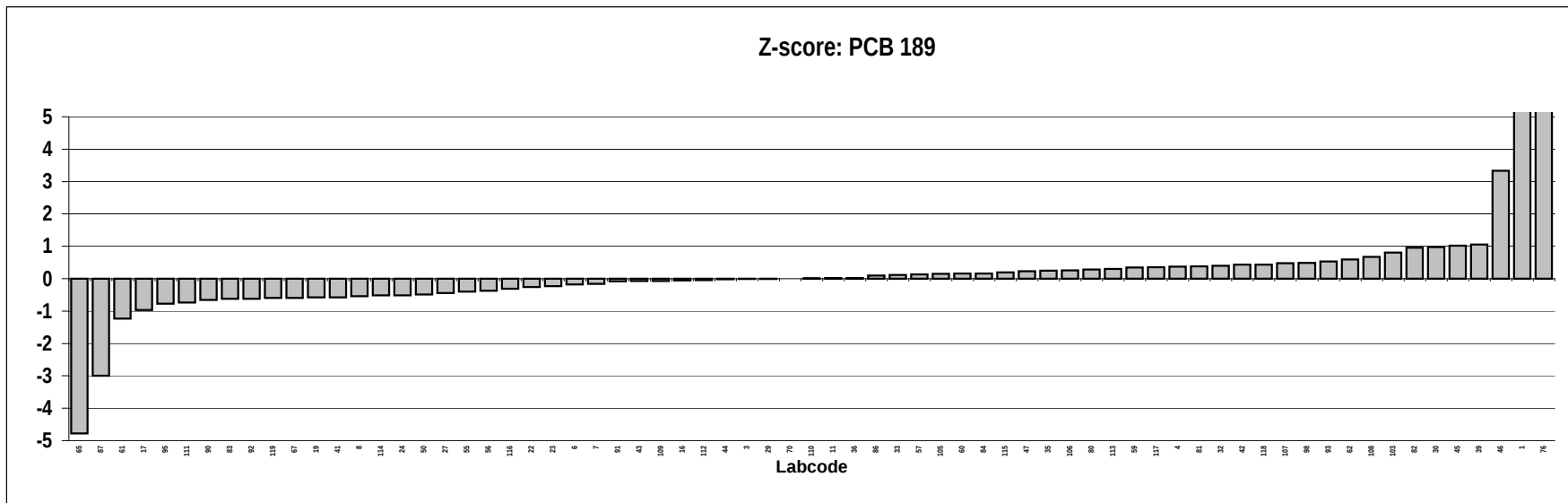
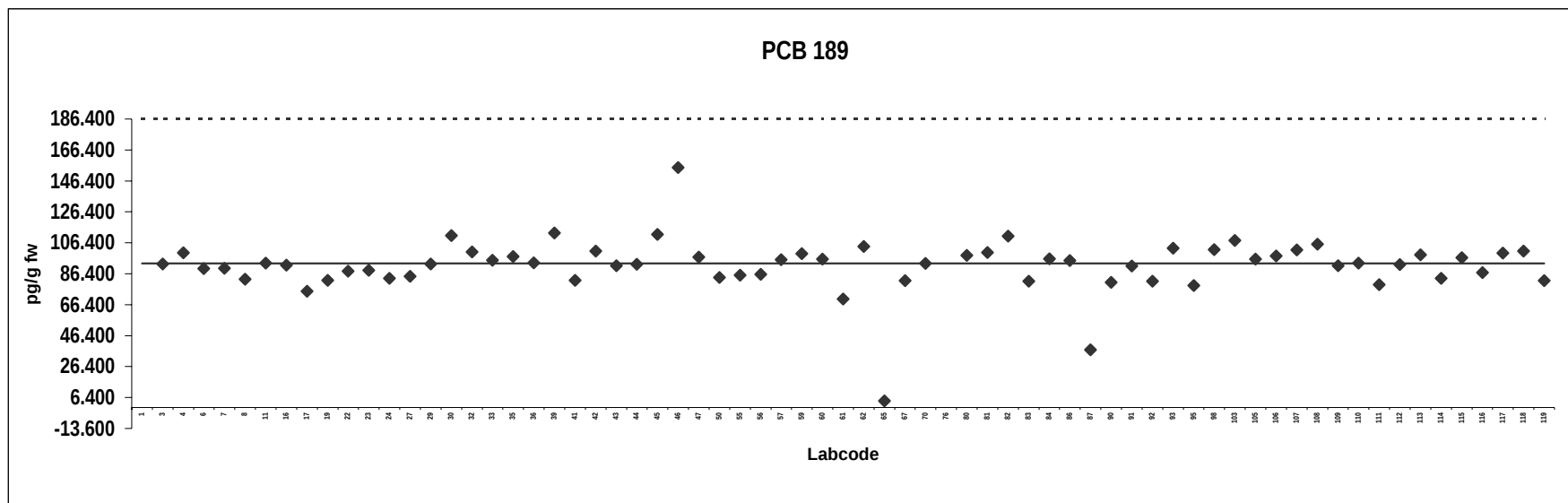
Consensus statistics	
Consensus median, pg/g	469
Median all values pg/g	476
Consensus mean, pg/g	455
Standard deviation, pg/g	113
Relative standard deviation, %	25
No. of values reported	69
No. of values removed	5
No. of reported non-detects	0



Salmon
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	262	Outlier	86	95	
3	93		87	37	
4	100		90	81	
6	90		91	92	
7	90		92	82	
8	83		93	103	
11	93		95	79	
16	92		98	102	
17	75		103	108	
19	82		105	96	
22	88		106	98	
23	89		107	102	
24	84		108	106	
27	85		109	92	
29	93		110	93	
30	111		111	79	
32	100		112	92	
33	95		113	99	
35	98		114	83	
36	93		115	97	
39	113		116	87	
41	82		117	100	
42	101		118	101	
43	92		119	82	
44	93				
45	112				
46	155				
47	97				
50	84				
55	86				
56	86				
57	96				
59	99				
60	96				
61	70				
62	104				
65	4.2				
67	82				
70	93				
76	287	Outlier			
80	98				
81	100				
82	111				
83	82				
84	96				

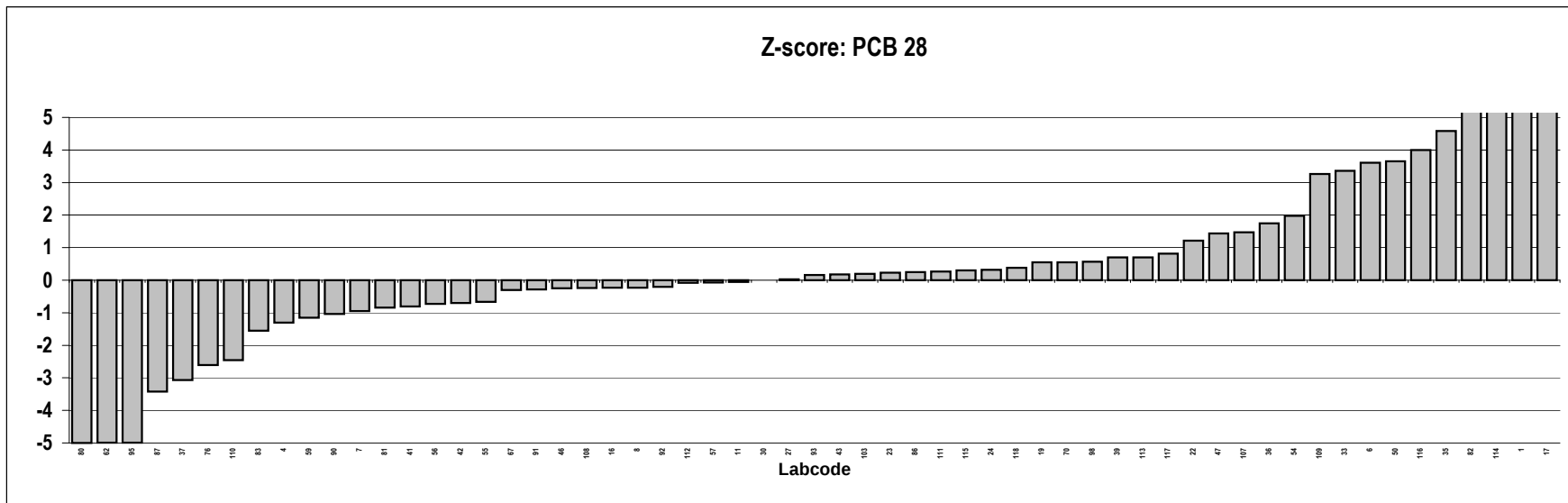
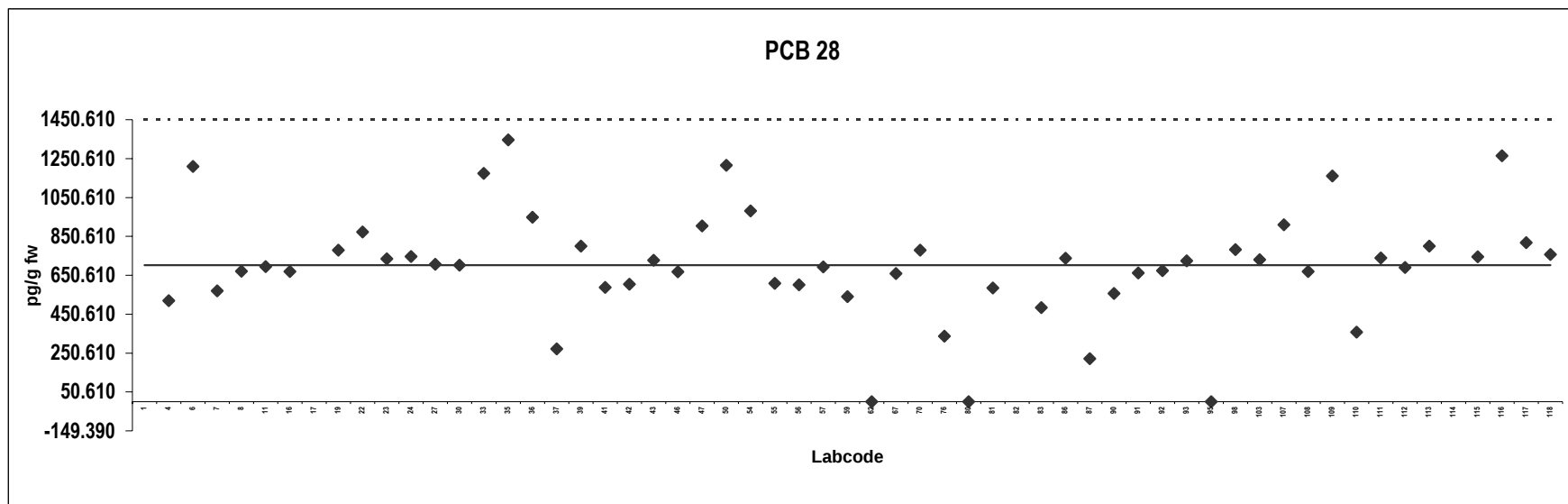
Consensus statistics	
Consensus median, pg/g	93
Median all values pg/g	93
Consensus mean, pg/g	92
Standard deviation, pg/g	17
Relative standard deviation, %	19
No. of values reported	69
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PCB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1826	Outlier	98	783	
4	520		103	731	
6	1210		107	910	
7	570		108	669	
8	671		109	1162	
11	695		110	358	
16	670		111	740	
17	8010	Outlier	112	691	
19	780		113	801	
22	873		114	1721	Outlier
23	736		115	746	
24	748		116	1266	
27	707		117	818	
30	703		118	757	
33	1175				
35	1347				
36	949				
37	272				
39	801				
41	589				
42	605				
43	728				
46	668				
47	905				
50	1216				
54	981				
55	609				
56	601				
57	693				
59	542				
62	0.71				
67	660				
70	780				
76	337				
80	0.52				
81	585				
82	1518	Outlier			
83	485				
86	738				
87	221				
90	557				
91	663				
92	675				
93	725				
95	0.77				

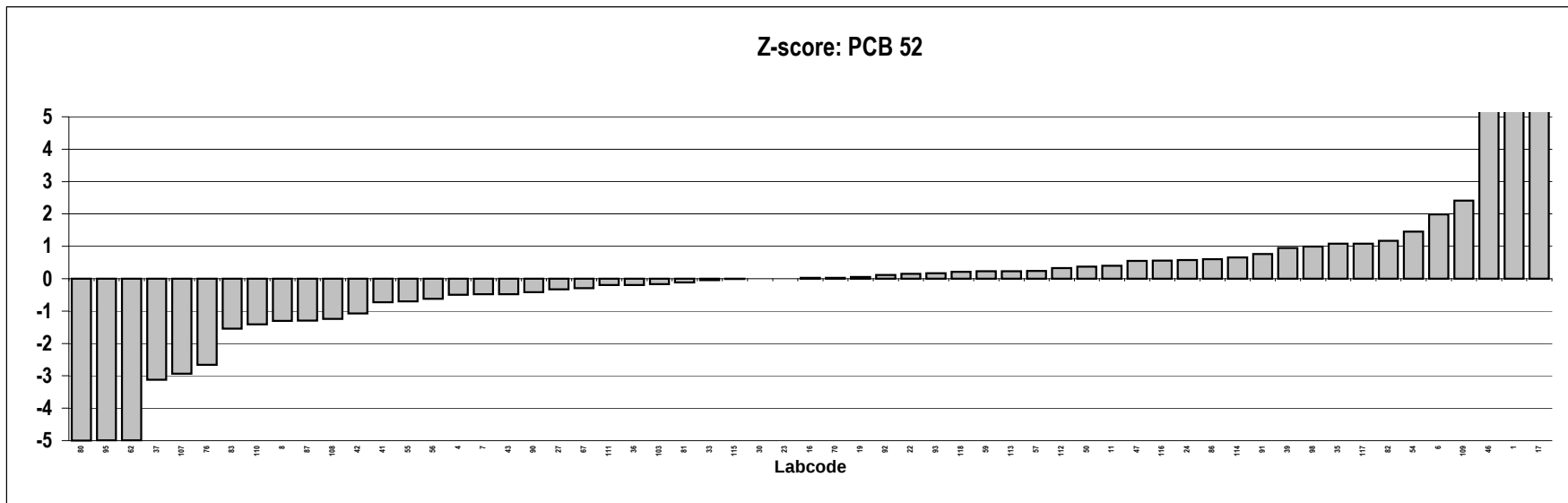
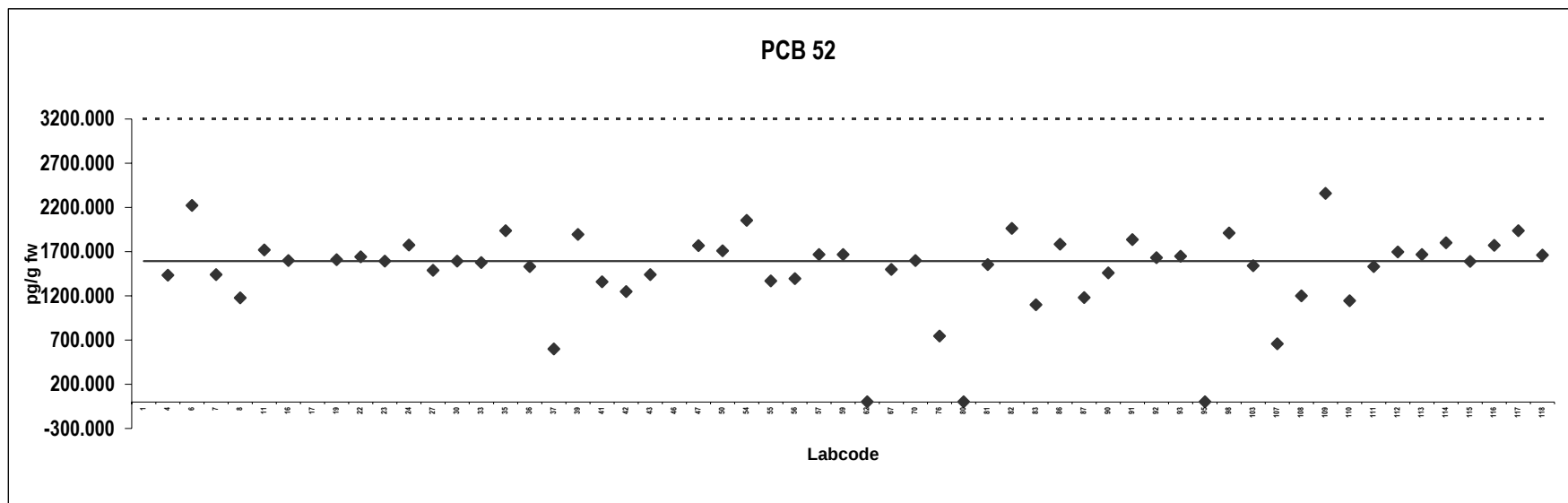
Consensus statistics	
Consensus median, pg/g	703
Median all values pg/g	725
Consensus mean, pg/g	699
Standard deviation, pg/g	284
Relative standard deviation, %	41
No. of values reported	59
No. of values removed	4
No. of reported non-detects	0



Salmon
Congener: PCB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4398	Outlier	98	1910	
4	1435		103	1540	
6	2224		107	659	
7	1440		108	1198	
8	1177		109	2361	
11	1719		110	1145	
16	1600		111	1530	
17	12300		112	1696	
19	1610		113	1667	
22	1640		114	1801	
23	1593	Outlier	115	1590	
24	1776		116	1771	
27	1488		117	1938	
30	1592		118	1660	
33	1578				
35	1936				
36	1531				
37	600				
39	1894				
41	1360				
42	1250	Outlier			
43	1440				
46	3550				
47	1767				
50	1711				
54	2055				
55	1370				
56	1396				
57	1668				
59	1666				
62	1.5				
67	1500				
70	1600				
76	747				
80	1.4				
81	1555				
82	1964				
83	1100				
86	1784				
87	1182				
90	1459				
91	1835				
92	1630				
93	1648				
95	1.4				

Consensus statistics	
Consensus median, pg/g	1593
Median all values pg/g	1600
Consensus mean, pg/g	1482
Standard deviation, pg/g	484
Relative standard deviation, %	33
No. of values reported	59
No. of values removed	3
No. of reported non-detects	0

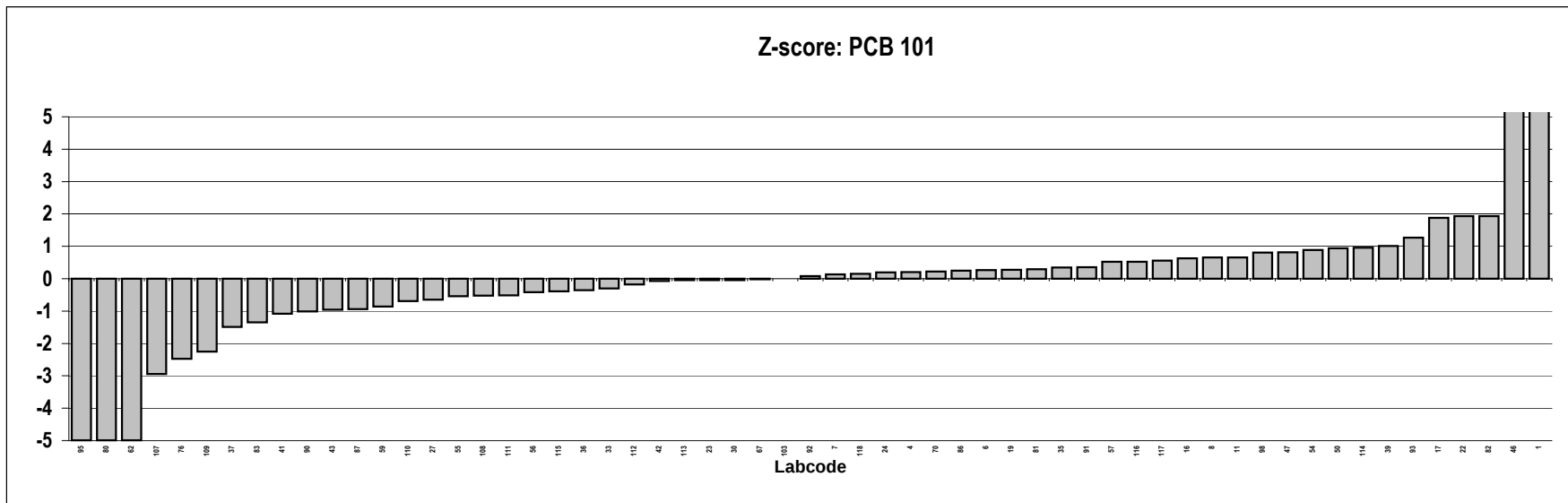
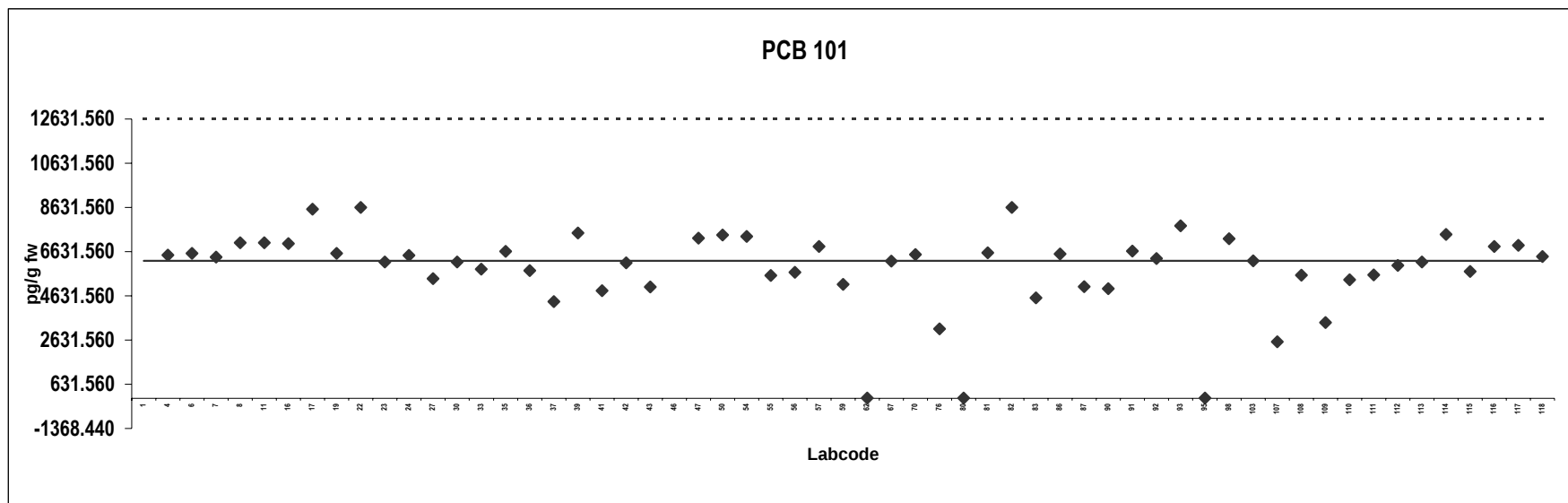


Salmon

Congener: PCB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	17484	Outlier	98	7220	
4	6475		103	6220	
6	6550		107	2557	
7	6390		108	5572	
8	7033		109	3418	
11	7034		110	5363	
16	7000		111	5580	
17	8560		112	6003	
19	6560		113	6164	
22	8626		114	7408	
23	6166		115	5730	
24	6463		116	6867	
27	5410		117	6914	
30	6168		118	6410	
33	5842				
35	6645				
36	5774				
37	4368				
39	7472				
41	4870				
42	6130				
43	5030				
46	17000	Outlier			
47	7237				
50	7389				
54	7325				
55	5550				
56	5697				
57	6867				
59	5147				
62	6.3				
67	6200				
70	6500				
76	3141				
80	5.8				
81	6580				
82	8628				
83	4540				
86	6532				
87	5048				
90	4961				
91	6656				
92	6316				
93	7794				
95	5.7				

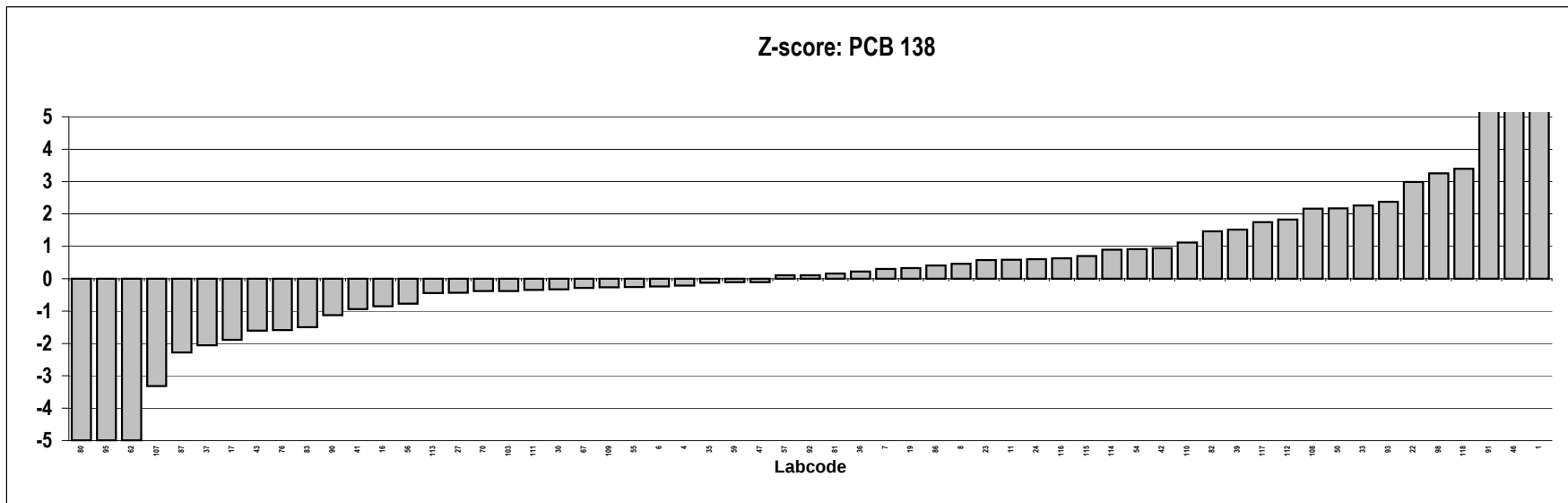
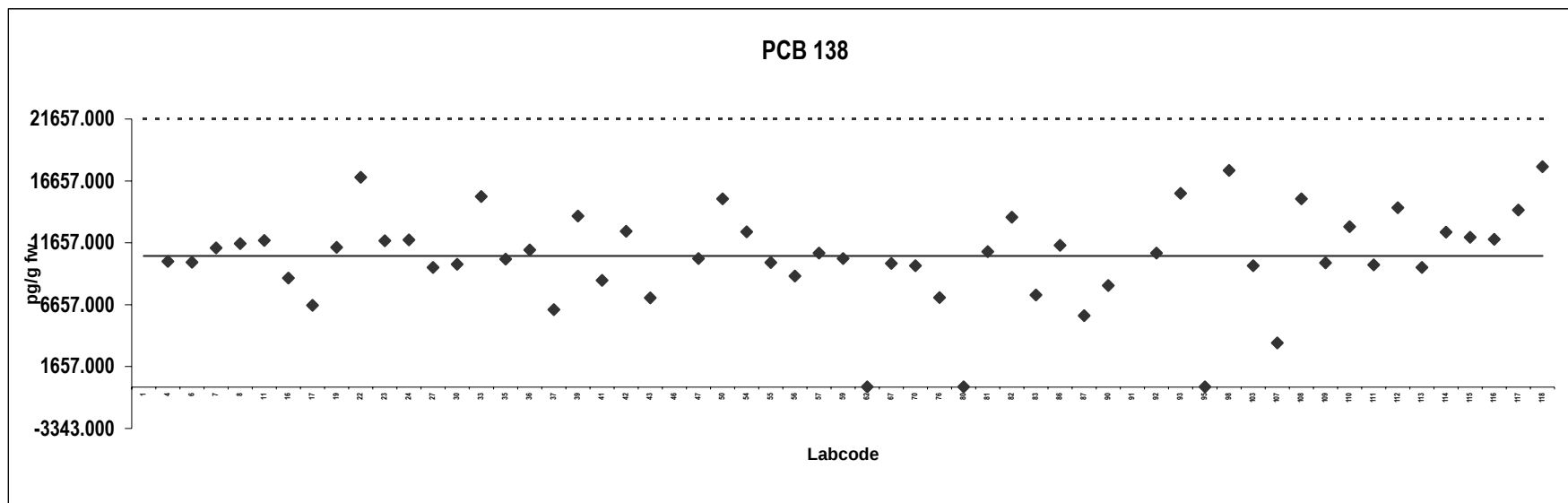
Consensus statistics	
Consensus median, pg/g	6220
Median all values pg/g	6316
Consensus mean, pg/g	5862
Standard deviation, pg/g	1832
Relative standard deviation, %	31
No. of values reported	59
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PCB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	30923	Outlier	98	17500	
4	10150		103	9800	
6	10092		107	3575	
7	11250		108	15202	
8	11591		109	10042	
11	11852		110	12970	
16	8800		111	9870	
17	6610		112	14485	
19	11300		113	9663	
22	16953		114	12510	
23	11824		115	12100	
24	11887		116	11951	
27	9676		117	14302	
30	9918		118	17800	
33	15400				
35	10350				
36	11070				
37	6251				
39	13826				
41	8620				
42	12600				
43	7210				
46	22300	Outlier			
47	10385				
50	15213				
54	12540				
55	10070				
56	8976				
57	10827				
59	10375				
62	9.9				
67	10000				
70	9800				
76	7243				
80	9.6				
81	10939				
82	13716				
83	7430				
86	11463				
87	5777				
90	8217				
91	22048	Outlier			
92	10829				
93	15643				
95	9.8				

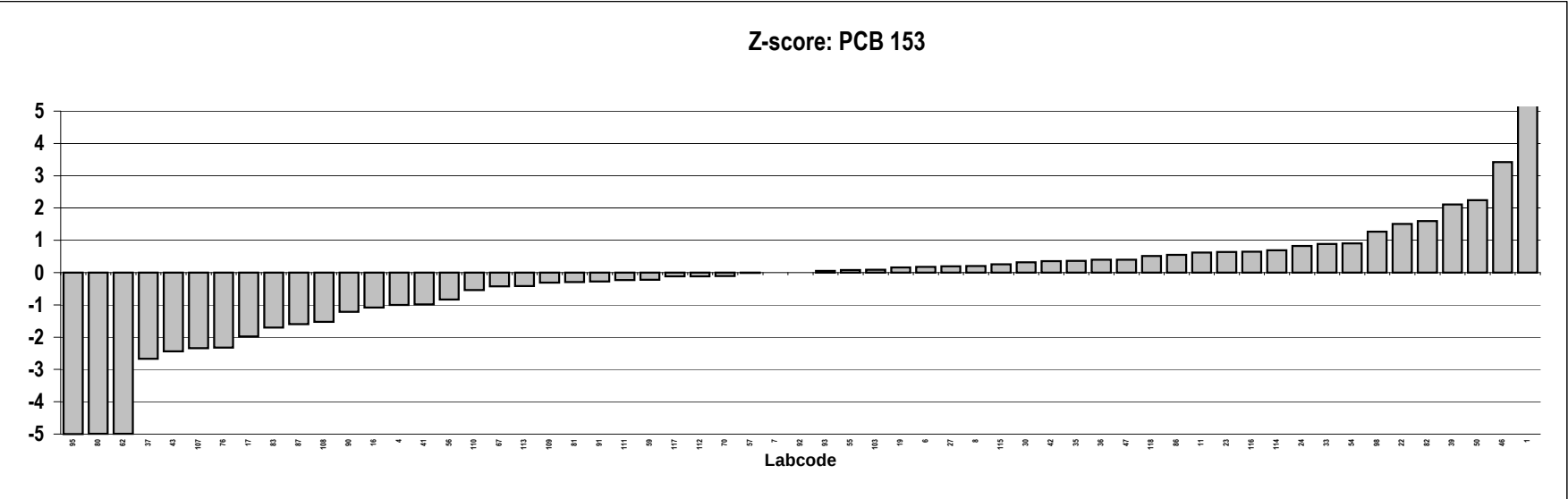
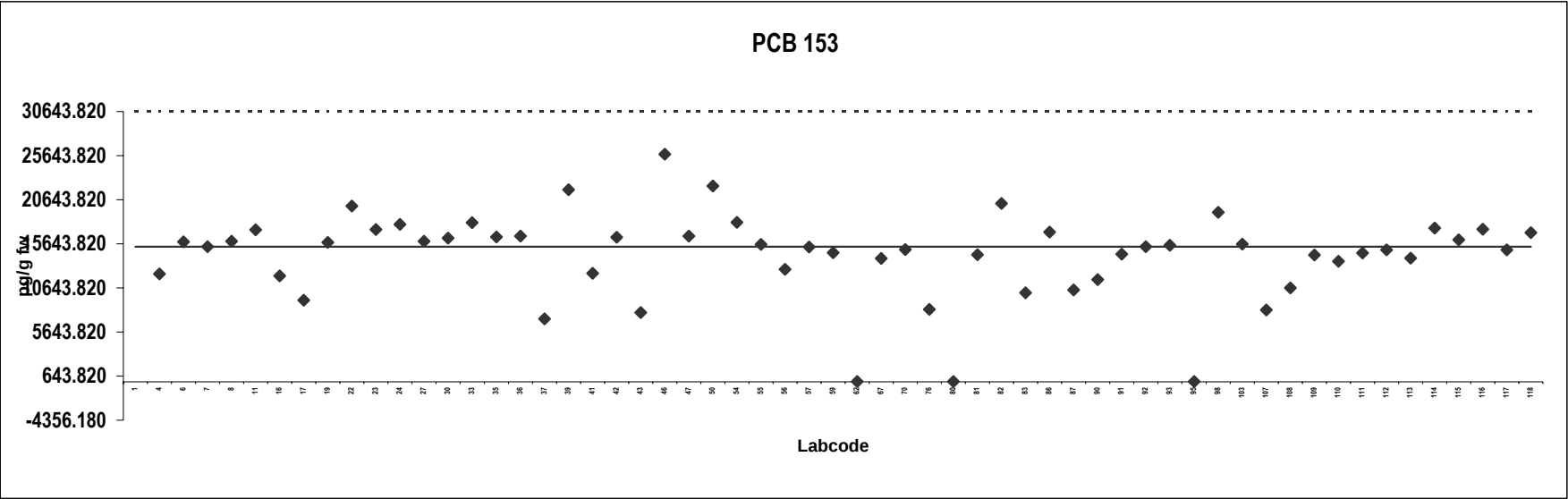
Consensus statistics	
Consensus median, pg/g	10606
Median all values pg/g	10829
Consensus mean, pg/g	10508
Standard deviation, pg/g	3828
Relative standard deviation, %	36
No. of values reported	59
No. of values removed	3
No. of reported non-detects	0



Salmon
Congener: PCB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	38421	Outlier	98	19200	
4	12250		103	15600	
6	15860		107	8141	
7	15310		108	10651	
8	15930		109	14375	
11	17228		110	13660	
16	12000		111	14600	
17	9250		112	14960	
19	15800		113	14030	
22	19926		114	17441	
23	17277		115	16100	
24	17853		116	17289	
27	15926		117	14951	
30	16284		118	16900	
33	18044				
35	16427				
36	16525				
37	7139				
39	21790				
41	12300				
42	16400				
43	7860				
46	25800				
47	16527				
50	22195				
54	18092				
55	15570				
56	12759				
57	15288				
59	14644				
62	16				
67	14000				
70	15000				
76	8205				
80	14				
81	14407				
82	20213				
83	10100				
86	16988				
87	10421				
90	11601				
91	14474				
92	15322				
93	15486				
95	13				

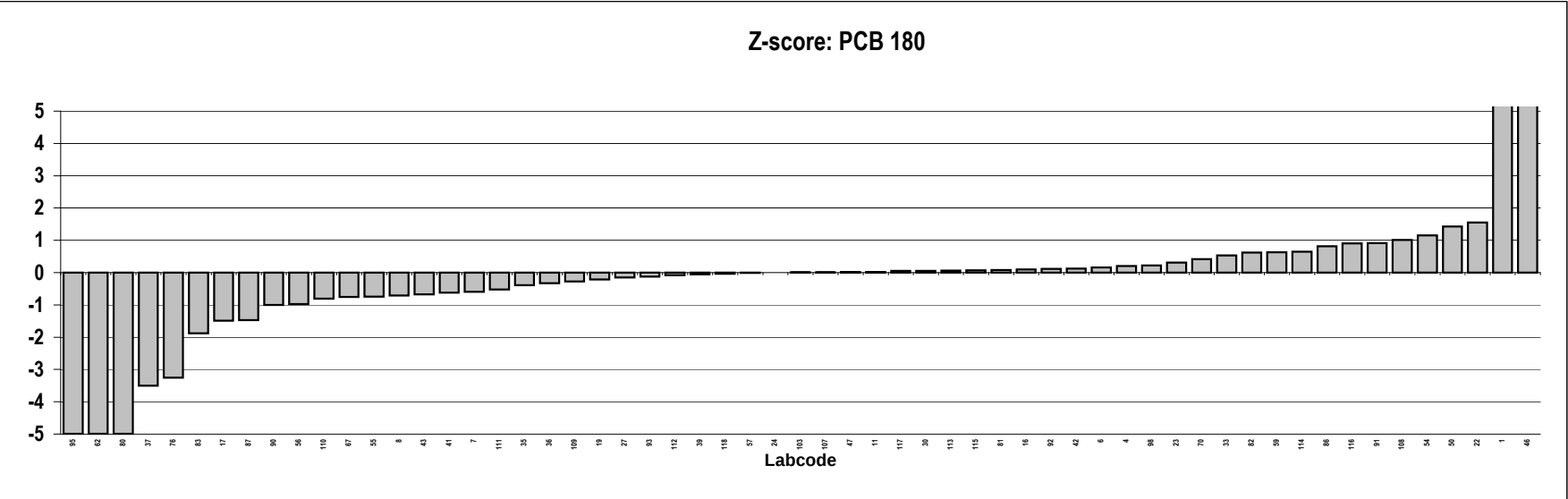
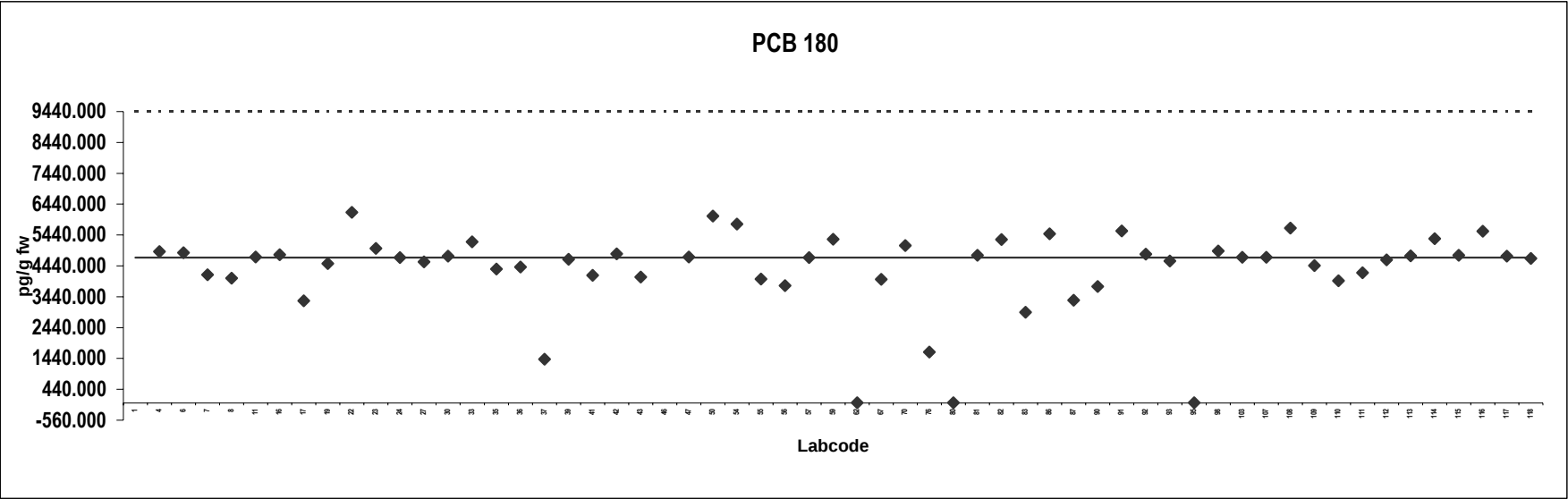
Consensus statistics	
Consensus median, pg/g	15316
Median all values pg/g	15322
Consensus mean, pg/g	14352
Standard deviation, pg/g	4872
Relative standard deviation, %	34
No. of values reported	59
No. of values removed	1
No. of reported non-detects	0



Salmon
Congener: PCB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	13192	Outlier	98	4920	
4	4900		103	4720	
6	4865		107	4721	
7	4150		108	5666	
8	4042		109	4449	
11	4731		110	3953	
16	4800		111	4220	
17	3310		112	4635	
19	4510		113	4767	
22	6171		114	5319	
23	5005		115	4780	
24	4711		116	5561	
27	4569		117	4758	
30	4759		118	4680	
33	5215				
35	4342				
36	4399				
37	1414				
39	4657				
41	4130				
42	4830				
43	4080	Outlier			
46	14700				
47	4728				
50	6053				
54	5796				
55	4010				
56	3796				
57	4705				
59	5303				
62	4.8				
67	4000				
70	5100				
76	1647				
80	5.0				
81	4785				
82	5297				
83	2940				
86	5475				
87	3325				
90	3769				
91	5569				
92	4817				
93	4595				
95	4.4				

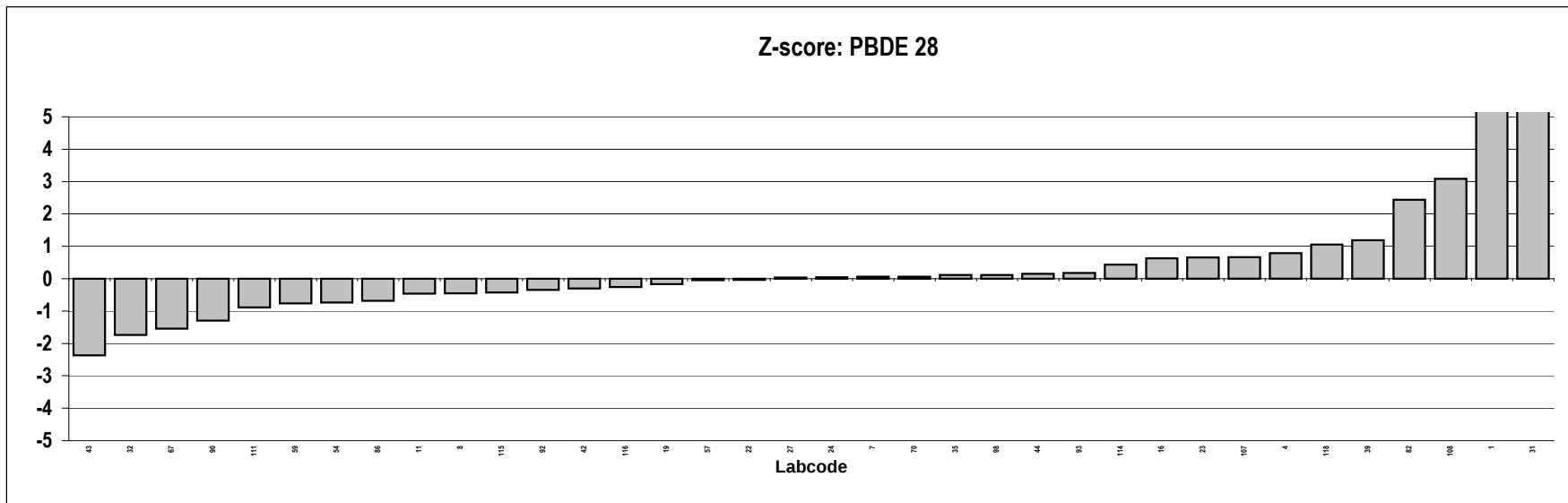
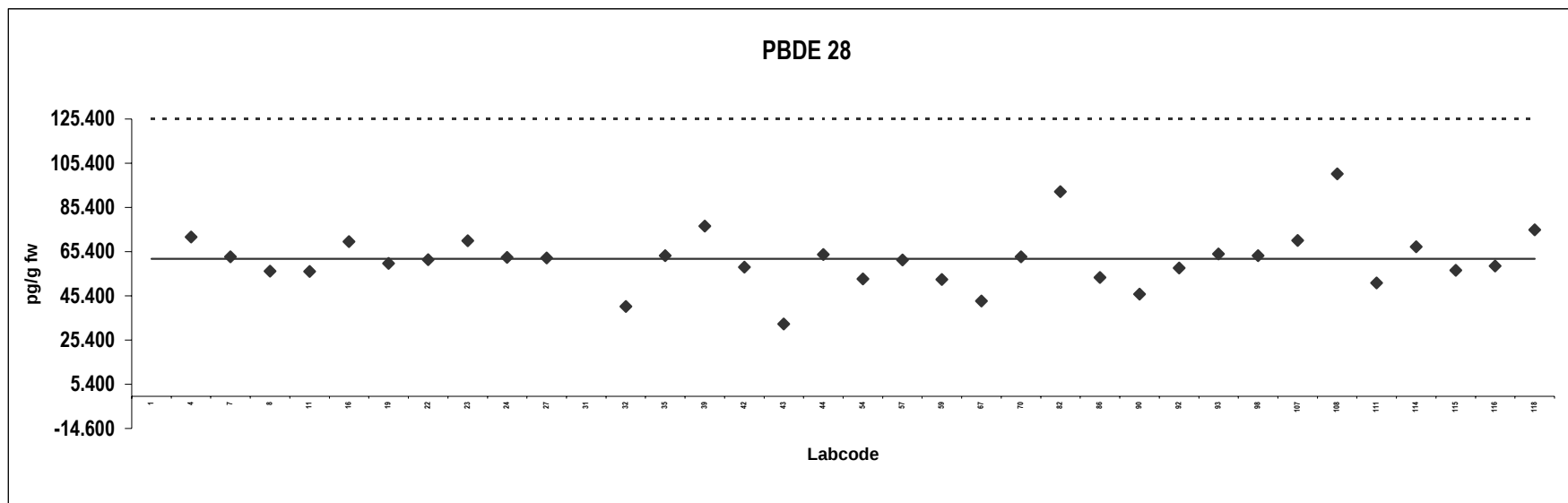
Consensus statistics	
Consensus median, pg/g	4711
Median all values pg/g	4720
Consensus mean, pg/g	4324
Standard deviation, pg/g	1339
Relative standard deviation, %	31
No. of values reported	59
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PBDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	296	Outlier			
4	72				
7	63				
8	57				
11	57				
16	70				
19	60				
22	62				
23	70				
24	63				
27	63				
31	52736	Outlier			
32	41				
35	64				
39	77				
42	58				
43	33				
44	64				
54	53				
57	62				
59	53				
67	43				
70	63				
82	93				
86	54				
90	46				
92	58				
93	64				
98	64				
107	70				
108	101				
111	51				
114	68				
115	57				
116	59				
118	75				

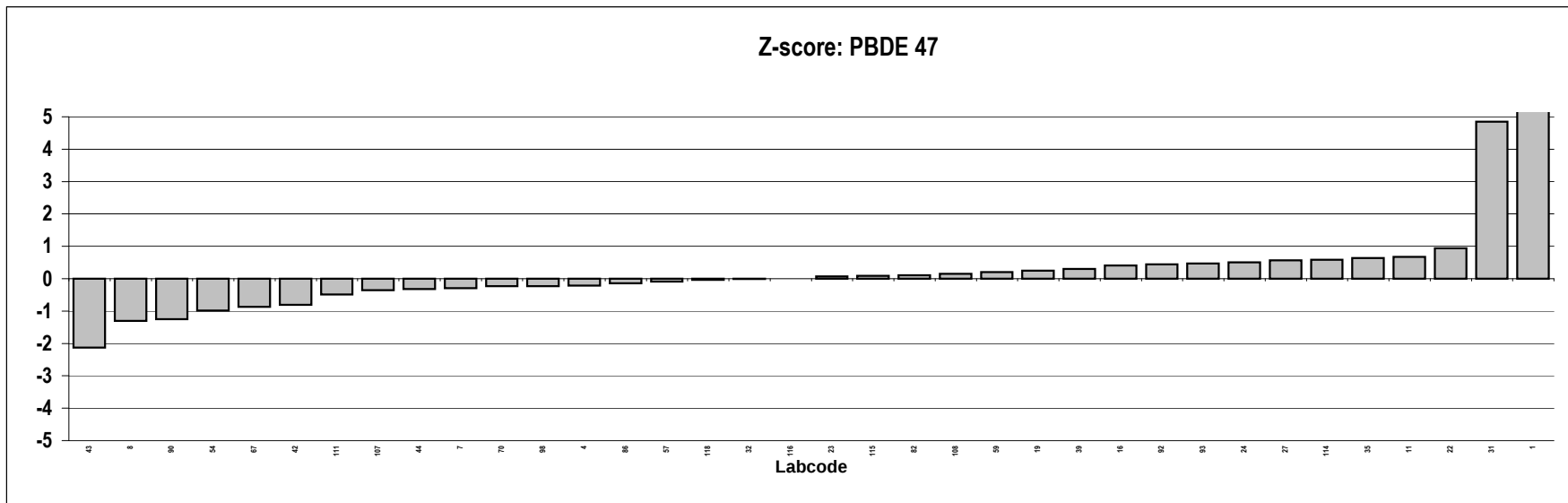
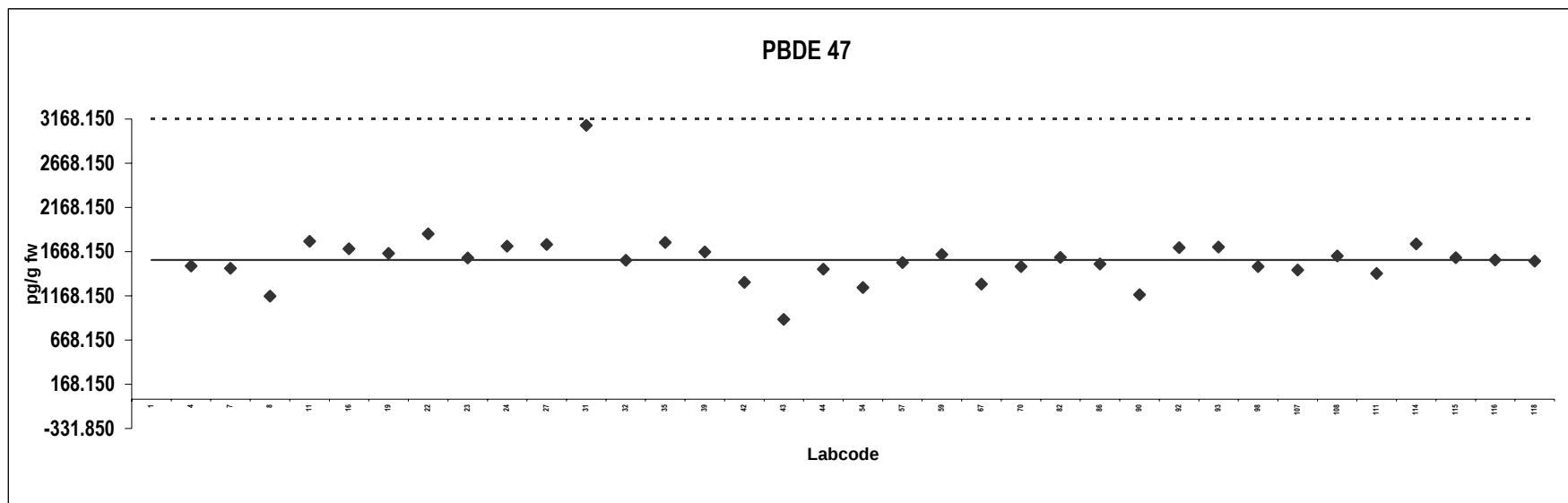
Consensus statistics	
Consensus median, pg/g	62
Median all values pg/g	63
Consensus mean, pg/g	62
Standard deviation, pg/g	13
Relative standard deviation, %	21
No. of values reported	36
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PBDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5126	Outlier			
4	1505				
7	1480				
8	1164				
11	1784				
16	1700				
19	1650				
22	1869				
23	1596				
24	1730				
27	1750				
31	3096				
32	1571				
35	1772				
39	1666				
42	1320				
43	903				
44	1471				
54	1262				
57	1545				
59	1637				
67	1300				
70	1500				
82	1605				
86	1528				
90	1180				
92	1713				
93	1720				
98	1500				
107	1460				
108	1619				
111	1420				
114	1756				
115	1600				
116	1572				
118	1560				

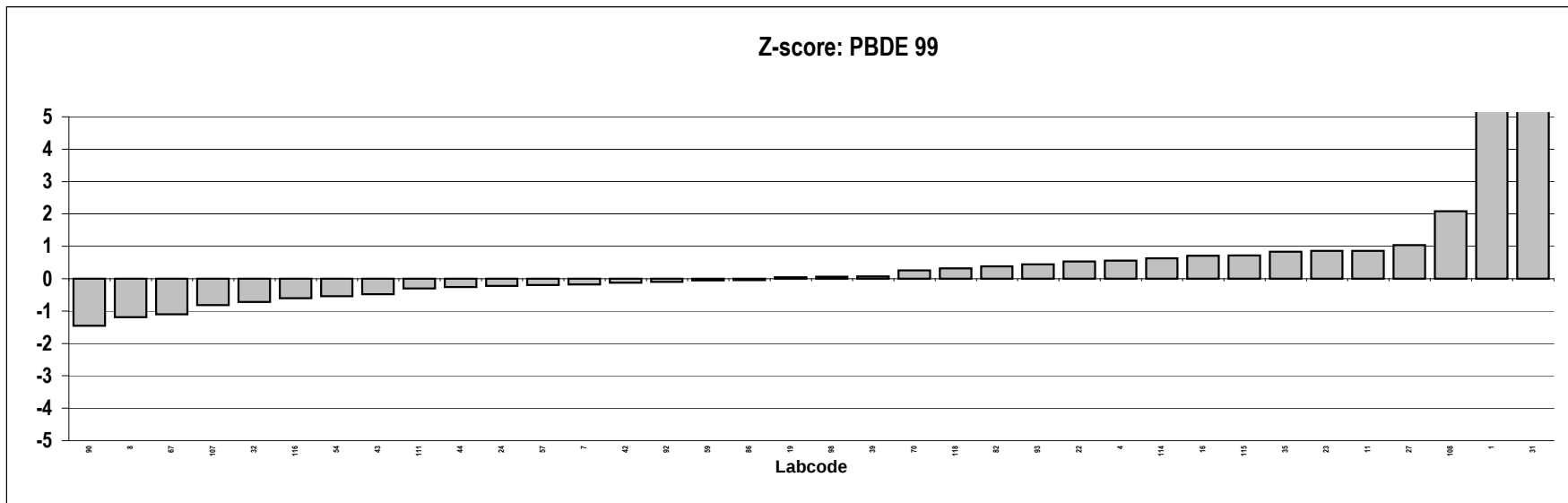
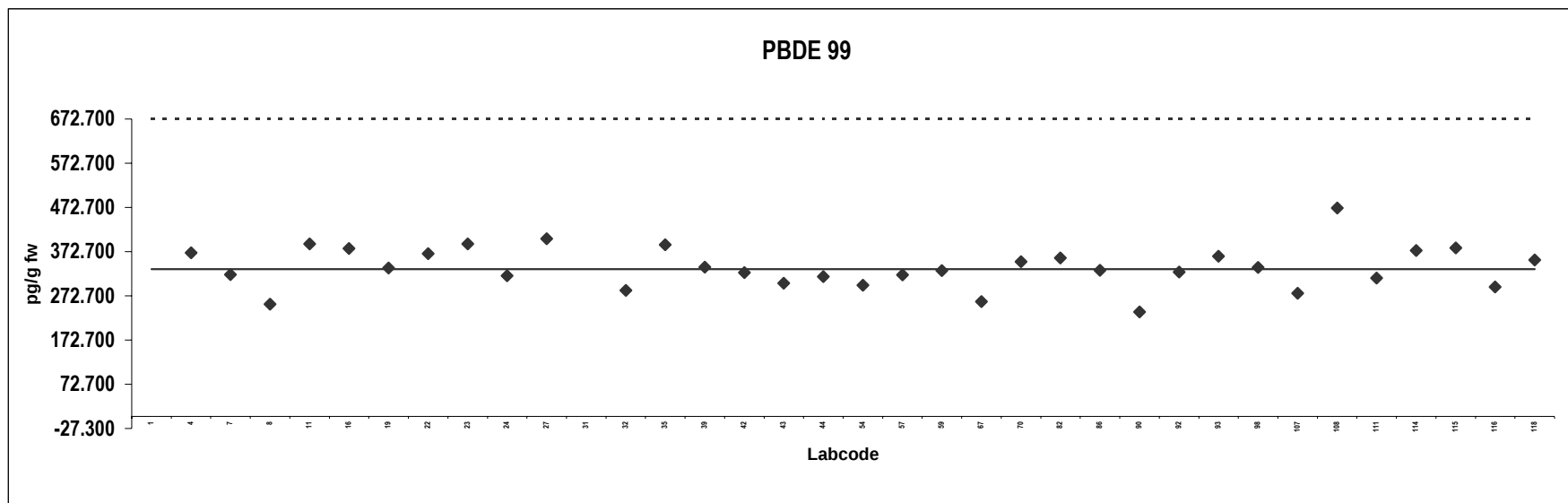
Consensus statistics	
Consensus median, pg/g	1572
Median all values pg/g	1584
Consensus mean, pg/g	1586
Standard deviation, pg/g	331
Relative standard deviation, %	21
No. of values reported	36
No. of values removed	1
No. of reported non-detects	0



Salmon
Congener: PBDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1165	Outlier			
4	370				
7	321				
8	254				
11	390				
16	380				
19	336				
22	368				
23	390				
24	318				
27	402				
31	3251	Outlier			
32	285				
35	388				
39	338				
42	325				
43	301				
44	316				
54	297				
57	320				
59	330				
67	260				
70	350				
82	359				
86	330				
90	236				
92	326				
93	363				
98	337				
107	279				
108	472				
111	313				
114	375				
115	381				
116	293				
118	354				

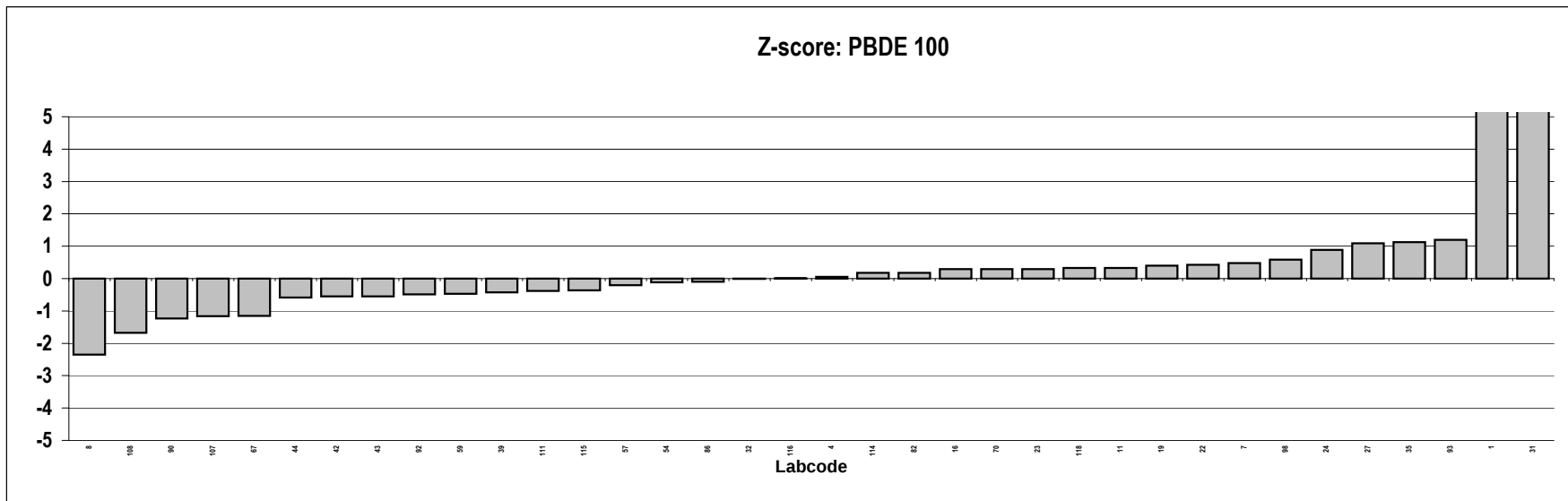
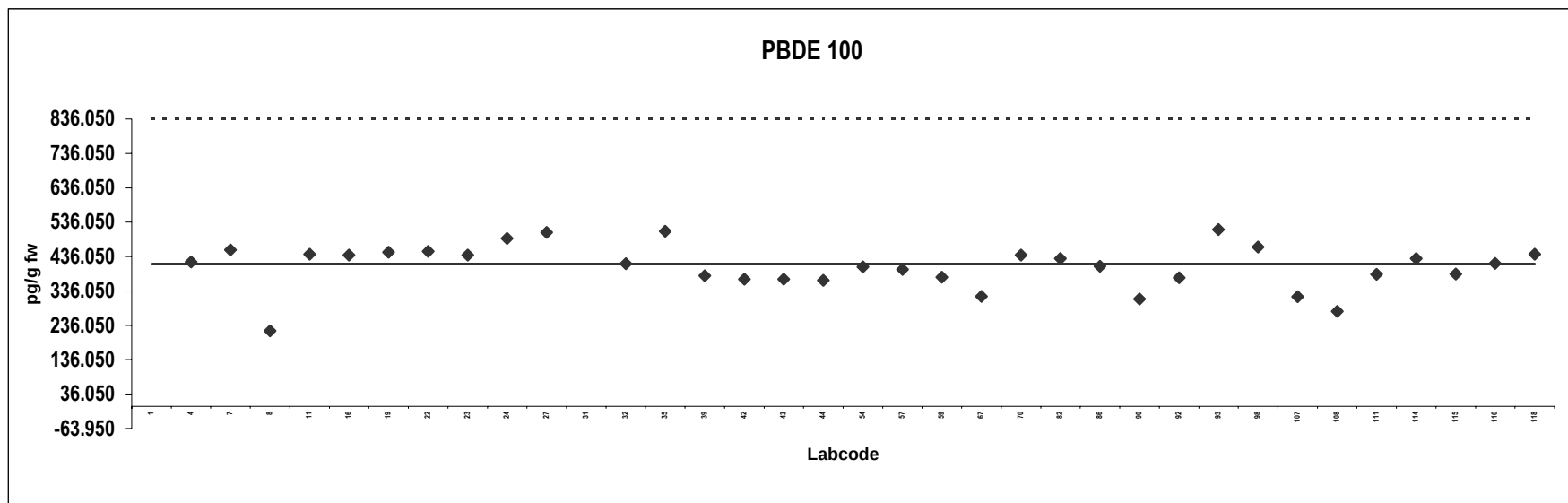
Consensus statistics	
Consensus median, pg/g	333
Median all values pg/g	336
Consensus mean, pg/g	337
Standard deviation, pg/g	48
Relative standard deviation, %	14
No. of values reported	36
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PBDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1468	Outlier			
4	420				
7	455				
8	220				
11	443				
16	440				
19	449				
22	451				
23	440				
24	489				
27	506				
31	3182	Outlier			
32	415				
35	509				
39	381				
42	370				
43	370				
44	367				
54	406				
57	399				
59	376				
67	320				
70	440				
82	430				
86	408				
90	313				
92	375				
93	515				
98	464				
107	319				
108	276				
111	384				
114	430				
115	385				
116	416				
118	443				

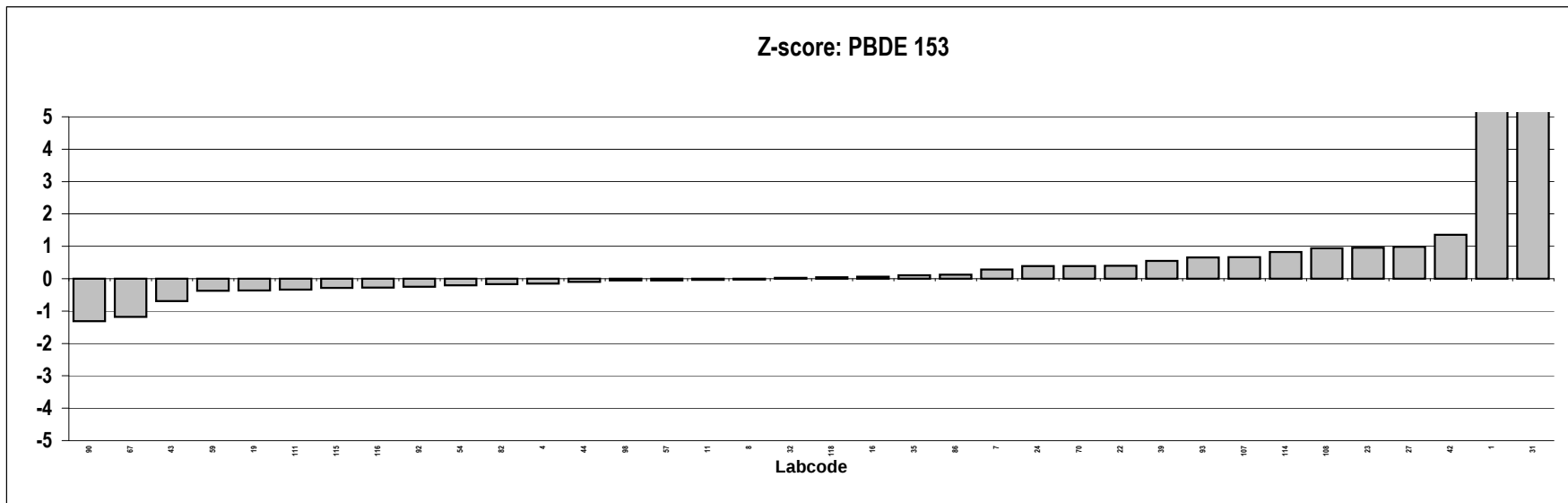
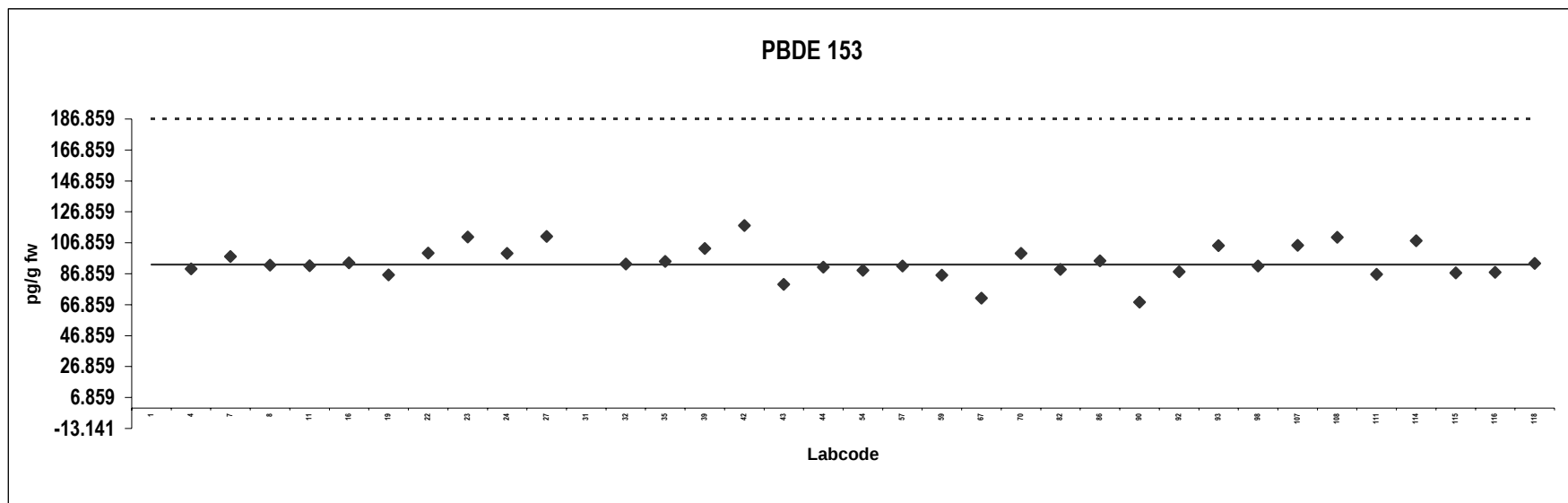
Consensus statistics	
Consensus median, pg/g	416
Median all values pg/g	418
Consensus mean, pg/g	407
Standard deviation, pg/g	65
Relative standard deviation, %	16
No. of values reported	36
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PBDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	351	Outlier			
4	90				
7	98				
8	92				
11	92				
16	94				
19	86				
22	100				
23	111				
24	100				
27	111				
31	3094				
32	93				
35	95				
39	103				
42	118				
43	80				
44	91				
54	89				
57	92				
59	86				
67	71				
70	100				
82	90				
86	95				
90	68				
92	88				
93	105				
98	92				
107	105				
108	110				
111	87				
114	108				
115	88				
116	88				
118	94				

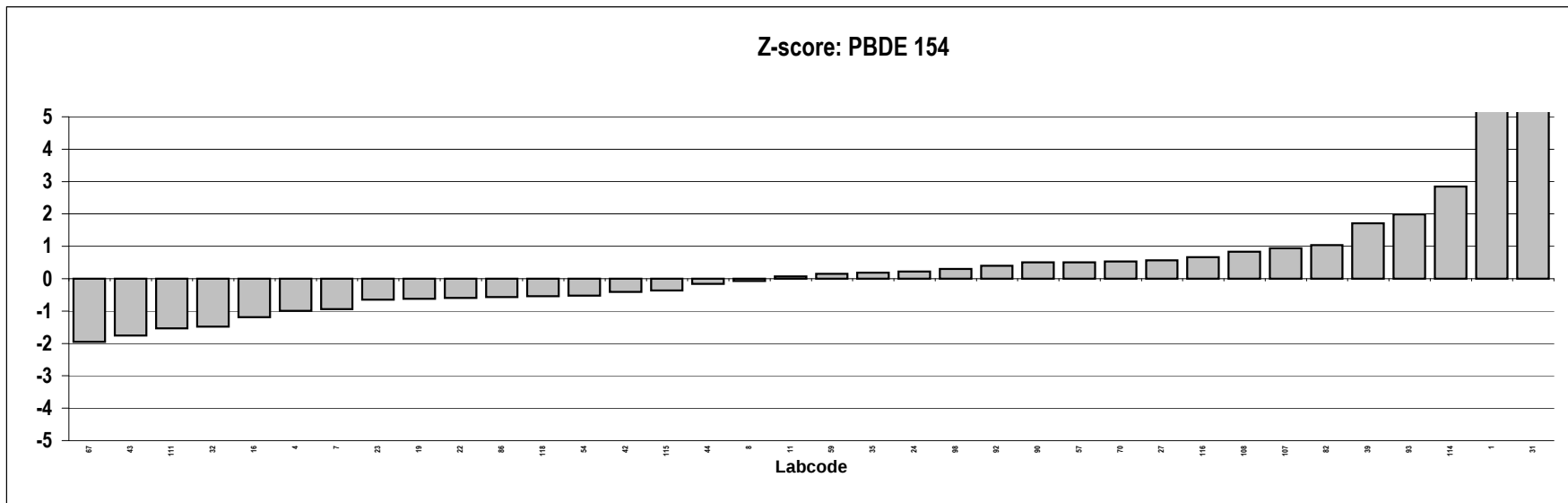
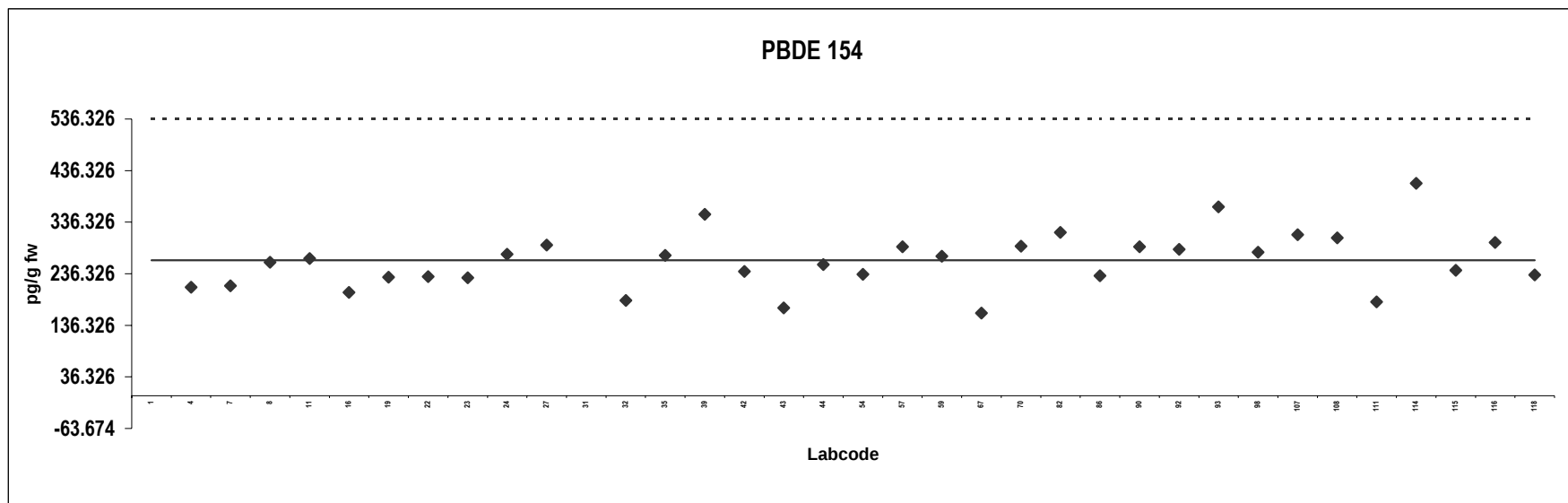
Consensus statistics	
Consensus median, pg/g	93
Median all values pg/g	93
Consensus mean, pg/g	94
Standard deviation, pg/g	11
Relative standard deviation, %	11
No. of values reported	36
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PBDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	864	Outlier			
4	210				
7	213				
8	259				
11	266				
16	200				
19	230				
22	231				
23	228				
24	274				
27	292				
31	2272	Outlier			
32	185				
35	272				
39	352				
42	241				
43	170				
44	254				
54	235				
57	289				
59	270				
67	160				
70	290				
82	317				
86	233				
90	289				
92	283				
93	366				
98	278				
107	312				
108	306				
111	182				
114	412				
115	243				
116	297				
118	234				

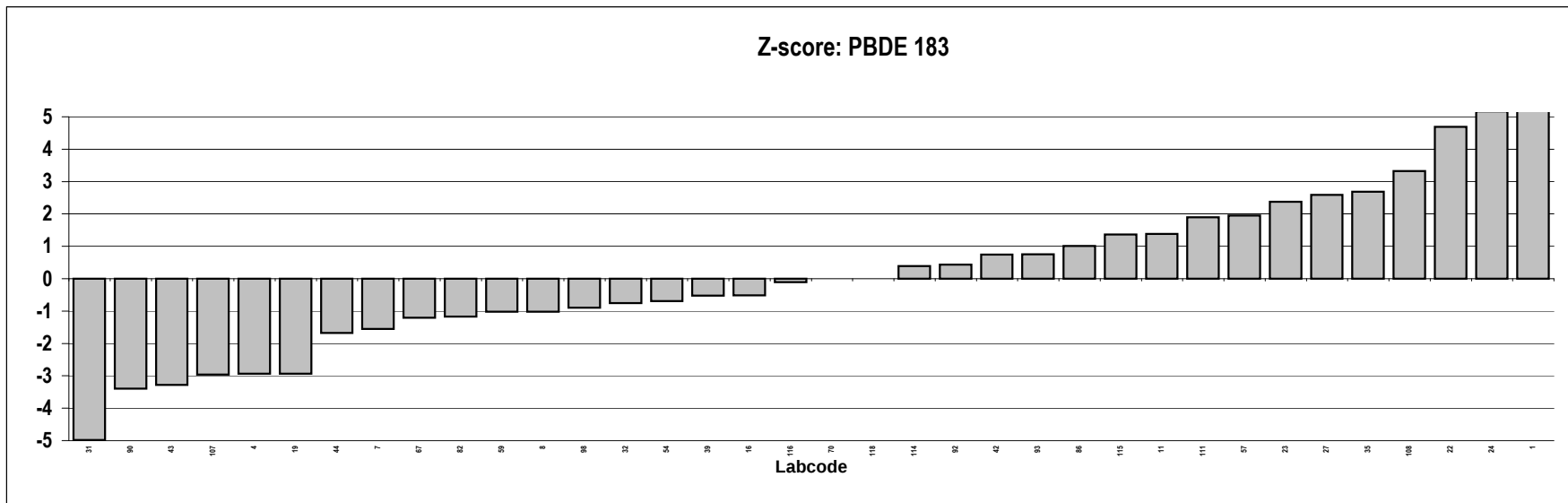
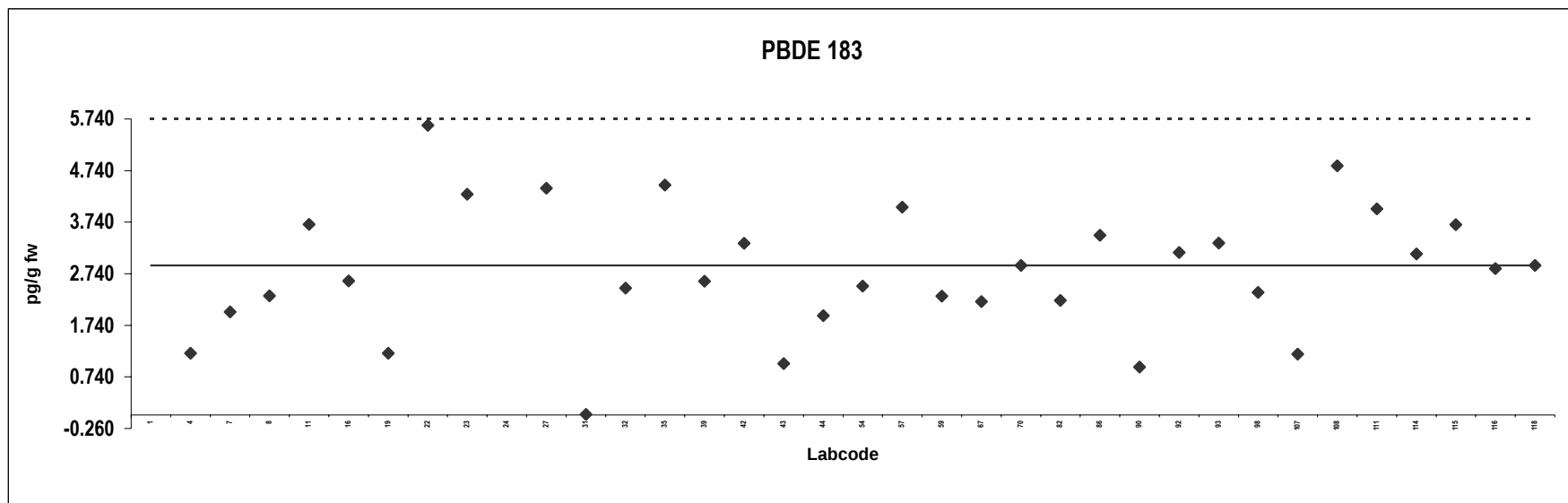
Consensus statistics	
Consensus median, pg/g	262
Median all values pg/g	268
Consensus mean, pg/g	261
Standard deviation, pg/g	55
Relative standard deviation, %	21
No. of values reported	36
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: PBDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	17	Outlier			
4	1.2	ND			
7	2.0	ND			
8	2.3				
11	3.7				
16	2.6				
19	1.2	ND			
22	5.6				
23	4.3				
24	5.9	Outlier,ND			
27	4.4				
31	0.010	ND			
32	2.5				
35	4.5				
39	2.6				
42	3.3				
43	1.0				
44	1.9				
54	2.5	ND			
57	4.0				
59	2.3				
67	2.2				
70	2.9				
82	2.2				
86	3.5				
90	0.93				
92	3.2				
93	3.3				
98	2.4				
107	1.2				
108	4.8	ND			
111	4.0	ND			
114	3.1				
115	3.7				
116	2.8				
118	2.9				

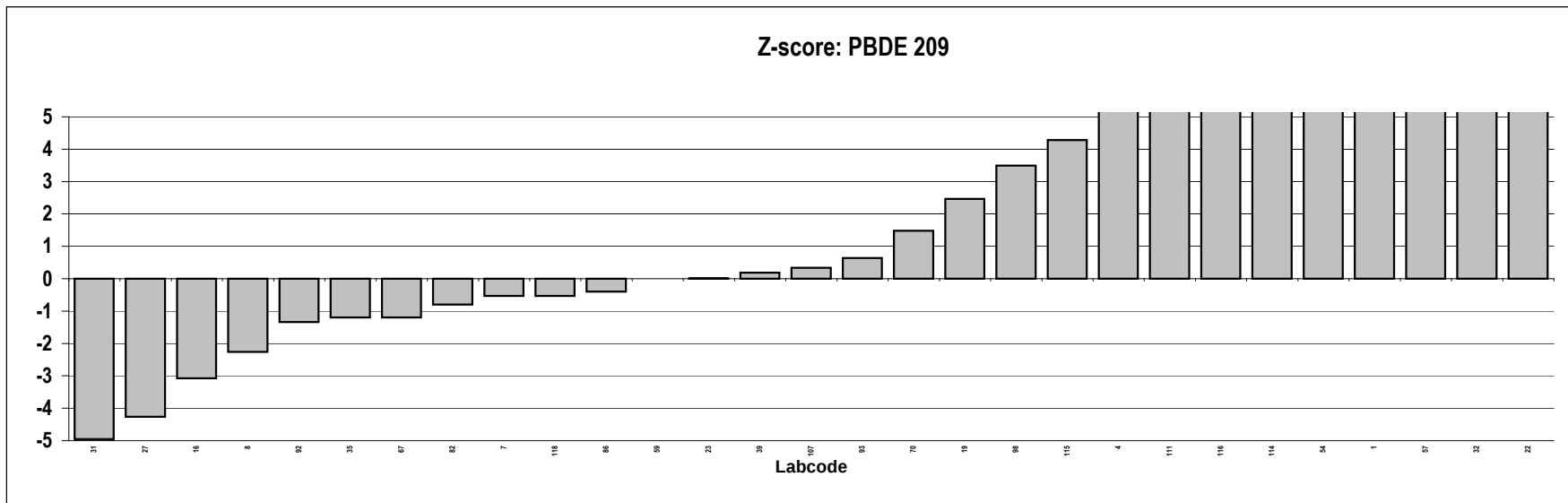
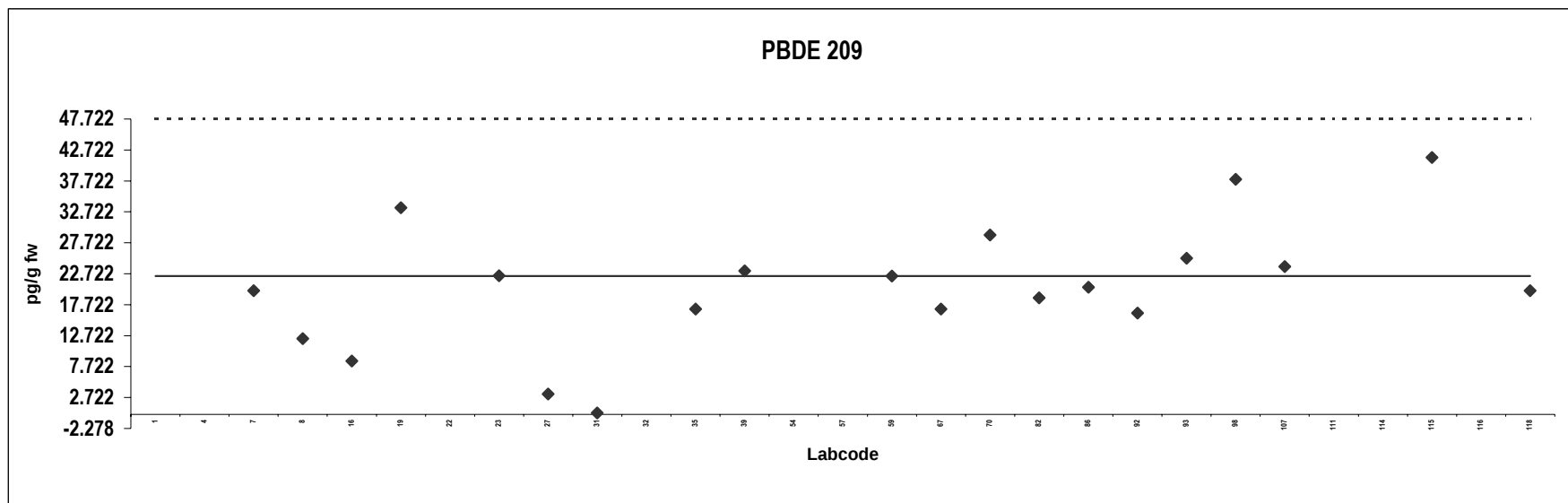
Consensus statistics	
Consensus median, pg/g	2.9
Median all values pg/g	2.9
Consensus mean, pg/g	2.8
Standard deviation, pg/g	1.2
Relative standard deviation, %	44
No. of values reported	36
No. of values removed	2
No. of reported non-detects	8



Salmon
Congener: PBDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	184	Outlier			
4	60	Outlier,ND			
7	20	ND			
8	12				
16	8.6				
19	33				
22	29057	Outlier			
23	22				
27	3.3				
31	0.21	ND			
32	343	Outlier			
35	17				
39	23				
54	100	Outlier,ND			
57	294	Outlier			
59	22				
67	17				
70	29				
82	19				
86	21				
92	16				
93	25				
98	38				
107	24				
111	62	Outlier			
114	79	Outlier			
115	42				
116	68	Outlier			
118	20	ND			

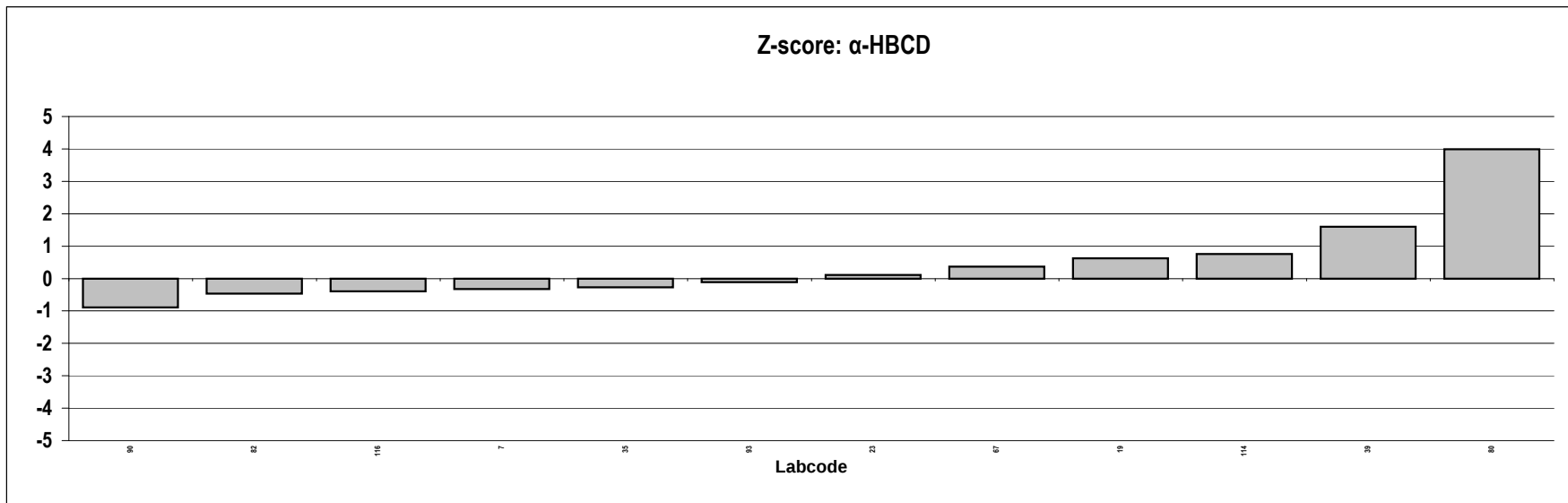
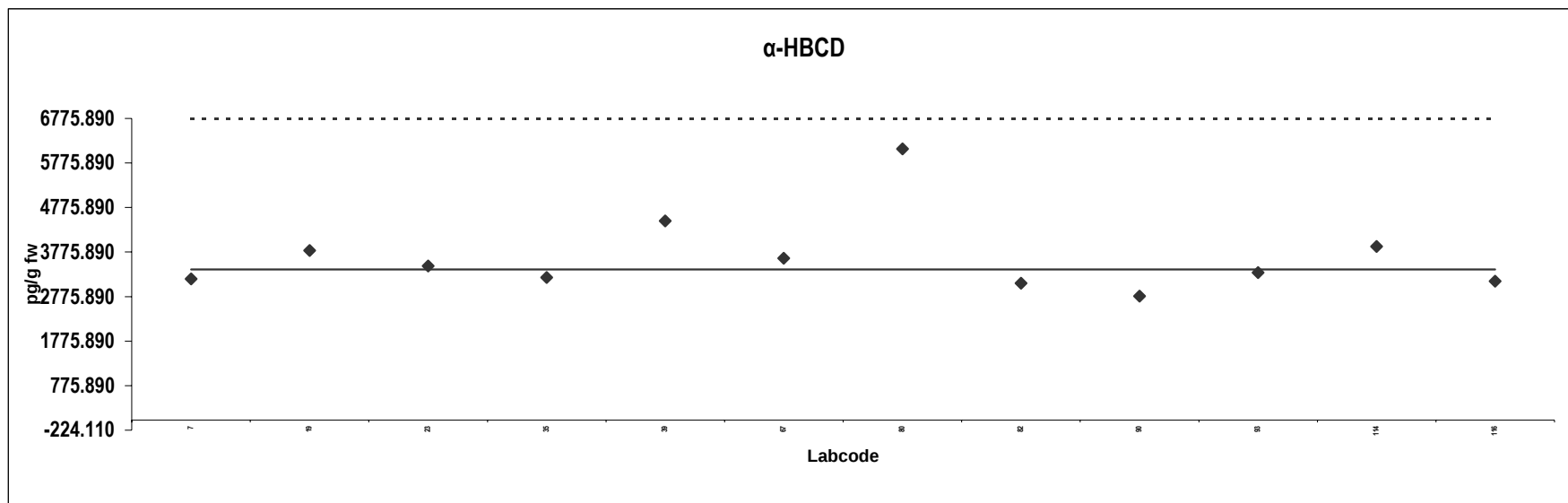
Consensus statistics	
Consensus median, pg/g	22
Median all values pg/g	24
Consensus mean, pg/g	21
Standard deviation, pg/g	10
Relative standard deviation, %	50
No. of values reported	29
No. of values removed	9
No. of reported non-detects	5



Salmon
Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
7	3170				
19	3809				
23	3460				
35	3204				
39	4473				
67	3640				
80	6090				
82	3074				
90	2786				
93	3316				
114	3898				
116	3121				

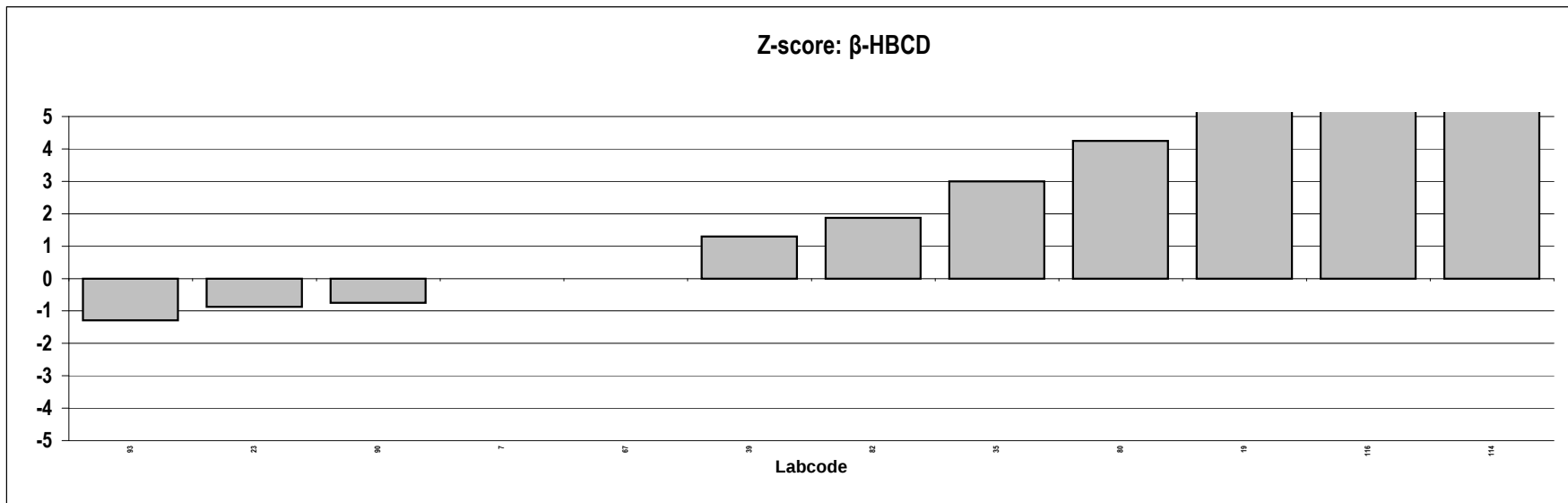
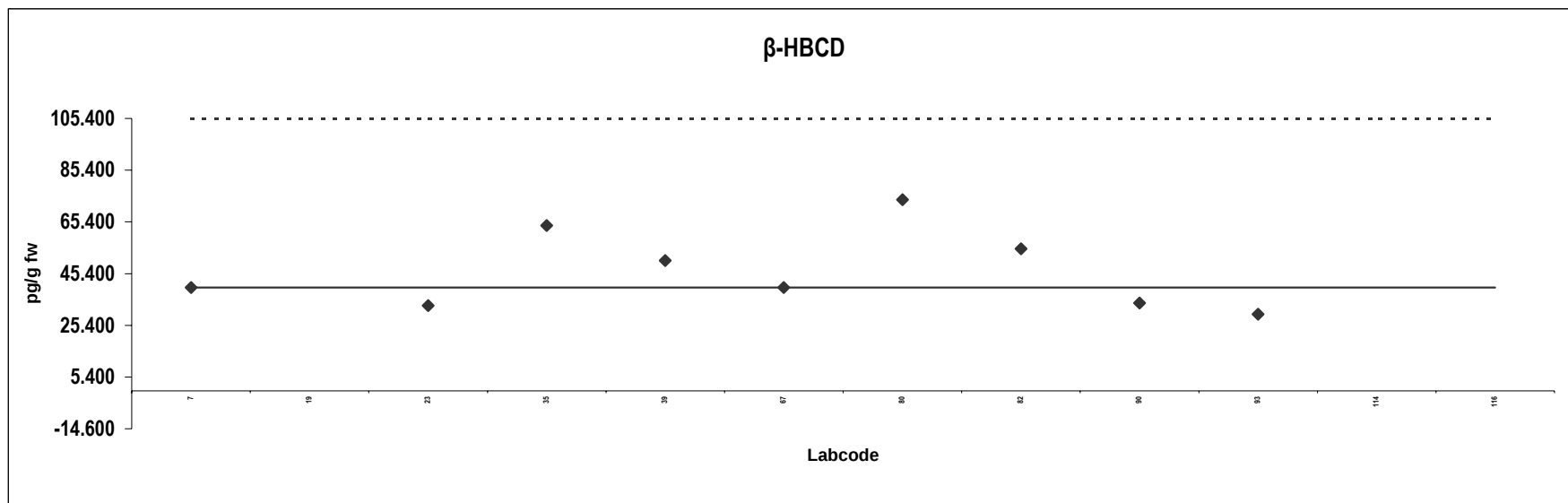
Consensus statistics	
Consensus median, pg/g	3388
Median all values pg/g	3388
Consensus mean, pg/g	3670
Standard deviation, pg/g	887
Relative standard deviation, %	24
No. of values reported	12
No. of values removed	0
No. of reported non-detects	0



Salmon
Congener: β -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
7	40	Outlier			
19	151				
23	33				
35	64				
39	50				
67	40				
80	74				
82	55				
90	34				
93	30				
114	516	Outlier			
116	154	Outlier			

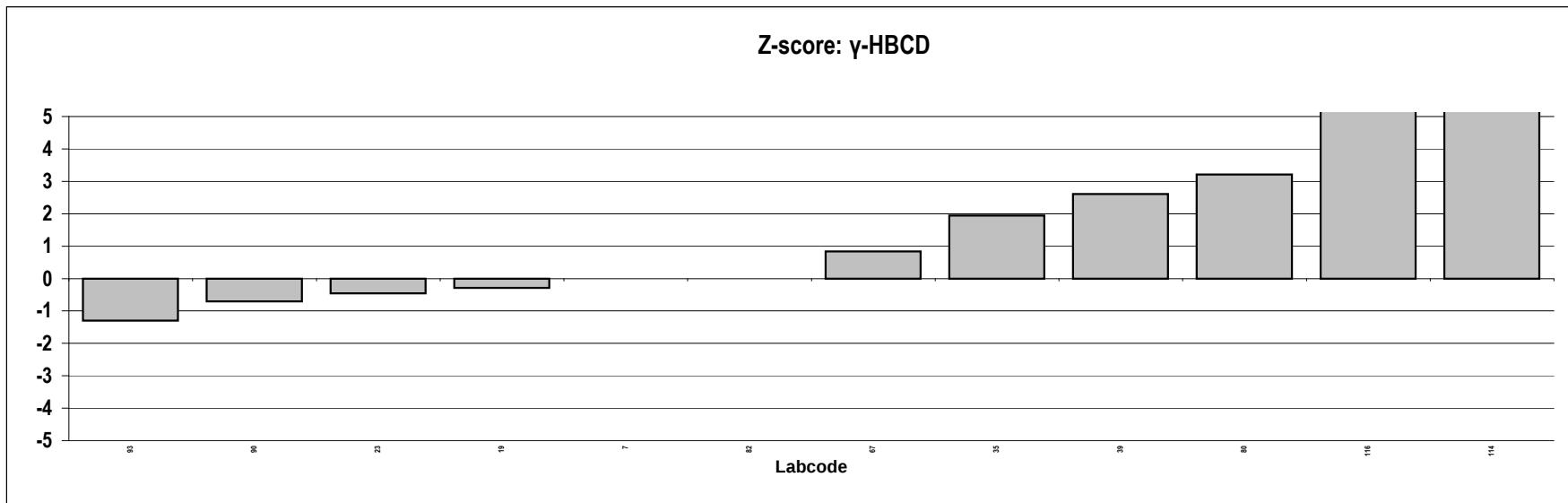
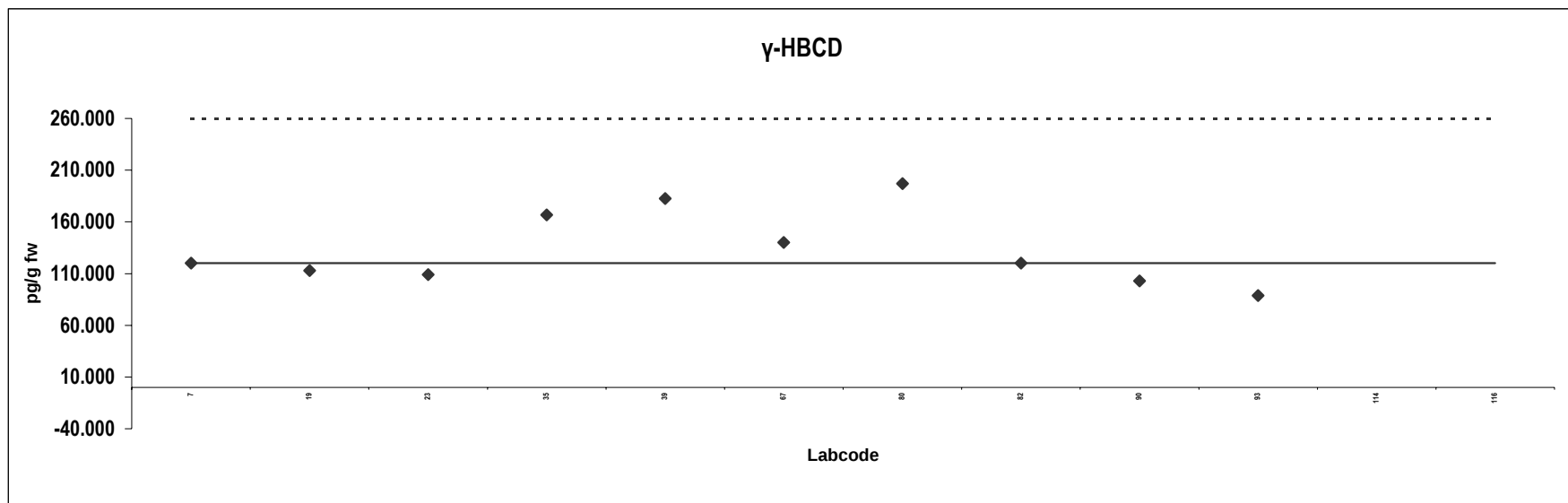
Consensus statistics	
Consensus median, pg/g	40
Median all values pg/g	53
Consensus mean, pg/g	47
Standard deviation, pg/g	15
Relative standard deviation, %	33
No. of values reported	12
No. of values removed	3
No. of reported non-detects	0



Salmon
Congener: γ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
7	120				
19	113				
23	109				
35	167				
39	183				
67	140				
80	197				
82	120				
90	103				
93	89				
114	1061	Outlier			
116	690	Outlier			

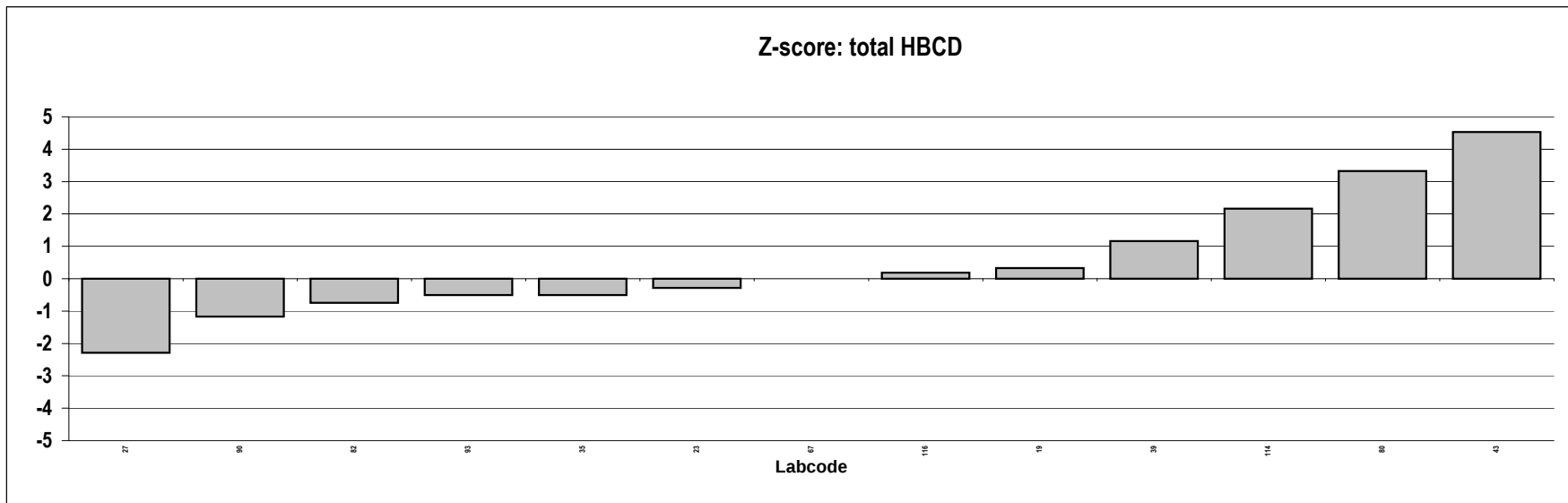
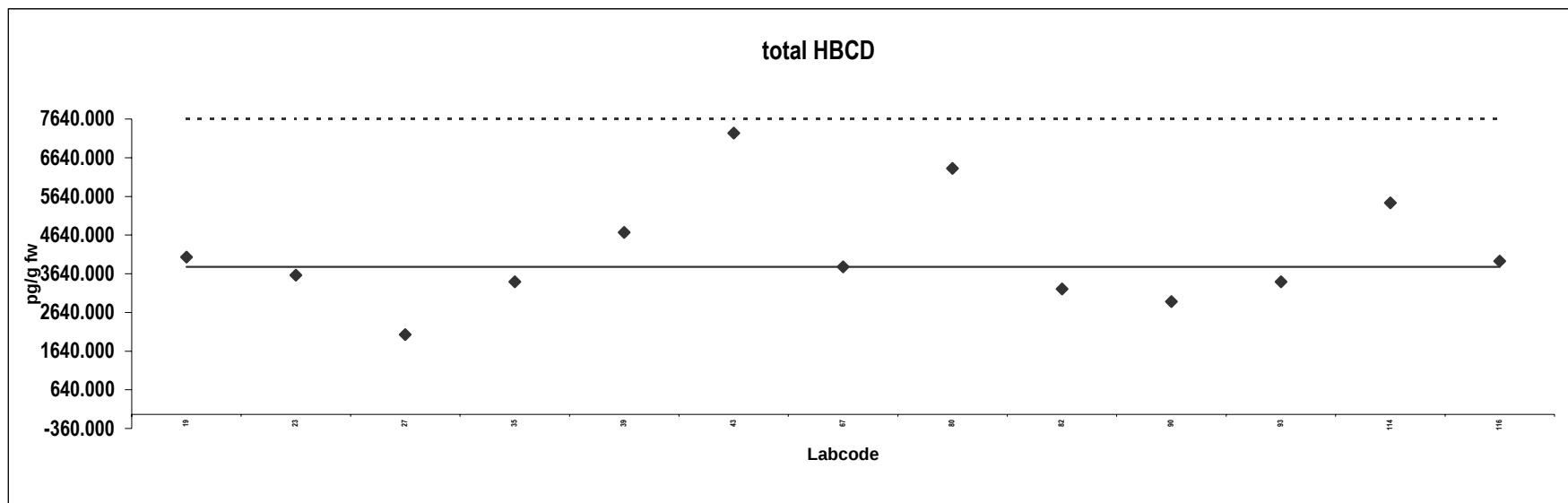
Consensus statistics	
Consensus median, pg/g	120
Median all values pg/g	130
Consensus mean, pg/g	134
Standard deviation, pg/g	36
Relative standard deviation, %	27
No. of values reported	12
No. of values removed	2
No. of reported non-detects	0



Salmon
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
19	4073				
23	3600				
27	2070				
35	3435				
39	4706				
43	7280				
67	3820				
80	6361				
82	3249				
90	2923				
93	3434				
114	5476				
116	3965				

Consensus statistics	
Consensus median, pg/g	3820
Median all values pg/g	3820
Consensus mean, pg/g	4184
Standard deviation, pg/g	1439
Relative standard deviation, %	34
No. of values reported	13
No. of values removed	0
No. of reported non-detects	0



Appendix 4:

Presentation of results
for cheese-2015

Appendix 2: Presentation of results: Cheese-2015

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:

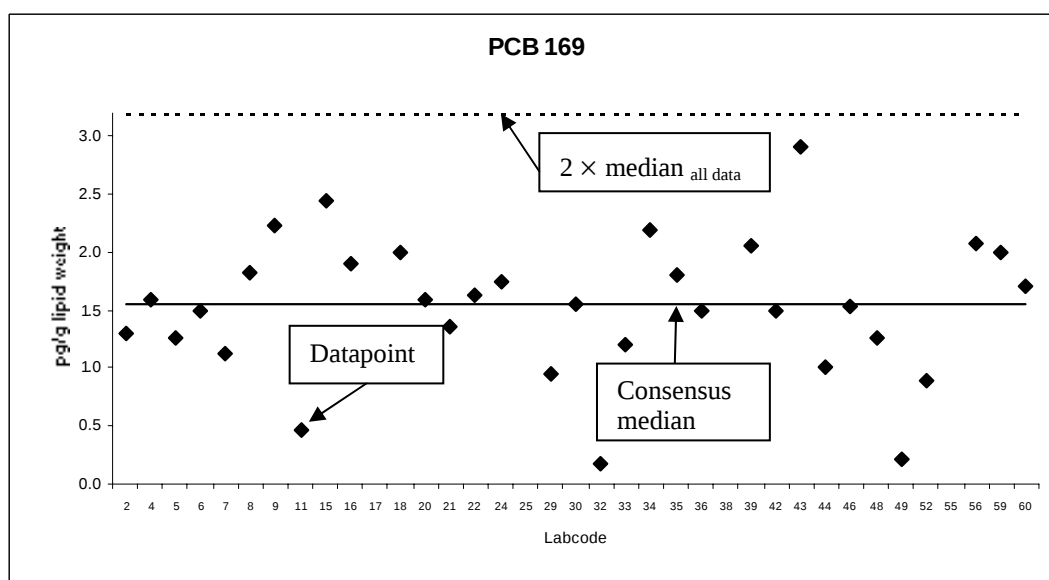
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding $2 \times$ this median were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

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

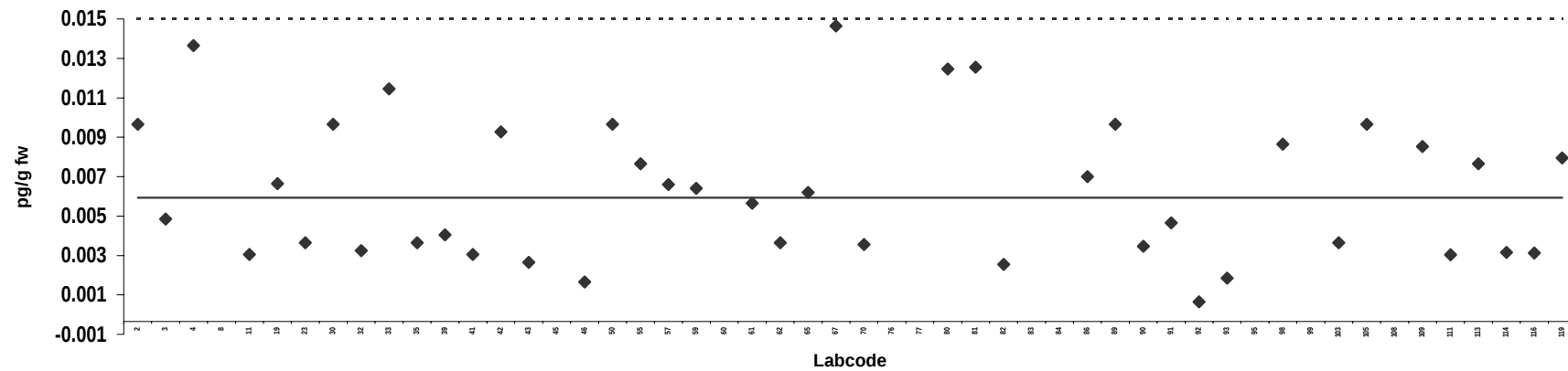
where x = reported value; X = assigned value (consensus); σ = target value for standard deviation. A σ of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of $\pm 20\%$ from the consensus value.

Cheese
Congener: 2,3,7,8 TCDD

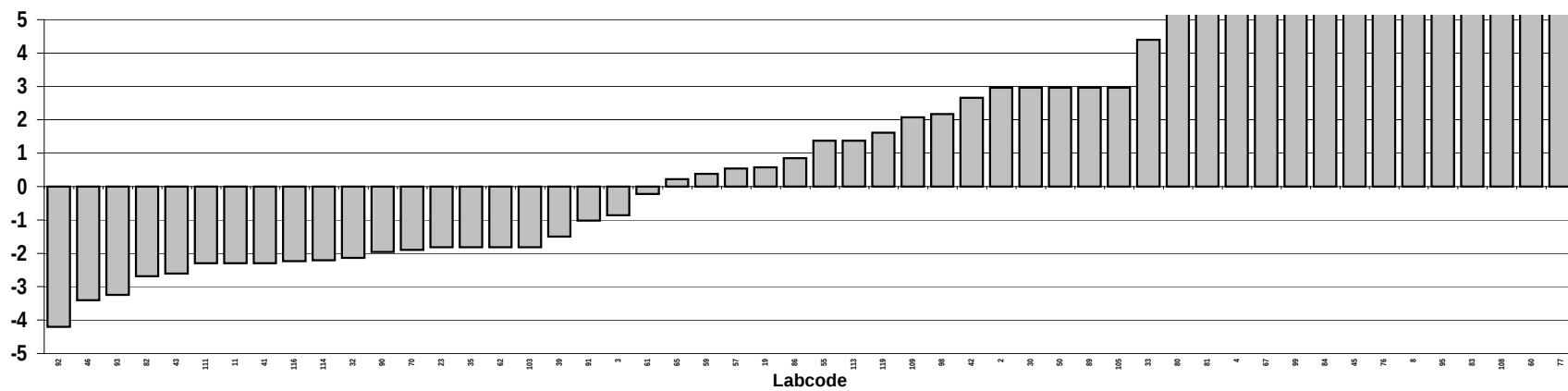
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	108	0.029	Outlier,ND
3	0.0052	ND	109	0.0089	
4	0.014	ND	111	0.0034	ND
8	0.020	Outlier,ND	113	0.0080	
11	0.0034	ND	114	0.0035	
19	0.0070	ND	116	0.0035	
23	0.0040		119	0.0083	
30	0.010	ND			
32	0.0036				
33	0.012	ND			
35	0.0040				
39	0.0044				
41	0.0034	ND			
42	0.0096				
43	0.0030	ND			
45	0.018	Outlier			
46	0.0020	ND			
50	0.010				
55	0.0080	ND			
57	0.0070				
59	0.0068	ND			
60	0.053	Outlier,ND			
61	0.0060				
62	0.0040				
65	0.0066	ND			
67	0.015				
70	0.0039	ND			
76	0.018	Outlier,ND			
77	0.31	Outlier,ND			
80	0.013	ND			
81	0.013	ND			
82	0.0029				
83	0.027	Outlier,ND			
84	0.017	Outlier			
86	0.0074	ND			
89	0.010	ND			
90	0.0038				
91	0.0050	ND			
92	0.0010	ND			
93	0.0022	ND			
95	0.025	Outlier,ND			
98	0.0090	ND			
99	0.016	Outlier,ND			
103	0.0040				
105	0.010	ND			

Consensus statistics	
Consensus median, pg/g	0.0063
Median all values pg/g	0.0077
Consensus mean, pg/g	0.0066
Standard deviation, pg/g	0.0036
Relative standard deviation, %	54
No. of values reported	52
No. of values removed	10
No. of reported non-detects	32

2,3,7,8 TCDD



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

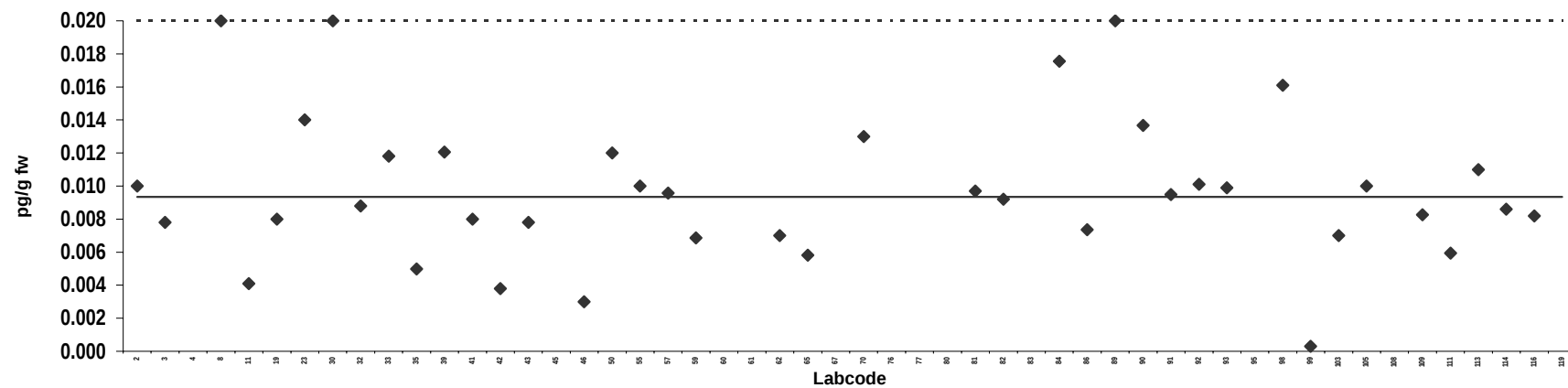


Cheese
Congener: 1,2,3,7,8 PeCDD

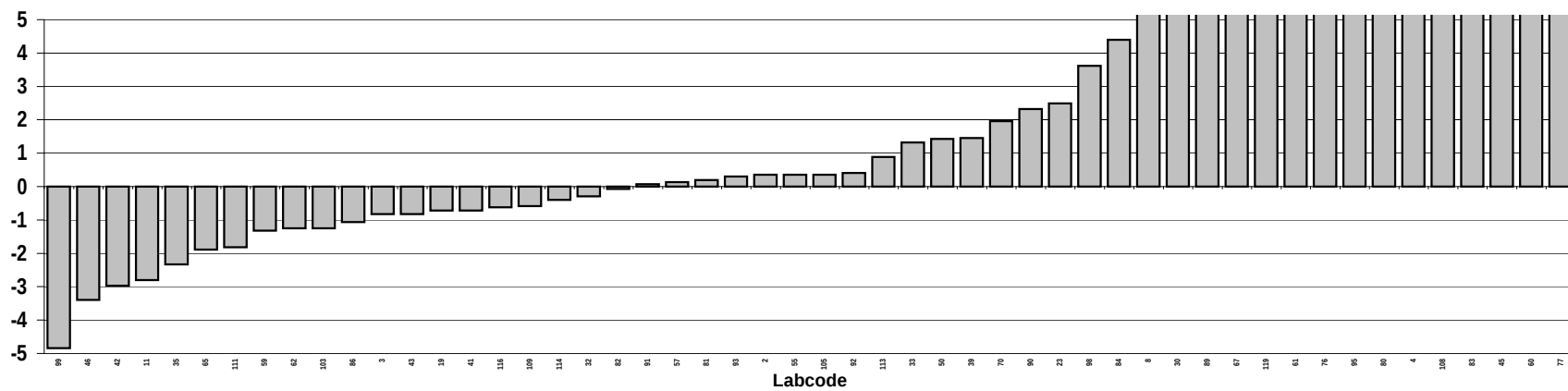
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	108	0.029	Outlier,ND
3	0.0078		109	0.0083	
4	0.027	Outlier,ND	111	0.0059	
8	0.020	ND	113	0.011	
11	0.0041	ND	114	0.0086	
19	0.0080		116	0.0082	
23	0.014		119	0.022	Outlier
30	0.020	ND			
32	0.0088				
33	0.012	ND			
35	0.0050				
39	0.012				
41	0.0080	ND			
42	0.0038				
43	0.0078				
45	0.050	Outlier			
46	0.0030	ND			
50	0.012				
55	0.010	ND			
57	0.0096				
59	0.0069	ND			
60	0.056	Outlier,ND			
61	0.025	Outlier,ND			
62	0.0070				
65	0.0058	ND			
67	0.021	Outlier			
70	0.013				
76	0.025	Outlier,ND			
77	0.27	Outlier,ND			
80	0.027	Outlier,ND			
81	0.0097	ND			
82	0.0092				
83	0.045	Outlier,ND			
84	0.018				
86	0.0074	ND			
89	0.020	ND			
90	0.014				
91	0.0095				
92	0.010				
93	0.0099				
95	0.025	Outlier,ND			
98	0.016				
99	0.00030	ND			
103	0.0070				
105	0.010				

Consensus statistics	
Consensus median, pg/g	0.0093
Median all values pg/g	0.010
Consensus mean, pg/g	0.010
Standard deviation, pg/g	0.0045
Relative standard deviation, %	46
No. of values reported	52
No. of values removed	12
No. of reported non-detects	23

1,2,3,7,8 PeCDD



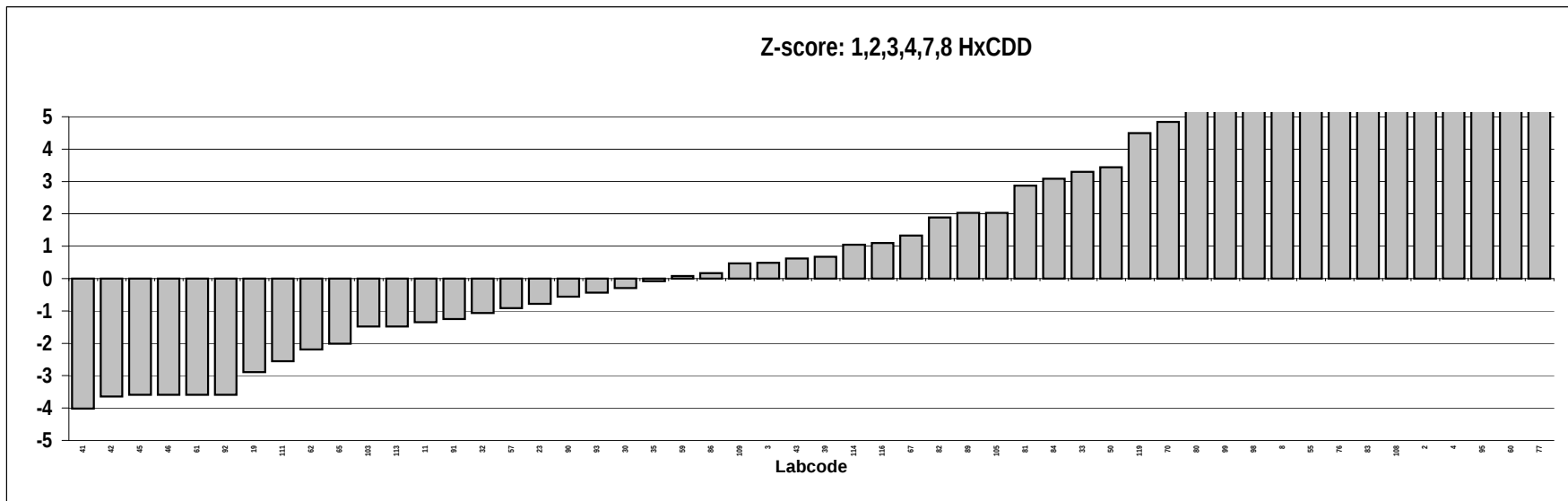
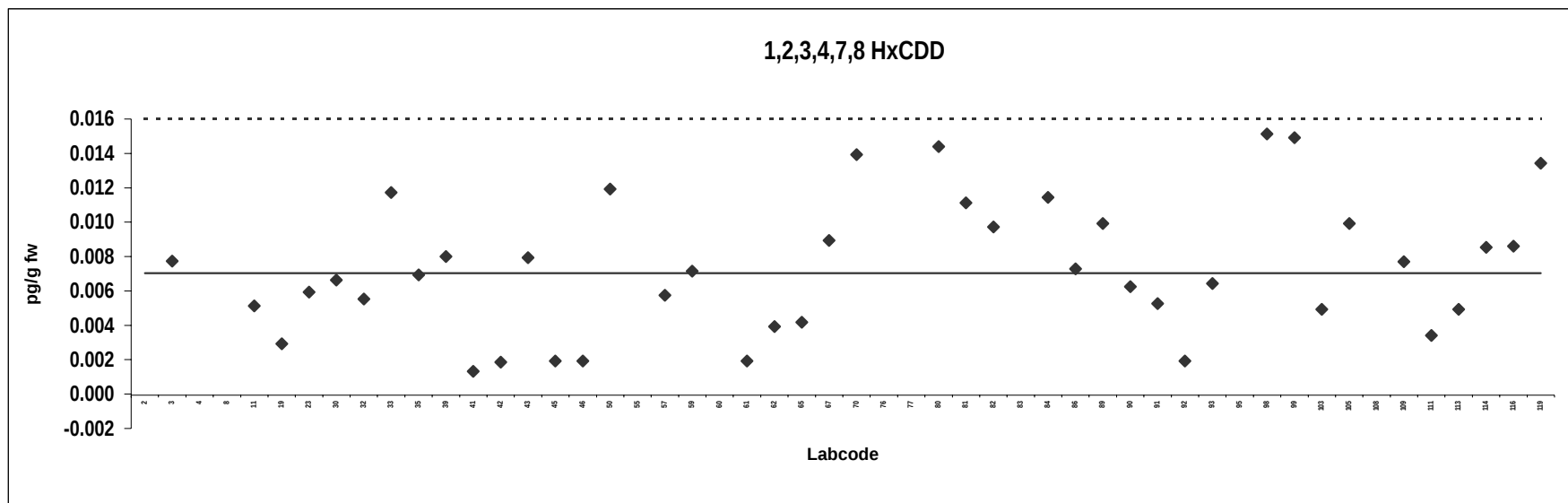
Z-score: 1,2,3,7,8 PeCDD



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	Outlier,ND	108	0.029	Outlier,ND
3	0.0078	ND	109	0.0078	
4	0.047	Outlier,ND	111	0.0035	ND
8	0.020	Outlier,ND	113	0.0050	ND
11	0.0052	ND	114	0.0086	
19	0.0030	ND	116	0.0087	
23	0.0060		119	0.014	
30	0.0067	ND			
32	0.0056				
33	0.012	ND			
35	0.0070				
39	0.0081				
41	0.0014	ND			
42	0.0019				
43	0.0080				
45	0.0020				
46	0.0020	ND			
50	0.012				
55	0.020	Outlier,ND			
57	0.0058				
59	0.0072	ND			
60	0.069	Outlier,ND			
61	0.0020				
62	0.0040				
65	0.0042	ND			
67	0.0090				
70	0.014				
76	0.020	Outlier,ND			
77	0.24	Outlier,ND			
80	0.014	ND			
81	0.011	ND			
82	0.0098				
83	0.025	Outlier,ND			
84	0.012				
86	0.0074	ND			
89	0.010	ND			
90	0.0063				
91	0.0053				
92	0.0020	ND			
93	0.0065				
95	0.050	Outlier,ND			
98	0.015				
99	0.015	ND			
103	0.0050				
105	0.010	ND			

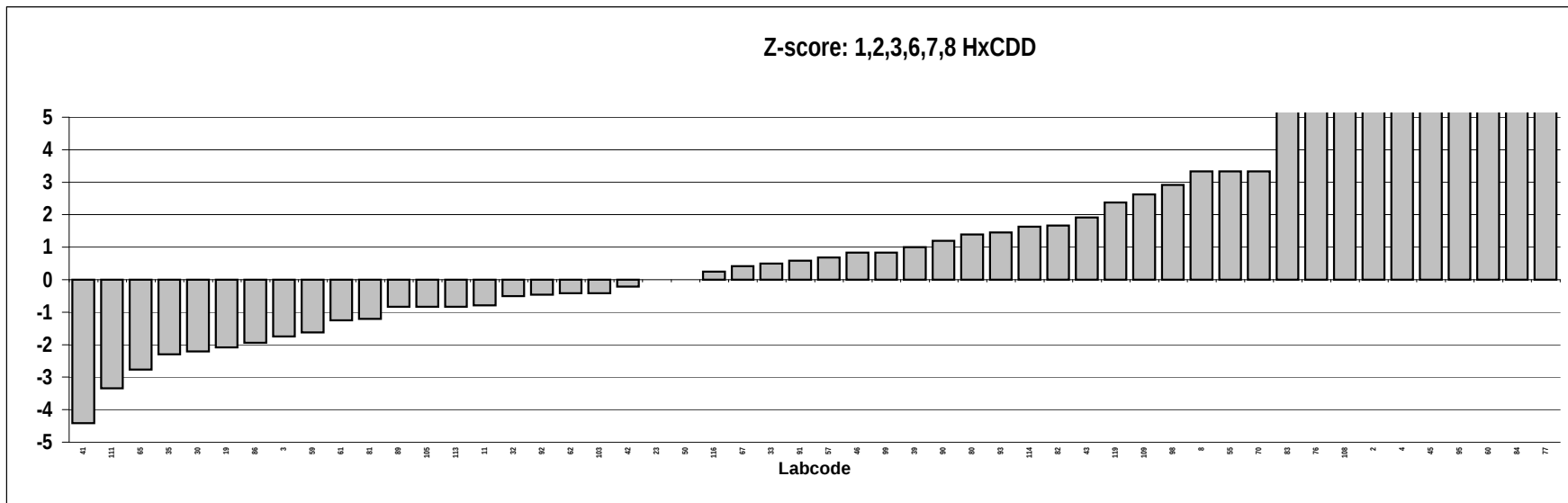
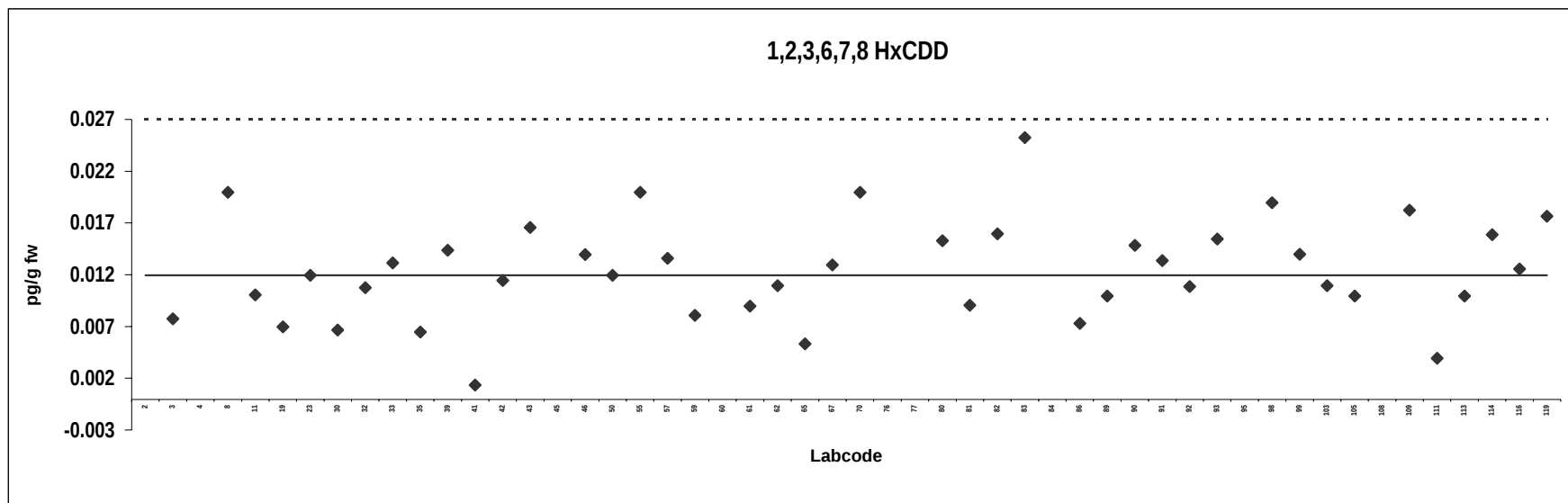
Consensus statistics	
Consensus median, pg/g	0.0071
Median all values pg/g	0.0080
Consensus mean, pg/g	0.0074
Standard deviation, pg/g	0.0039
Relative standard deviation, %	52
No. of values reported	52
No. of values removed	10
No. of reported non-detects	28



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	Outlier,ND	108	0.029	Outlier,ND
3	0.0078		109	0.018	
4	0.047	Outlier,ND	111	0.0040	
8	0.020	ND	113	0.010	
11	0.010		114	0.016	
19	0.0070	ND	116	0.013	
23	0.012		119	0.018	
30	0.0067	ND			
32	0.011				
33	0.013				
35	0.0065				
39	0.014				
41	0.0014	ND			
42	0.012				
43	0.017				
45	0.048	Outlier			
46	0.014				
50	0.012				
55	0.020	ND			
57	0.014				
59	0.0081	ND			
60	0.064	Outlier,ND			
61	0.0090				
62	0.011				
65	0.0054	ND			
67	0.013				
70	0.020				
76	0.028	Outlier,ND			
77	0.25	Outlier,ND			
80	0.015	ND			
81	0.0091	ND			
82	0.016				
83	0.025	ND			
84	0.069	Outlier			
86	0.0074	ND			
89	0.010	ND			
90	0.015				
91	0.013				
92	0.011				
93	0.016				
95	0.050	Outlier,ND			
98	0.019				
99	0.014	ND			
103	0.011				
105	0.010				

Consensus statistics	
Consensus median, pg/g	0.012
Median all values pg/g	0.014
Consensus mean, pg/g	0.012
Standard deviation, pg/g	0.0048
Relative standard deviation, %	39
No. of values reported	52
No. of values removed	9
No. of reported non-detects	20

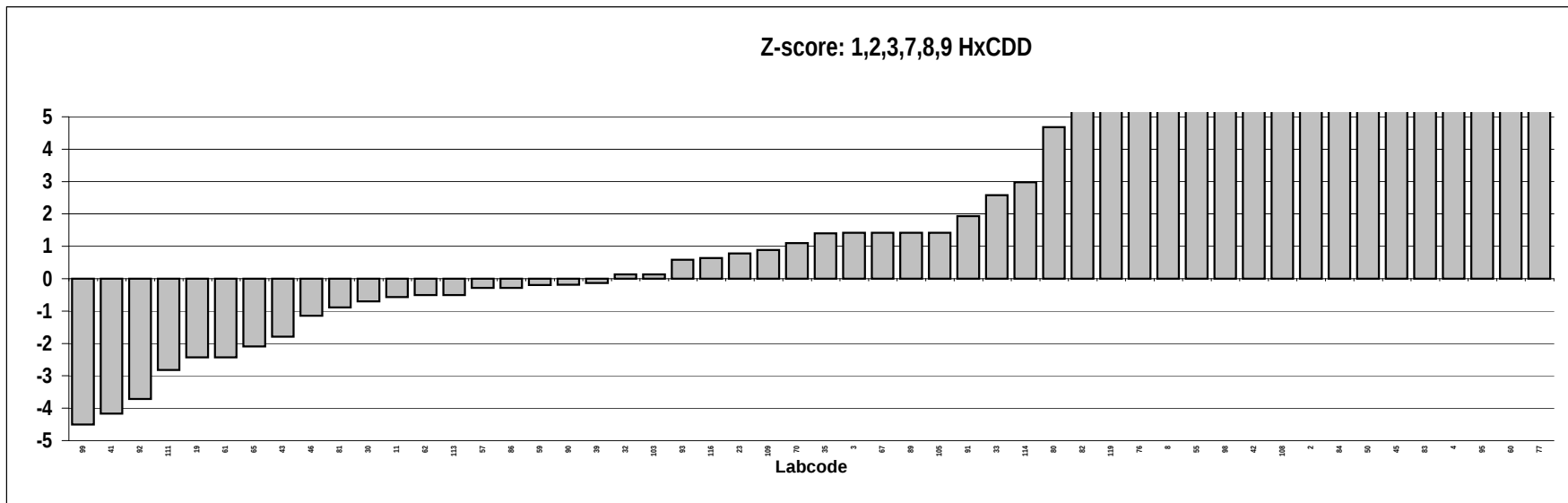
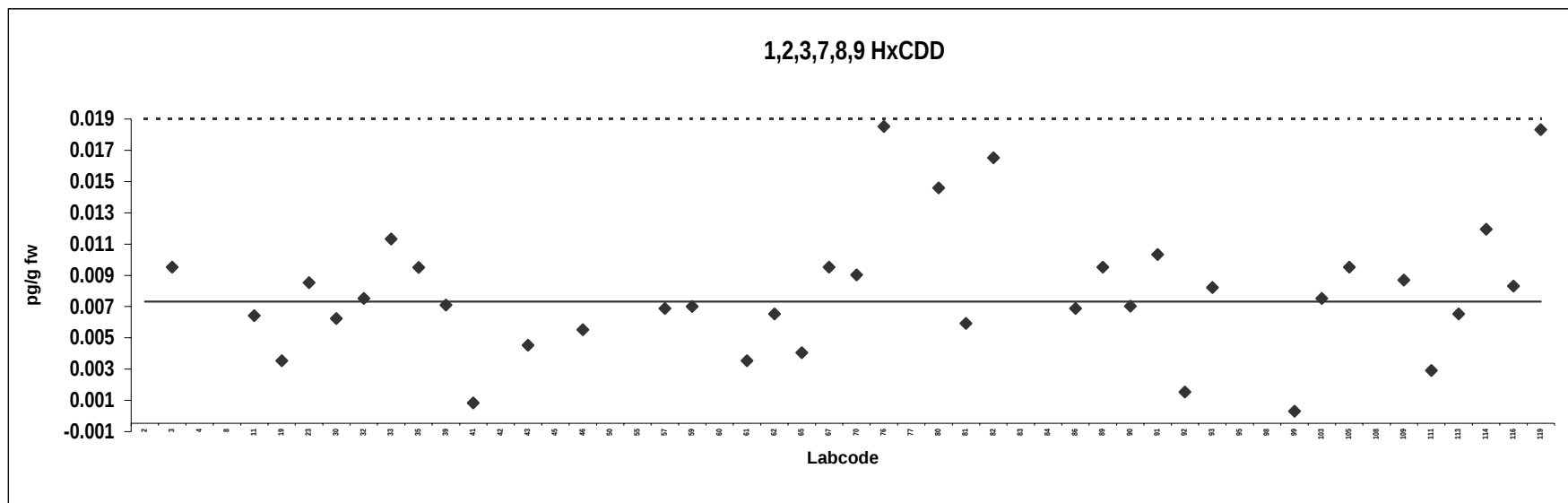


Cheese

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	Outlier,ND	108	0.029	Outlier,ND
3	0.010		109	0.0092	
4	0.043	Outlier,ND	111	0.0034	ND
8	0.020	Outlier,ND	113	0.0070	ND
11	0.0069		114	0.012	
19	0.0040	ND	116	0.0088	
23	0.0090		119	0.019	
30	0.0067	ND			
32	0.0080				
33	0.012	ND			
35	0.010				
39	0.0076				
41	0.0013	ND			
42	0.024	Outlier			
43	0.0050	ND			
45	0.036	Outlier			
46	0.0060				
50	0.032	Outlier			
55	0.020	Outlier,ND			
57	0.0073				
59	0.0075	ND			
60	0.068	Outlier,ND			
61	0.0040				
62	0.0070				
65	0.0045	ND			
67	0.010				
70	0.0095	ND			
76	0.019	ND			
77	0.23	Outlier,ND			
80	0.015	ND			
81	0.0064	ND			
82	0.017				
83	0.041	Outlier			
84	0.031	Outlier			
86	0.0074	ND			
89	0.010	ND			
90	0.0075				
91	0.011				
92	0.0020	ND			
93	0.0087				
95	0.050	Outlier,ND			
98	0.023	Outlier			
99	0.00078	ND			
103	0.0080				
105	0.010	ND			

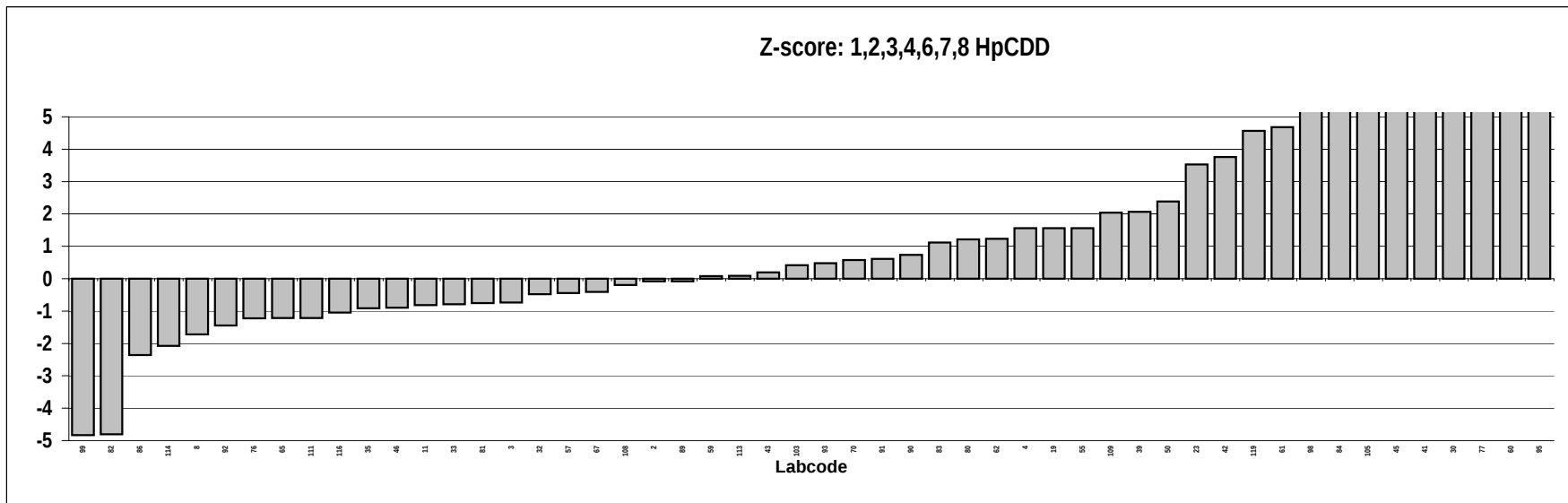
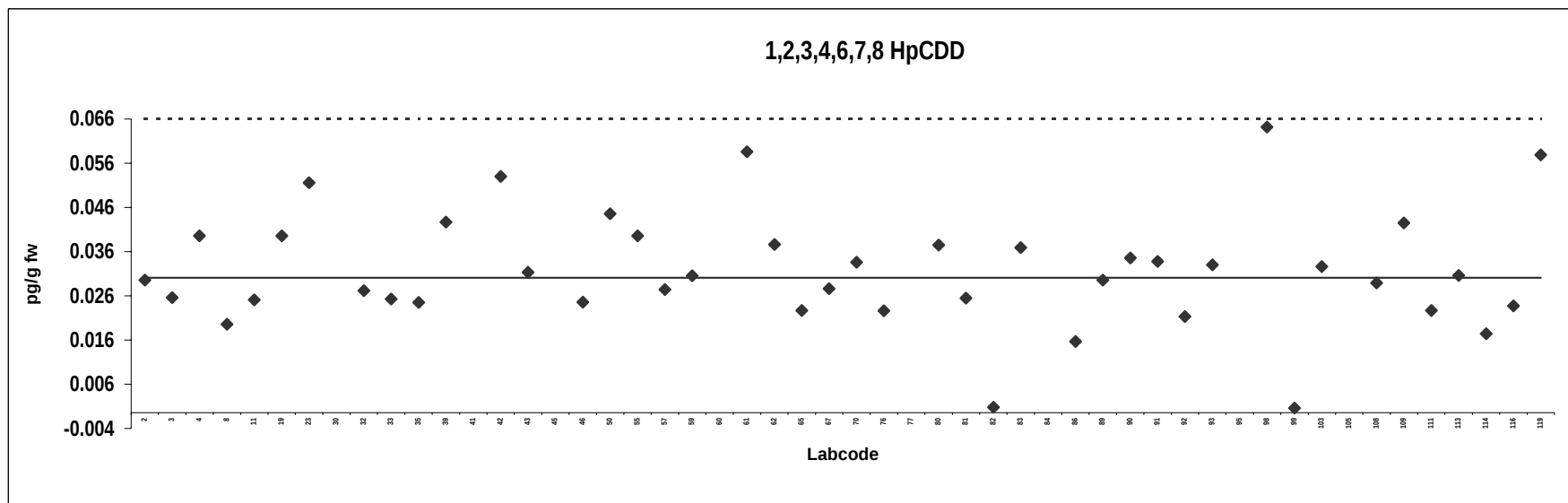
Consensus statistics	
Consensus median, pg/g	0.0078
Median all values pg/g	0.010
Consensus mean, pg/g	0.0084
Standard deviation, pg/g	0.0042
Relative standard deviation, %	50
No. of values reported	52
No. of values removed	14
No. of reported non-detects	26



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	ND	108	0.029	ND
3	0.026	ND	109	0.043	
4	0.040	ND	111	0.023	
8	0.020	ND	113	0.031	
11	0.026		114	0.018	
19	0.040	ND	116	0.024	
23	0.052		119	0.058	
30	0.13	Outlier			
32	0.028				
33	0.026				
35	0.025				
39	0.043				
41	0.11	Outlier			
42	0.053				
43	0.032				
45	0.090	Outlier			
46	0.025				
50	0.045				
55	0.040	ND			
57	0.028				
59	0.031				
60	0.33	Outlier			
61	0.059				
62	0.038				
65	0.023				
67	0.028				
70	0.034				
76	0.023	ND			
77	0.31	Outlier,ND			
80	0.038				
81	0.026				
82	0.0012	ND			
83	0.037				
84	0.079	Outlier			
86	0.016				
89	0.030	ND			
90	0.035				
91	0.034				
92	0.022				
93	0.033				
95	0.80	Outlier			
98	0.065				
99	0.0010	ND			
103	0.033				
105	0.086	Outlier			

Consensus statistics	
Consensus median, pg/g	0.030
Median all values pg/g	0.033
Consensus mean, pg/g	0.032
Standard deviation, pg/g	0.013
Relative standard deviation, %	41
No. of values reported	52
No. of values removed	8
No. of reported non-detects	12



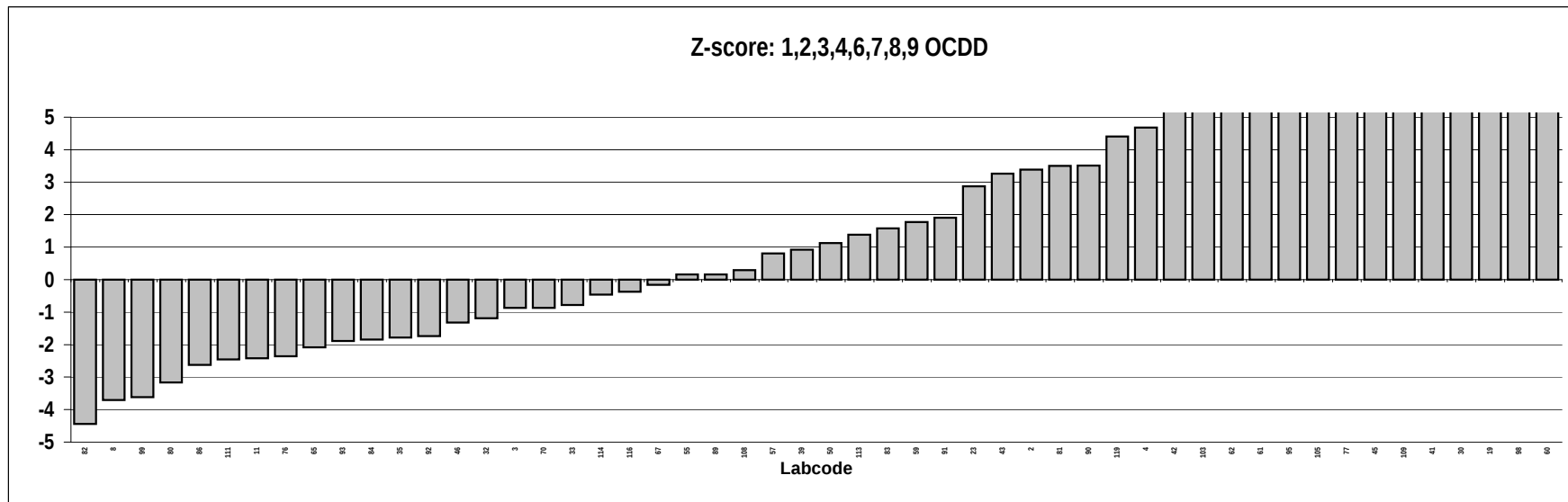
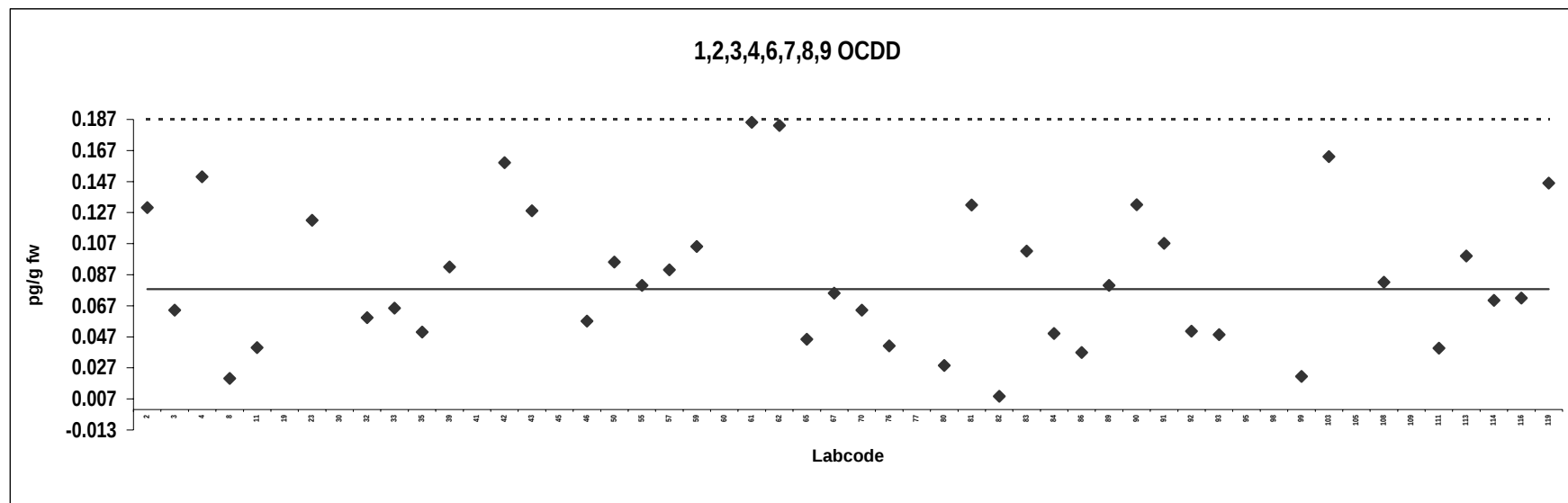
Cheese

Congener: 1,2,3,4,6,7,8,9 OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.13	ND	108	0.082	
3	0.064		109	0.31	Outlier
4	0.15	ND	111	0.040	
8	0.020	ND	113	0.099	
11	0.040		114	0.070	
19	0.57	Outlier,ND	116	0.072	
23	0.12		119	0.15	
30	0.54	Outlier			
32	0.059				
33	0.065				
35	0.050				
39	0.092				
41	0.46	Outlier			
42	0.16				
43	0.13				
45	0.30	Outlier			
46	0.057				
50	0.095				
55	0.080	ND			
57	0.090	ND			
59	0.10				
60	4.6	Outlier			
61	0.19				
62	0.18				
65	0.045				
67	0.075				
70	0.064				
76	0.041	ND			
77	0.29	Outlier,ND			
80	0.028				
81	0.13				
82	0.0086	ND			
83	0.10				
84	0.049				
86	0.037	ND			
89	0.080	ND			
90	0.13				
91	0.11				
92	0.051				
93	0.048				
95	0.20	Outlier,ND			
98	0.92	Outlier			
99	0.021	ND			
103	0.16				
105	0.21	Outlier			

Consensus statistics

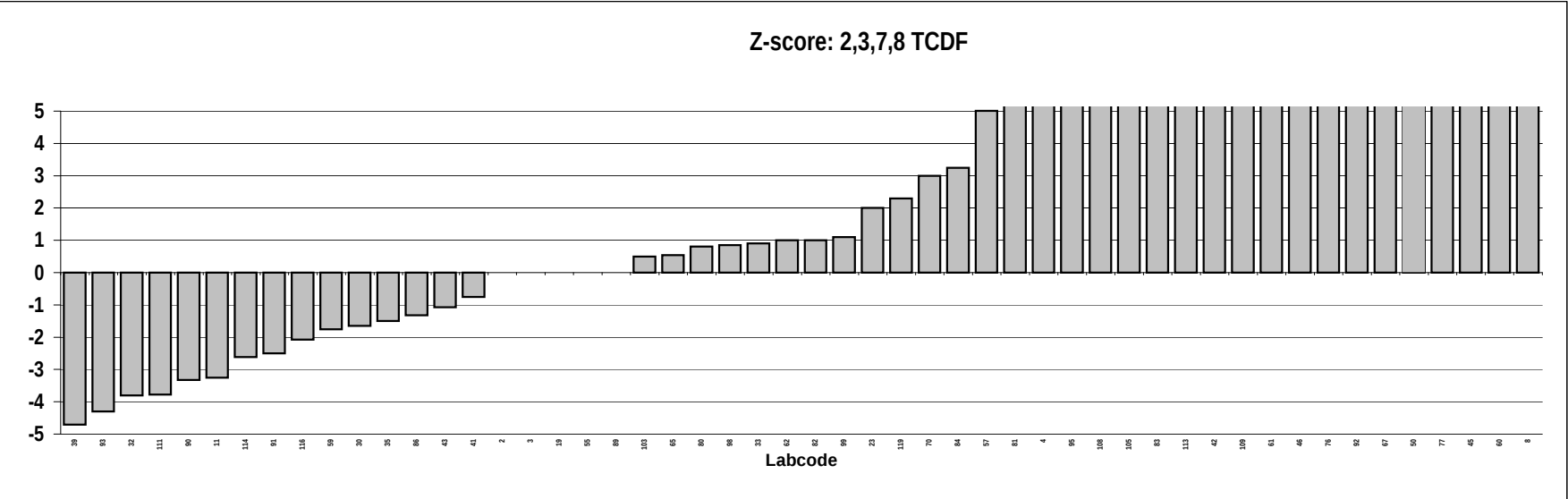
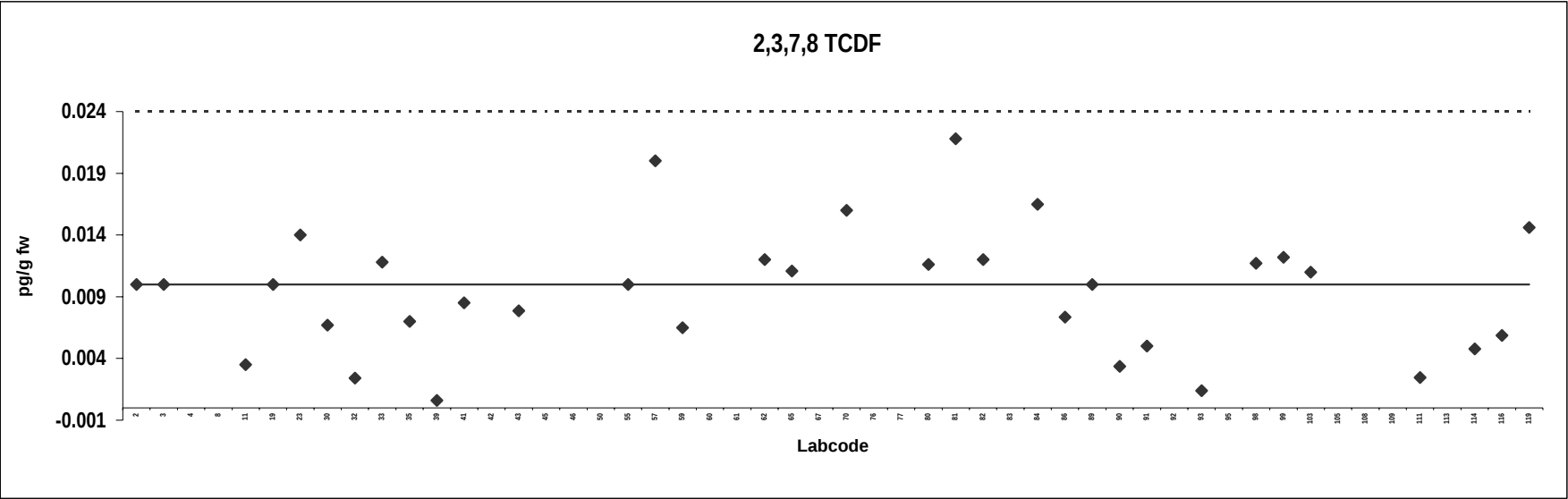
Consensus median, pg/g	0.078
Median all values pg/g	0.093
Consensus mean, pg/g	0.085
Standard deviation, pg/g	0.046
Relative standard deviation, %	54
No. of values reported	52
No. of values removed	10
No. of reported non-detects	13



Cheese
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	108	0.029	Outlier,ND
3	0.010		109	0.042	Outlier
4	0.025	Outlier,ND	111	0.0025	ND
8	0.65	Outlier	113	0.036	Outlier
11	0.0035	ND	114	0.0048	
19	0.010	ND	116	0.0059	
23	0.014		119	0.015	ND
30	0.0067	ND			
32	0.0024				
33	0.012	ND			
35	0.0070				
39	0.00059				
41	0.0085				
42	0.038	Outlier			
43	0.0079				
45	0.31	Outlier			
46	0.051	Outlier			
50	0.13	Outlier			
55	0.010	ND			
57	0.020				
59	0.0065	ND			
60	0.43	Outlier			
61	0.045	Outlier			
62	0.012				
65	0.011				
67	0.091	Outlier			
70	0.016				
76	0.058	Outlier			
77	0.18	Outlier,ND			
80	0.012	ND			
81	0.022				
82	0.012				
83	0.033	Outlier,ND			
84	0.016				
86	0.0074	ND			
89	0.010	ND			
90	0.0034				
91	0.0050	ND			
92	0.062	Outlier			
93	0.0014	ND			
95	0.025	Outlier,ND			
98	0.012				
99	0.012	ND			
103	0.011				
105	0.033	Outlier			

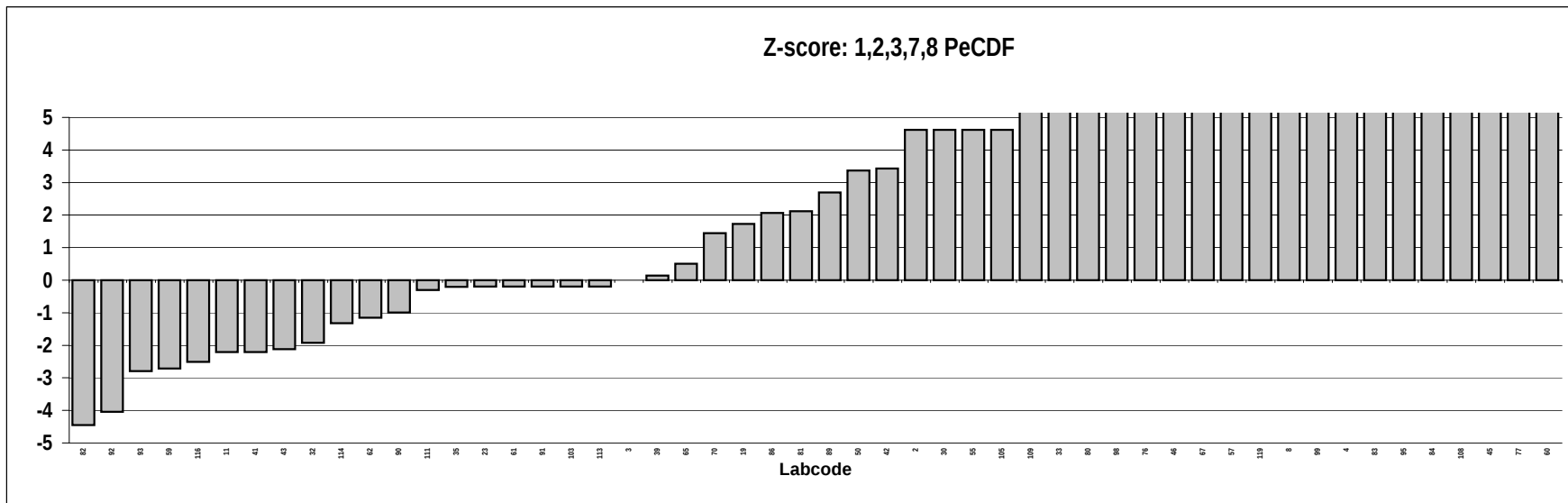
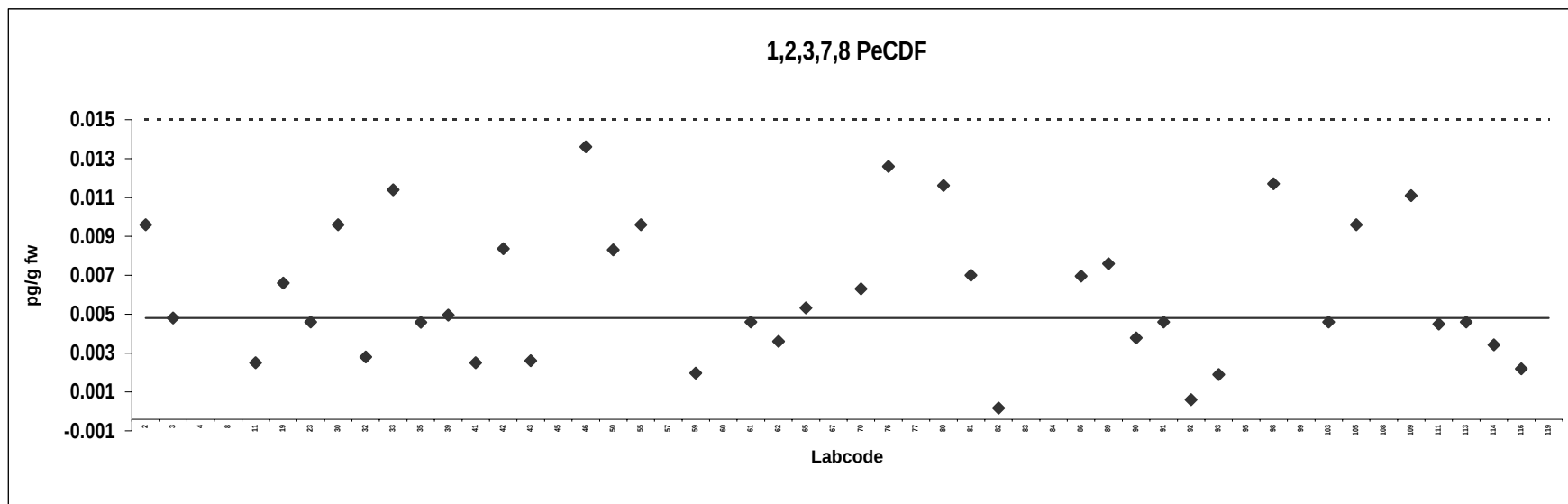
Consensus statistics	
Consensus median, pg/g	0.010
Median all values pg/g	0.012
Consensus mean, pg/g	0.0094
Standard deviation, pg/g	0.0051
Relative standard deviation, %	54
No. of values reported	52
No. of values removed	18
No. of reported non-detects	20



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	108	0.032	Outlier
3	0.0052	ND	109	0.011	
4	0.022	Outlier,ND	111	0.0049	ND
8	0.020	Outlier,ND	113	0.0050	ND
11	0.0029	ND	114	0.0038	
19	0.0070	ND	116	0.0026	
23	0.0050		119	0.019	Outlier
30	0.010	ND			
32	0.0032				
33	0.012	ND			
35	0.0050				
39	0.0054				
41	0.0029	ND			
42	0.0088				
43	0.0030	ND			
45	0.068	Outlier			
46	0.014				
50	0.0087	ND			
55	0.010	ND			
57	0.016	Outlier			
59	0.0024				
60	0.22	Outlier			
61	0.0050				
62	0.0040				
65	0.0057	ND			
67	0.016	Outlier			
70	0.0067				
76	0.013	ND			
77	0.20	Outlier,ND			
80	0.012	ND			
81	0.0074	ND			
82	0.00057	ND			
83	0.024	Outlier,ND			
84	0.028	Outlier			
86	0.0074	ND			
89	0.0080	ND			
90	0.0042				
91	0.0050	ND			
92	0.0010	ND			
93	0.0023	ND			
95	0.025	Outlier,ND			
98	0.012				
99	0.022	Outlier,ND			
103	0.0050				
105	0.010	ND			

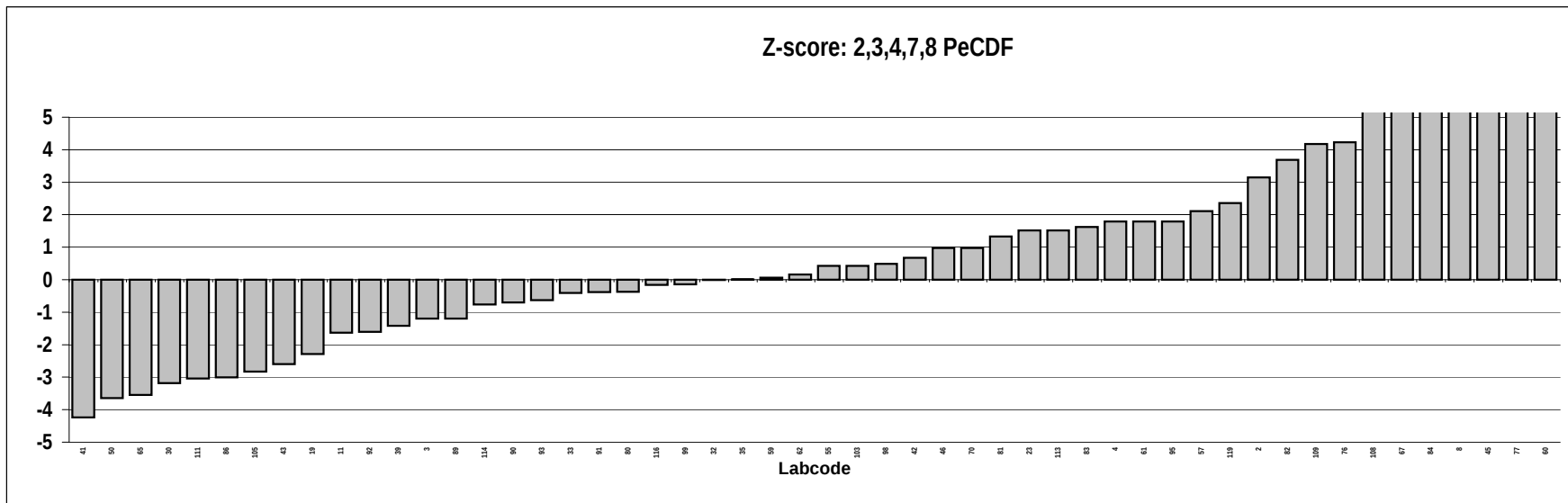
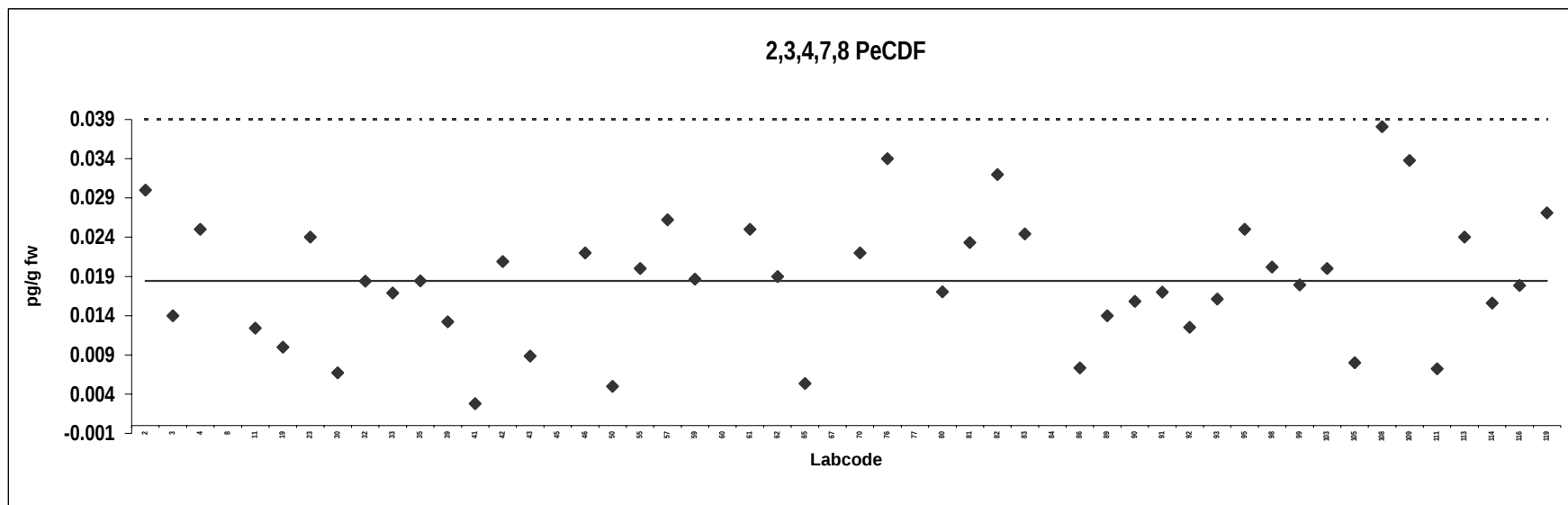
Consensus statistics	
Consensus median, pg/g	0.0052
Median all values pg/g	0.0077
Consensus mean, pg/g	0.0065
Standard deviation, pg/g	0.0036
Relative standard deviation, %	55
No. of values reported	52
No. of values removed	13
No. of reported non-detects	29



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	ND	108	0.038	
3	0.014		109	0.034	
4	0.025	ND	111	0.0072	
8	0.12	Outlier	113	0.024	
11	0.012		114	0.016	
19	0.010		116	0.018	
23	0.024		119	0.027	
30	0.0067	ND			
32	0.018				
33	0.017				
35	0.018				
39	0.013				
41	0.0028	ND			
42	0.021				
43	0.0089				
45	0.17	Outlier			
46	0.022				
50	0.0050				
55	0.020	ND			
57	0.026				
59	0.019				
60	0.56	Outlier			
61	0.025	ND			
62	0.019				
65	0.0054	ND			
67	0.044	Outlier			
70	0.022				
76	0.034	ND			
77	0.19	Outlier,ND			
80	0.017				
81	0.023				
82	0.032				
83	0.024	ND			
84	0.078	Outlier			
86	0.0074	ND			
89	0.014				
90	0.016				
91	0.017				
92	0.013				
93	0.016				
95	0.025	ND			
98	0.020				
99	0.018	ND			
103	0.020				
105	0.0080				

Consensus statistics	
Consensus median, pg/g	0.018
Median all values pg/g	0.020
Consensus mean, pg/g	0.019
Standard deviation, pg/g	0.0082
Relative standard deviation, %	44
No. of values reported	52
No. of values removed	6
No. of reported non-detects	13

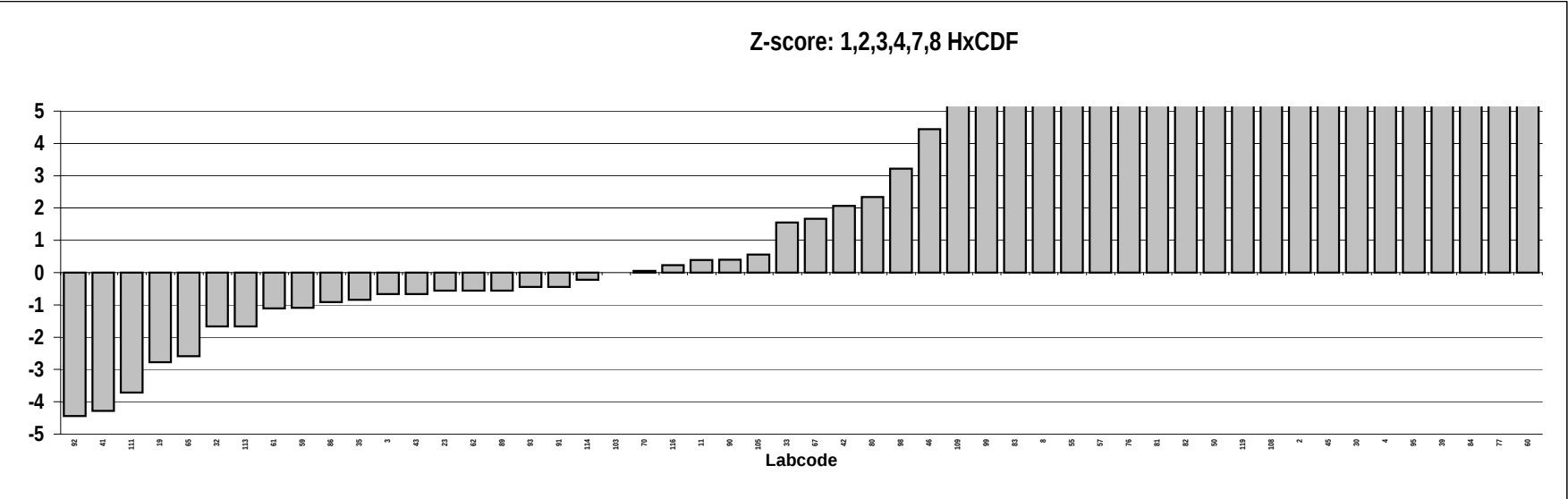
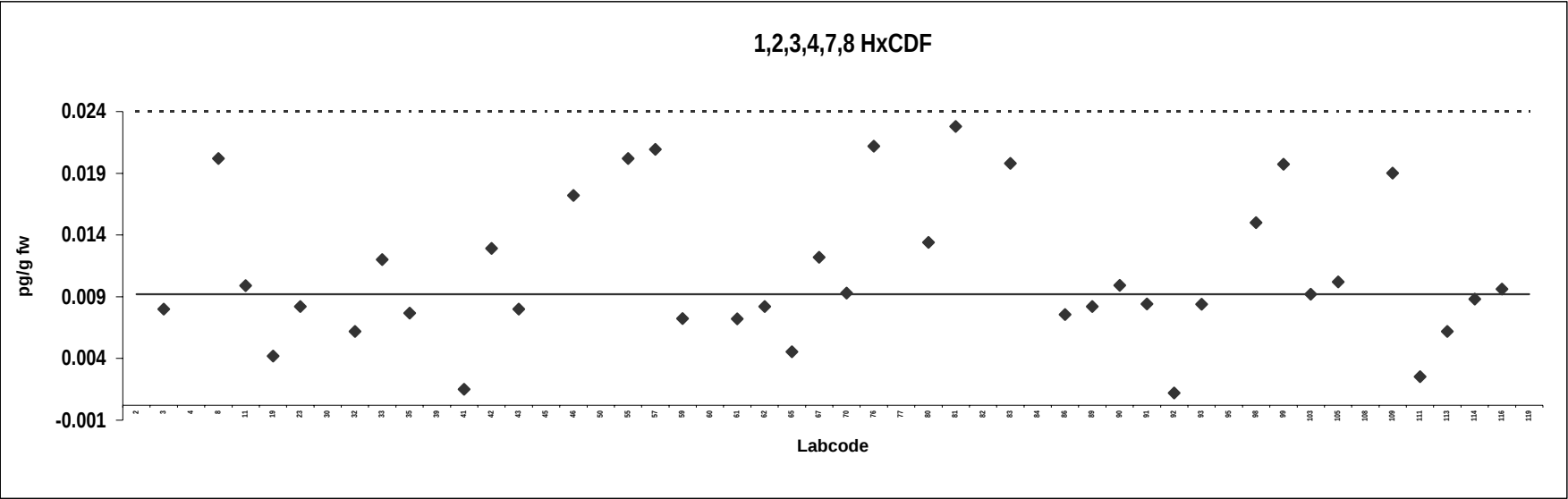


Cheese

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	Outlier,ND	108	0.029	Outlier
3	0.0078	ND	109	0.019	
4	0.037	Outlier,ND	111	0.0023	ND
8	0.020	ND	113	0.0060	
11	0.0097		114	0.0086	
19	0.0040	ND	116	0.0094	
23	0.0080		119	0.027	Outlier
30	0.037	Outlier			
32	0.0060				
33	0.012	ND			
35	0.0075				
39	0.053	Outlier			
41	0.0013	ND			
42	0.013				
43	0.0078				
45	0.036	Outlier			
46	0.017				
50	0.026	Outlier			
55	0.020	ND			
57	0.021				
59	0.0070				
60	0.83	Outlier			
61	0.0070				
62	0.0080				
65	0.0043	ND			
67	0.012				
70	0.0091				
76	0.021	ND			
77	0.23	Outlier,ND			
80	0.013	ND			
81	0.023				
82	0.025	Outlier			
83	0.020	ND			
84	0.10	Outlier			
86	0.0074	ND			
89	0.0080	ND			
90	0.0097				
91	0.0082				
92	0.0010	ND			
93	0.0082				
95	0.050	Outlier,ND			
98	0.015				
99	0.020	ND			
103	0.0090				
105	0.010	ND			

Consensus statistics	
Consensus median, pg/g	0.009
Median all values pg/g	0.012
Consensus mean, pg/g	0.011
Standard deviation, pg/g	0.0059
Relative standard deviation, %	55
No. of values reported	52
No. of values removed	13
No. of reported non-detects	20



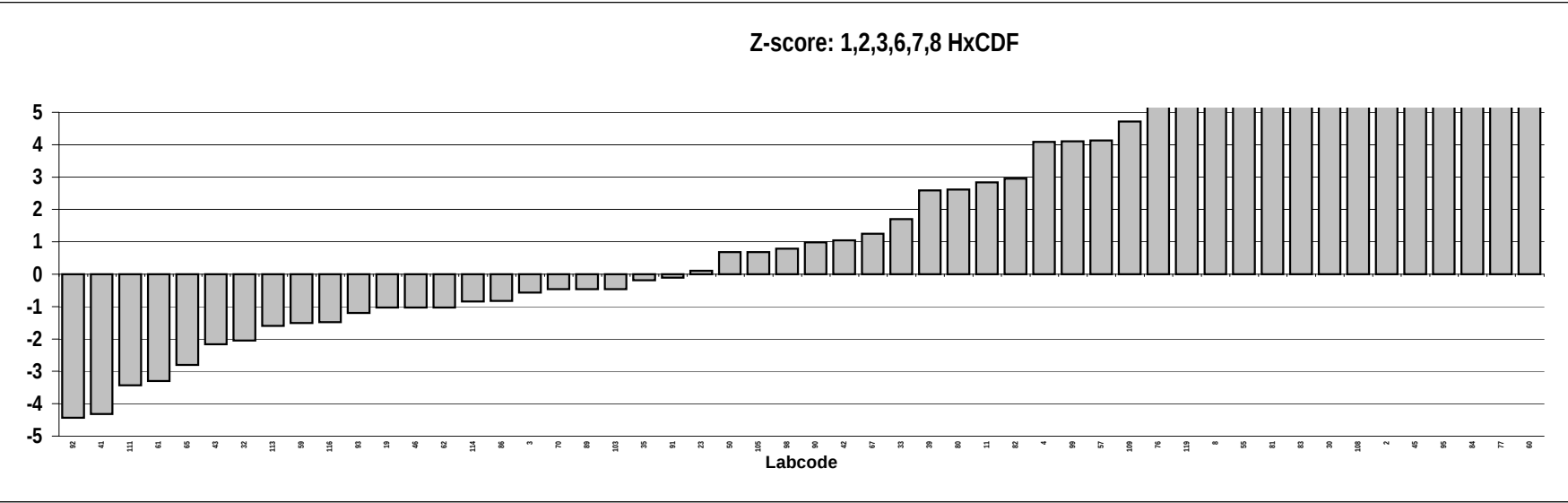
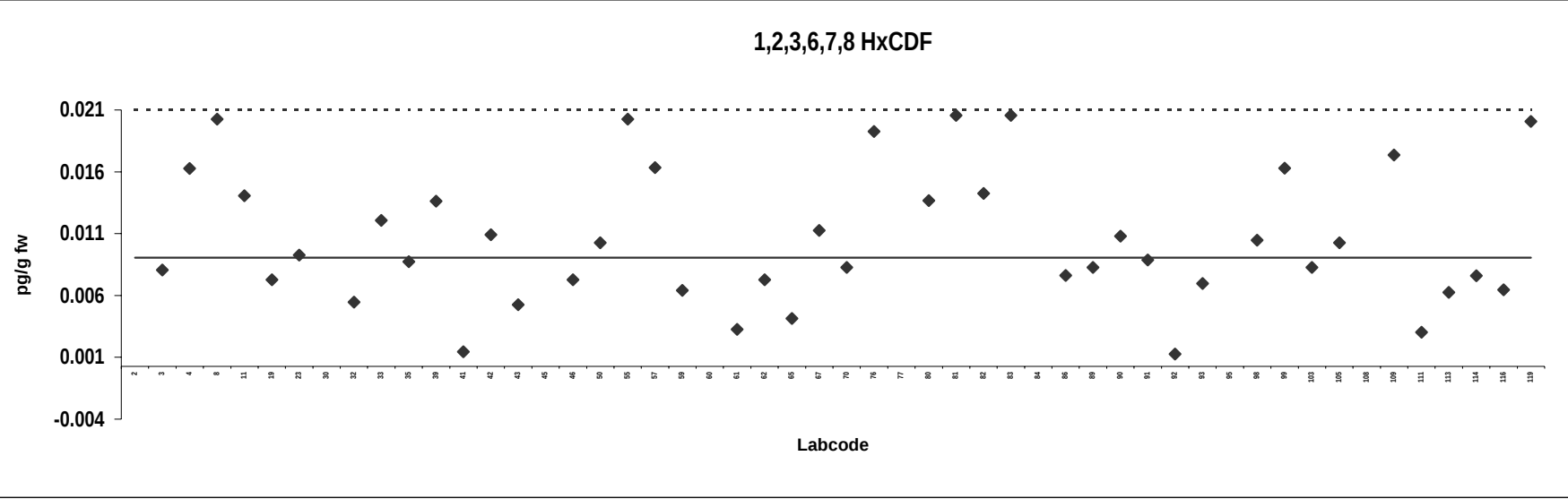
Cheese

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	Outlier,ND	108	0.029	Outlier,ND
3	0.0078	ND	109	0.017	
4	0.016	ND	111	0.0028	
8	0.020	ND	113	0.0060	
11	0.014		114	0.0073	
19	0.0070	ND	116	0.0062	
23	0.0090		119	0.020	
30	0.027	Outlier			
32	0.0052				
33	0.012	ND			
35	0.0085				
39	0.013				
41	0.0012	ND			
42	0.011				
43	0.0050				
45	0.032	Outlier			
46	0.0070				
50	0.010				
55	0.020	ND			
57	0.016				
59	0.0062				
60	0.25	Outlier			
61	0.0030				
62	0.0070				
65	0.0039	ND			
67	0.011				
70	0.0080				
76	0.019	ND			
77	0.23	Outlier,ND			
80	0.013	ND			
81	0.020				
82	0.014				
83	0.020	ND			
84	0.055	Outlier			
86	0.0074	ND			
89	0.0080	ND			
90	0.011				
91	0.0086				
92	0.0010	ND			
93	0.0067				
95	0.050	Outlier,ND			
98	0.010				
99	0.016	ND			
103	0.0080				
105	0.010	ND			

Consensus statistics

Consensus median, pg/g	0.0088
Median all values pg/g	0.010
Consensus mean, pg/g	0.010
Standard deviation, pg/g	0.0054
Relative standard deviation, %	53
No. of values reported	52
No. of values removed	8
No. of reported non-detects	20

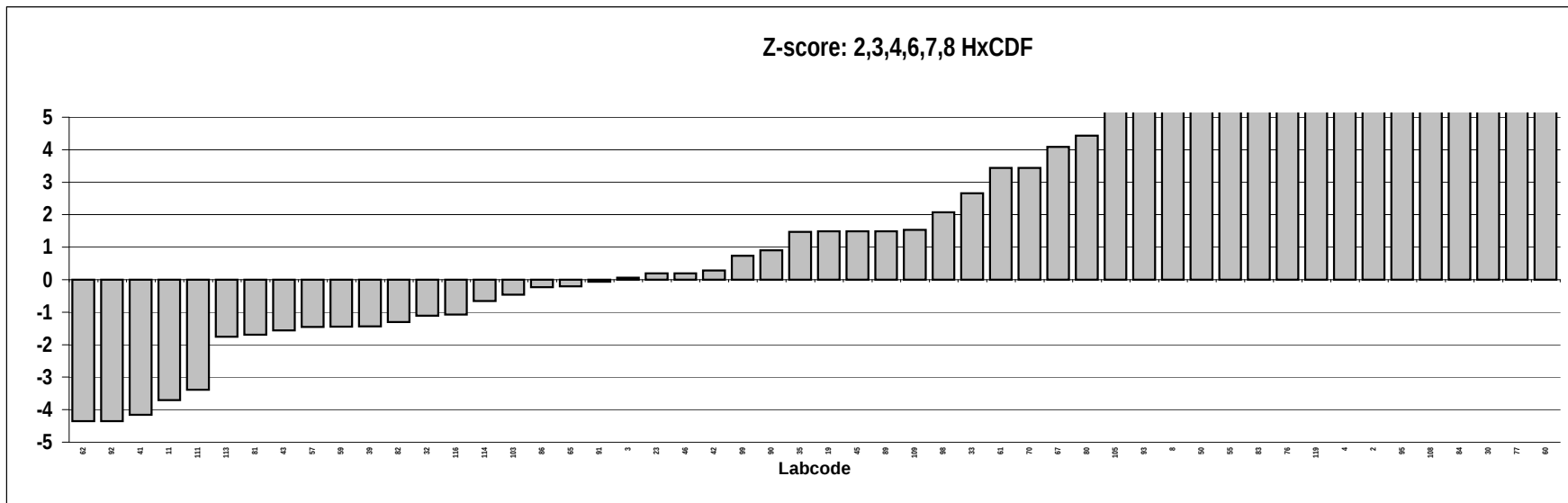
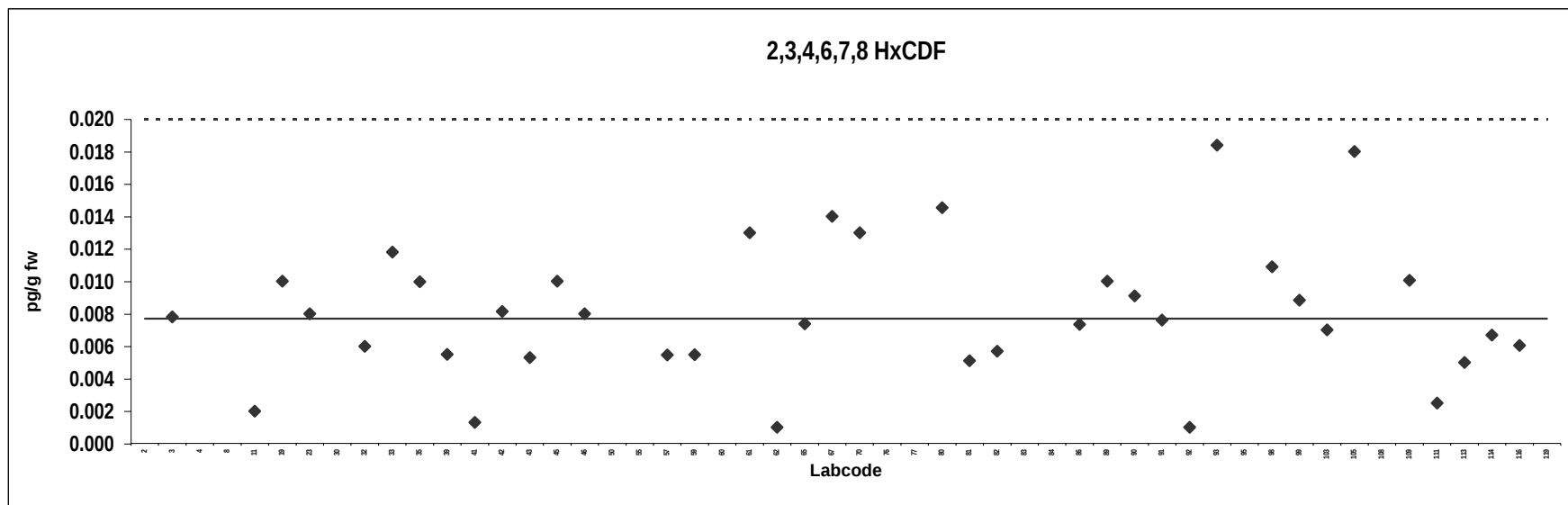


Cheese

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	Outlier,ND	108	0.056	Outlier
3	0.0078	ND	109	0.010	
4	0.028	Outlier,ND	111	0.0025	ND
8	0.020	Outlier,ND	113	0.0050	ND
11	0.0020	ND	114	0.0067	
19	0.010	ND	116	0.0061	
23	0.0080		119	0.026	Outlier
30	0.11	Outlier			
32	0.0060				
33	0.012	ND			
35	0.010				
39	0.0055				
41	0.0013	ND			
42	0.0081				
43	0.0053				
45	0.010				
46	0.0080				
50	0.020	Outlier			
55	0.020	Outlier,ND			
57	0.0055				
59	0.0055	ND			
60	0.25	Outlier			
61	0.013				
62	0.0010	ND			
65	0.0074				
67	0.014				
70	0.013				
76	0.026	Outlier,ND			
77	0.21	Outlier,ND			
80	0.015	ND			
81	0.0051	ND			
82	0.0057				
83	0.021	Outlier,ND			
84	0.065	Outlier			
86	0.0074	ND			
89	0.010	ND			
90	0.0091				
91	0.0076				
92	0.0010	ND			
93	0.018				
95	0.050	Outlier,ND			
98	0.011				
99	0.0088	ND			
103	0.0070				
105	0.018				

Consensus statistics	
Consensus median, pg/g	0.0077
Median all values pg/g	0.010
Consensus mean, pg/g	0.0081
Standard deviation, pg/g	0.0042
Relative standard deviation, %	52
No. of values reported	52
No. of values removed	14
No. of reported non-detects	23



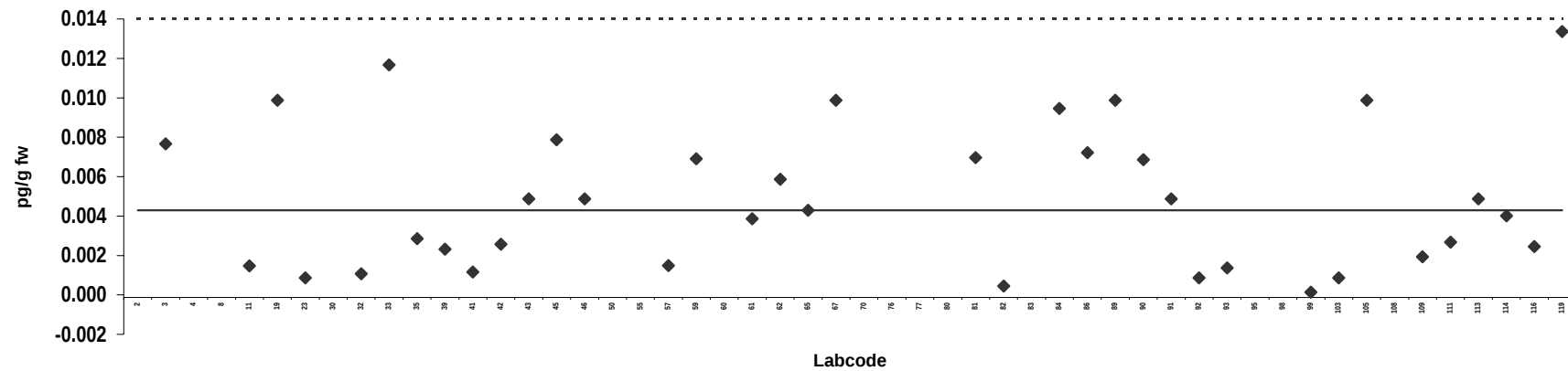
Cheese

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

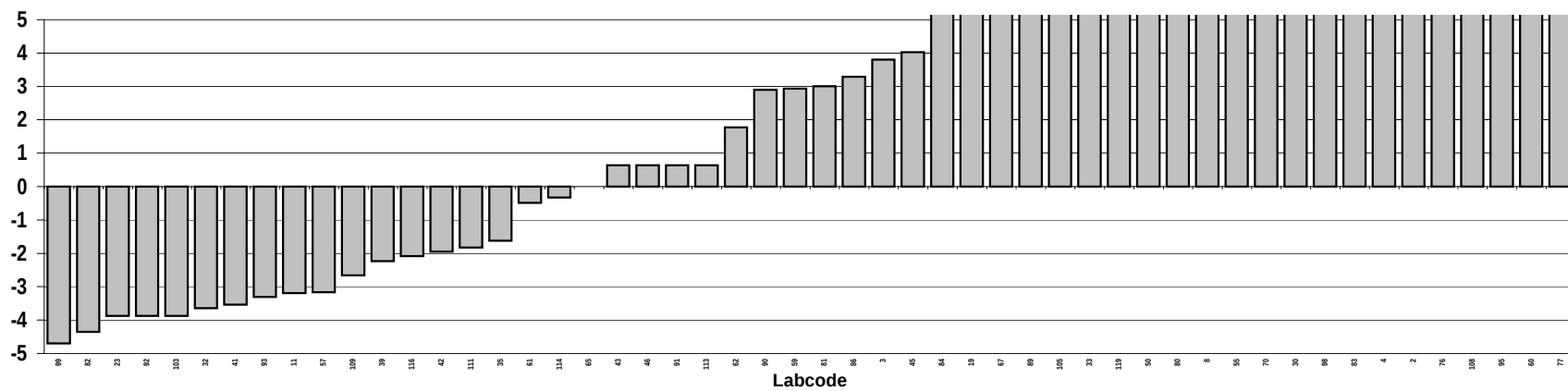
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	Outlier,ND	108	0.032	Outlier
3	0.0078	ND	109	0.0021	ND
4	0.029	Outlier,ND	111	0.0028	ND
8	0.020	Outlier,ND	113	0.0050	ND
11	0.0016	ND	114	0.0041	
19	0.010	ND	116	0.0026	
23	0.0010		119	0.014	
30	0.023	Outlier			
32	0.0012				
33	0.012	ND			
35	0.0030				
39	0.0025	ND			
41	0.0013	ND			
42	0.0027	ND			
43	0.0050	ND			
45	0.0080				
46	0.0050				
50	0.015	Outlier			
55	0.020	Outlier,ND			
57	0.0016	ND			
59	0.0070	ND			
60	0.099	Outlier			
61	0.0040				
62	0.0060				
65	0.0044	ND			
67	0.010	ND			
70	0.020	Outlier,ND			
76	0.030	Outlier,ND			
77	0.25	Outlier,ND			
80	0.018	Outlier,ND			
81	0.0071	ND			
82	0.00057	ND			
83	0.026	Outlier,ND			
84	0.0096				
86	0.0074	ND			
89	0.010	ND			
90	0.0070	ND			
91	0.0050	ND			
92	0.0010	ND			
93	0.0015	ND			
95	0.050	Outlier,ND			
98	0.025	Outlier			
99	0.00027	ND			
103	0.0010	ND			
105	0.010	ND			

Consensus statistics	
Consensus median, pg/g	0.0044
Median all values pg/g	0.0071
Consensus mean, pg/g	0.0050
Standard deviation, pg/g	0.0036
Relative standard deviation, %	72
No. of values reported	52
No. of values removed	15
No. of reported non-detects	36

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



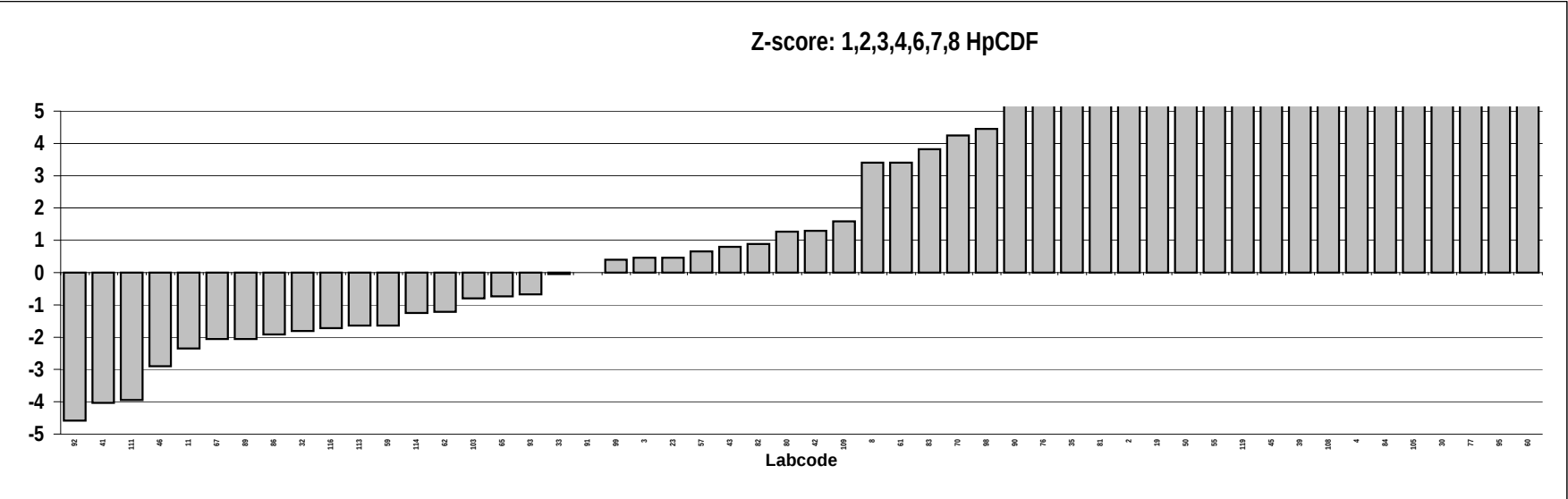
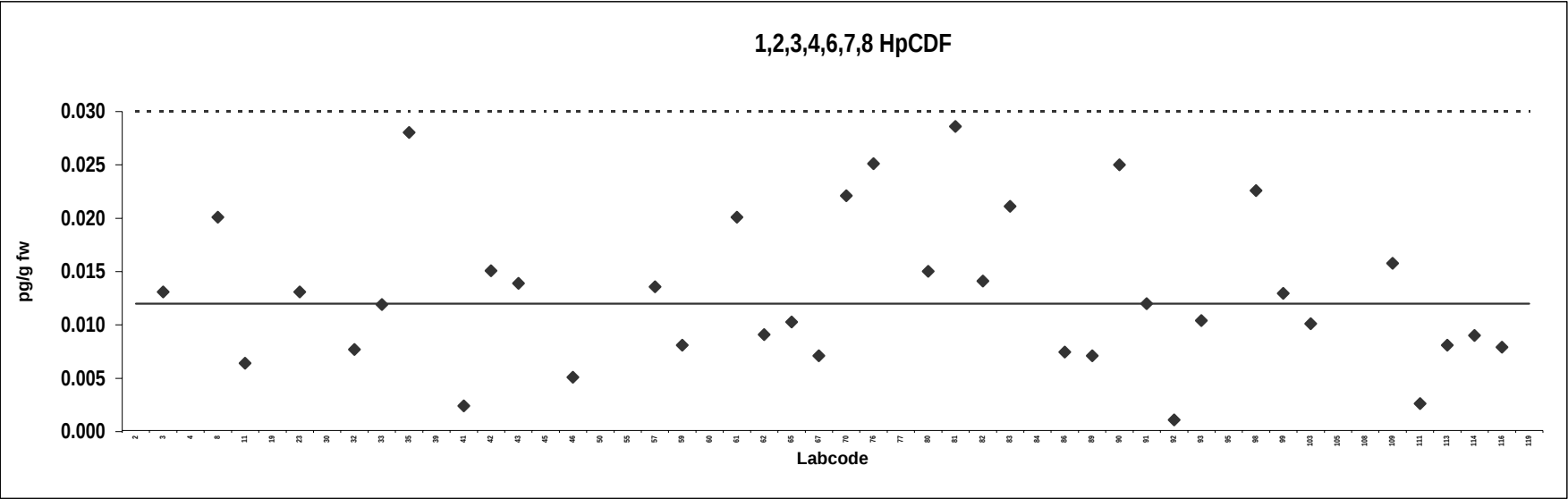
Z-score: 1,2,3,7,8,9 HxCDF



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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	Outlier,ND	108	0.070	Outlier
3	0.013	ND	109	0.016	
4	0.079	Outlier,ND	111	0.0025	ND
8	0.020	ND	113	0.0080	
11	0.0063		114	0.0089	
19	0.030	Outlier,ND	116	0.0078	
23	0.013		119	0.050	Outlier
30	0.18	Outlier			
32	0.0076				
33	0.012	ND			
35	0.028				
39	0.070	Outlier			
41	0.0023	ND			
42	0.015				
43	0.014				
45	0.062	Outlier			
46	0.0050				
50	0.033	Outlier			
55	0.040	Outlier,ND			
57	0.013				
59	0.0080				
60	4.5	Outlier			
61	0.020				
62	0.0090				
65	0.010				
67	0.0070				
70	0.022	ND			
76	0.025	ND			
77	0.19	Outlier,ND			
80	0.015				
81	0.029				
82	0.014				
83	0.021				
84	0.10	Outlier			
86	0.0074	ND			
89	0.0070	ND			
90	0.025				
91	0.012				
92	0.0010	ND			
93	0.010				
95	0.37	Outlier			
98	0.023				
99	0.013	ND			
103	0.010				
105	0.10	Outlier			

Consensus statistics	
Consensus median, pg/g	0.012
Median all values pg/g	0.015
Consensus mean, pg/g	0.013
Standard deviation, pg/g	0.0072
Relative standard deviation, %	55
No. of values reported	52
No. of values removed	15
No. of reported non-detects	16

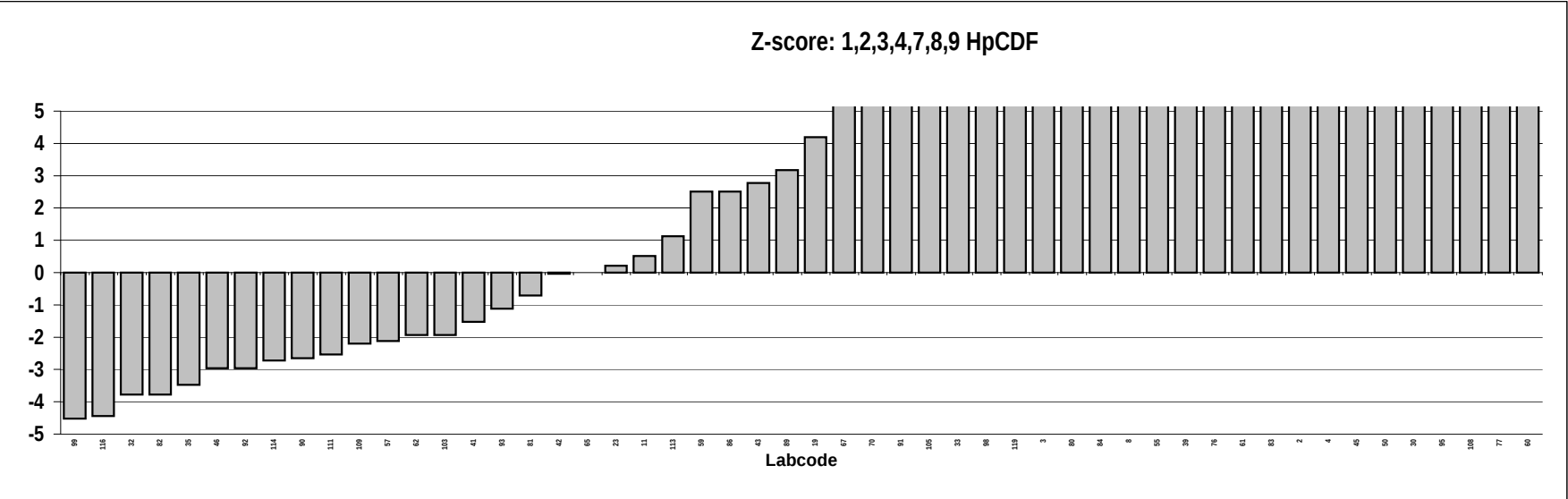
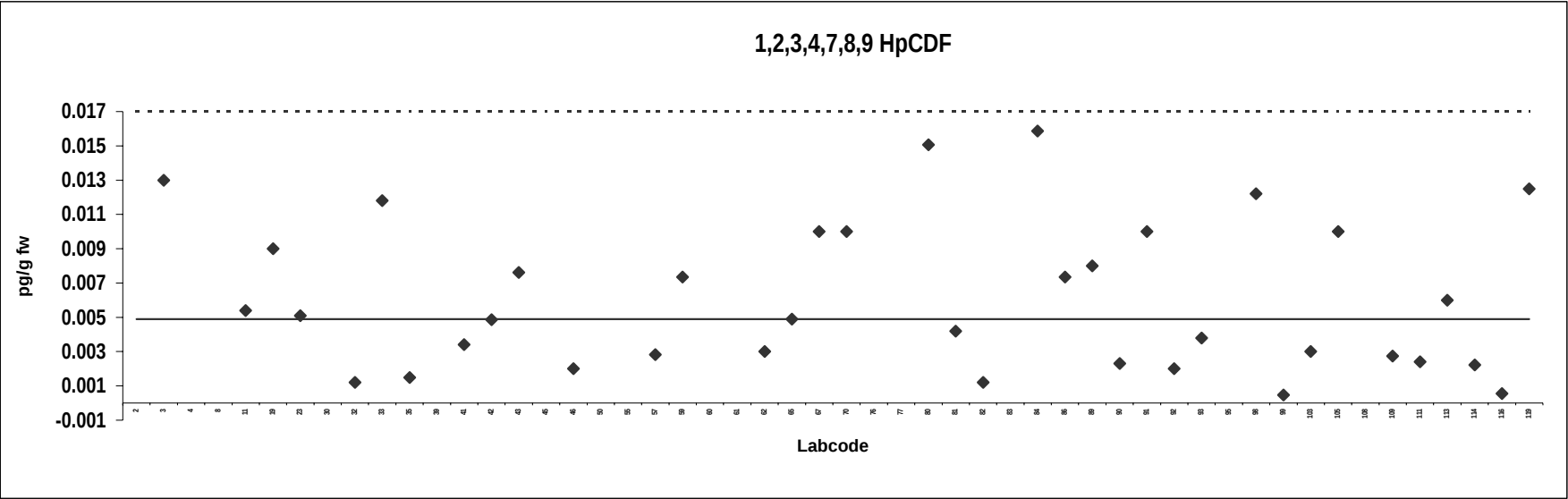


Cheese

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

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	Outlier,ND	108	0.10	Outlier
3	0.013	ND	109	0.0027	
4	0.031	Outlier,ND	111	0.0024	ND
8	0.020	Outlier,ND	113	0.0060	ND
11	0.0054	ND	114	0.0022	ND
19	0.0090	ND	116	0.00054	ND
23	0.0051	ND	119	0.013	
30	0.063	Outlier			
32	0.0012				
33	0.012	ND			
35	0.0015				
39	0.021	Outlier			
41	0.0034	ND			
42	0.0049	ND			
43	0.0076				
45	0.036	Outlier			
46	0.0020	ND			
50	0.045	Outlier			
55	0.020	Outlier,ND			
57	0.0028				
59	0.0073	ND			
60	0.50	Outlier			
61	0.026	Outlier			
62	0.0030	ND			
65	0.0049	ND			
67	0.010	ND			
70	0.010	ND			
76	0.024	Outlier,ND			
77	0.20	Outlier,ND			
80	0.015	ND			
81	0.0042	ND			
82	0.0012	ND			
83	0.029	Outlier,ND			
84	0.016				
86	0.0074	ND			
89	0.0080	ND			
90	0.0023	ND			
91	0.010	ND			
92	0.0020	ND			
93	0.0038	ND			
95	0.10	Outlier,ND			
98	0.012				
99	0.00047	ND			
103	0.0030	ND			
105	0.010	ND			

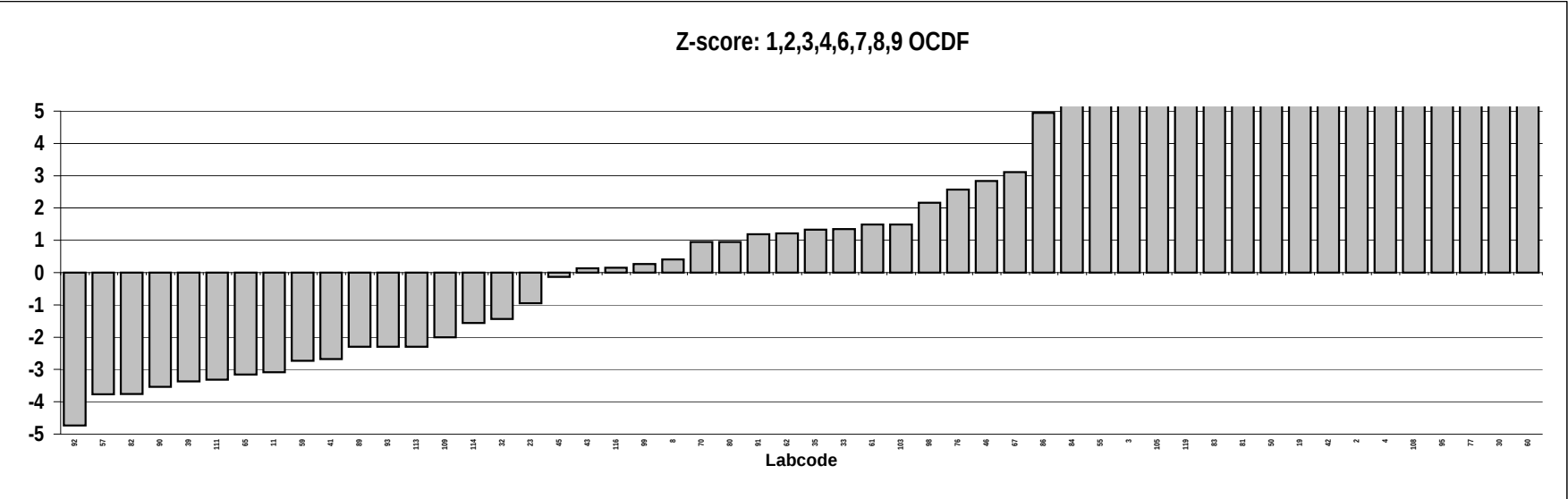
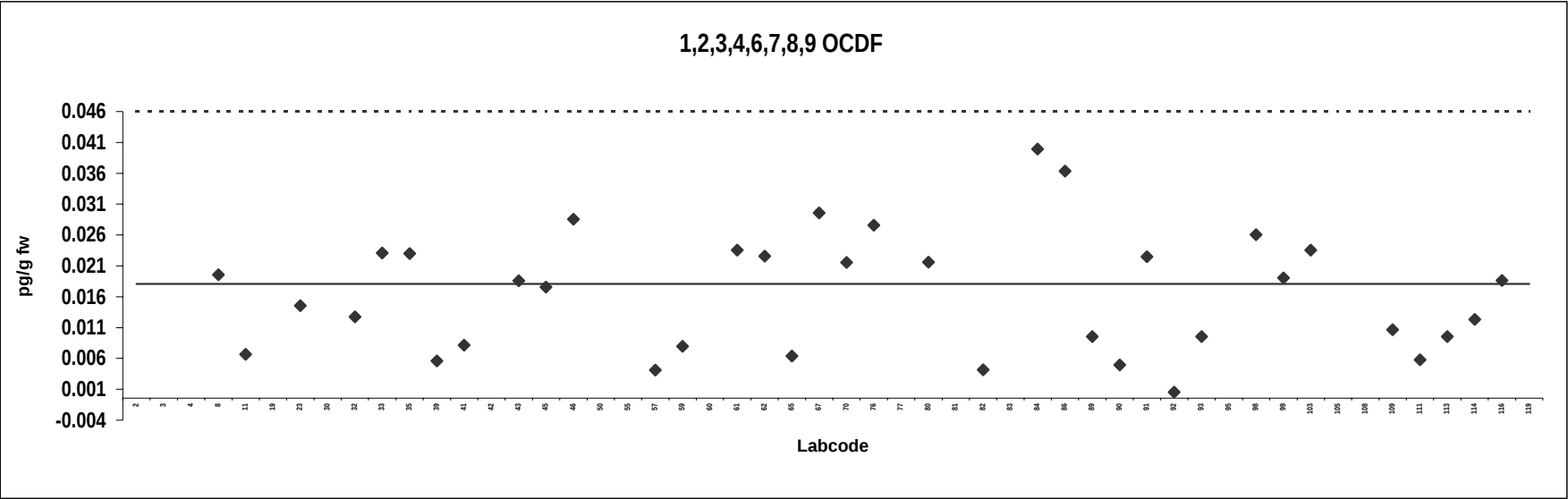
Consensus statistics	
Consensus median, pg/g	0.0049
Median all values pg/g	0.0085
Consensus mean, pg/g	0.0061
Standard deviation, pg/g	0.0044
Relative standard deviation, %	72
No. of values reported	52
No. of values removed	15
No. of reported non-detects	37



Cheese
Congener: 1,2,3,4,6,7,8,9 OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.13	Outlier,ND	108	0.18	Outlier
3	0.052	Outlier,ND	109	0.011	
4	0.16	Outlier,ND	111	0.0062	ND
8	0.020	ND	113	0.010	ND
11	0.0071	ND	114	0.013	
19	0.10	Outlier,ND	116	0.019	
23	0.015		119	0.068	Outlier
30	0.33	Outlier			
32	0.013				
33	0.024	ND			
35	0.023				
39	0.0060	ND			
41	0.0086	ND			
42	0.10	Outlier			
43	0.019				
45	0.018				
46	0.029				
50	0.097	Outlier			
55	0.050	Outlier,ND			
57	0.0045				
59	0.0084	ND			
60	8.4	Outlier			
61	0.024				
62	0.023				
65	0.0068	ND			
67	0.030	ND			
70	0.022	ND			
76	0.028	ND			
77	0.21	Outlier,ND			
80	0.022				
81	0.074	Outlier			
82	0.0046	ND			
83	0.069	Outlier,ND			
84	0.040				
86	0.037	ND			
89	0.010	ND			
90	0.0054				
91	0.023				
92	0.0010	ND			
93	0.010				
95	0.20	Outlier,ND			
98	0.027				
99	0.020	ND			
103	0.024				
105	0.060	Outlier			

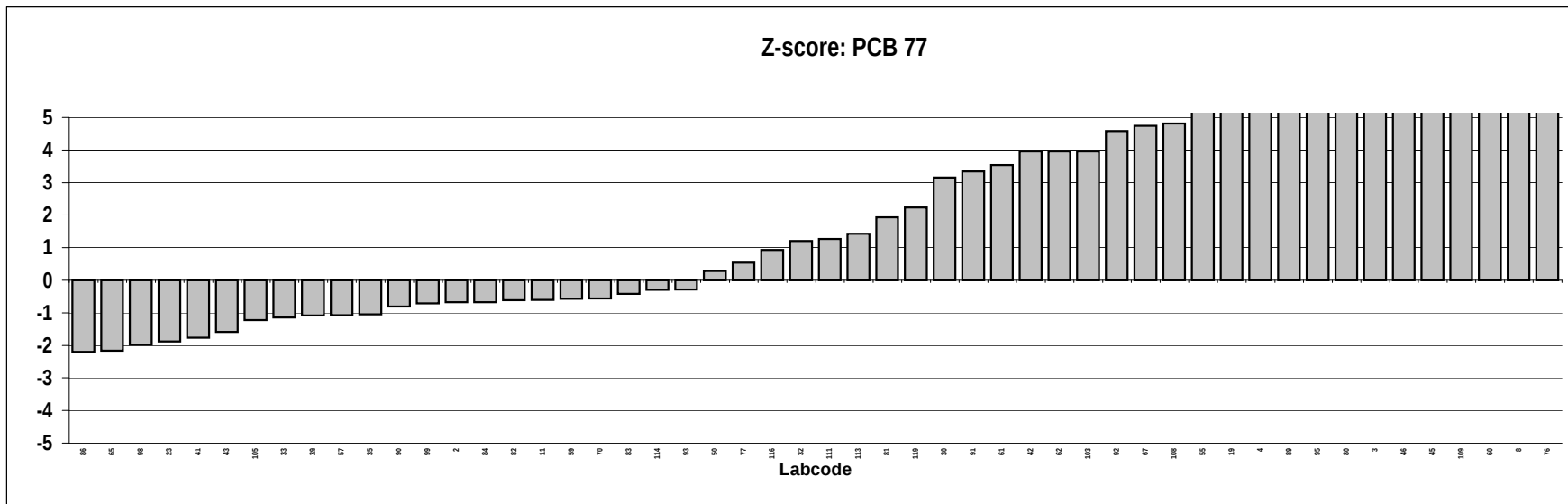
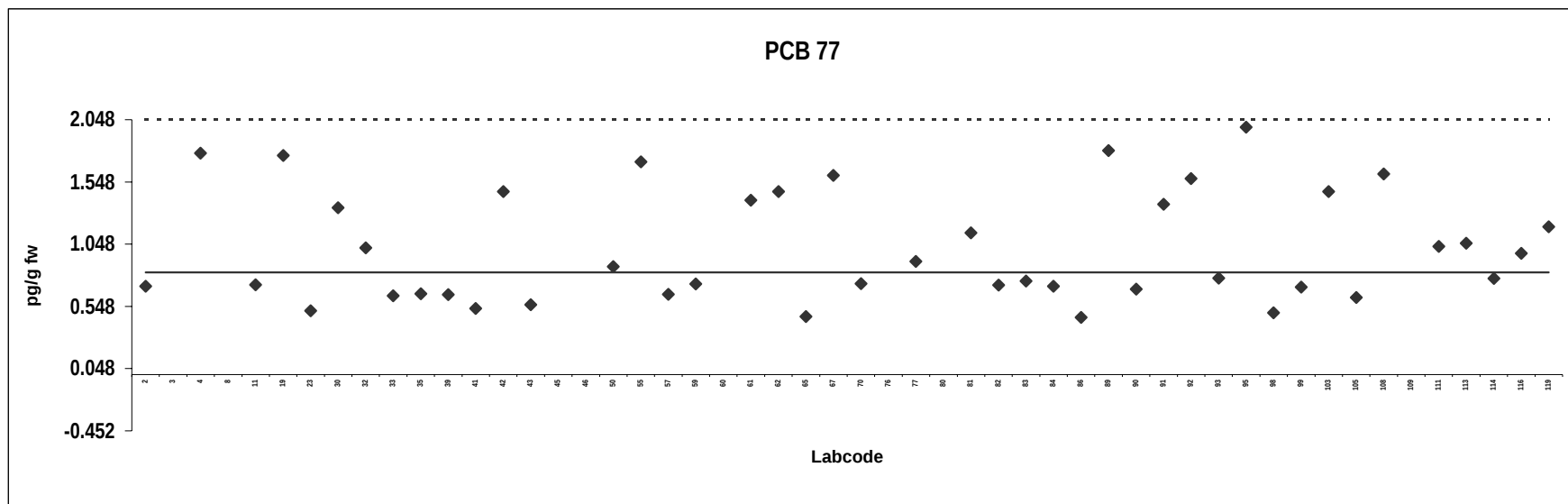
Consensus statistics	
Consensus median, pg/g	0.019
Median all values pg/g	0.023
Consensus mean, pg/g	0.017
Standard deviation, pg/g	0.0097
Relative standard deviation, %	57
No. of values reported	52
No. of values removed	16
No. of reported non-detects	25



Cheese
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.71		108	1.6	
3	3.0	Outlier	109	5.0	Outlier
4	1.8		111	1.0	
8	22	Outlier	113	1.1	
11	0.72		114	0.77	
19	1.8	ND	116	0.97	
23	0.51		119	1.2	
30	1.3				
32	1.0				
33	0.63				
35	0.65				
39	0.64				
41	0.53				
42	1.5				
43	0.56				
45	4.4	Outlier			
46	4.3	Outlier			
50	0.87				
55	1.7				
57	0.65				
59	0.73				
60	10	Outlier			
61	1.4				
62	1.5				
65	0.47				
67	1.6				
70	0.73	ND			
76	27	Outlier			
77	0.91	ND			
80	2.2	Outlier			
81	1.1				
82	0.72				
83	0.75				
84	0.71				
86	0.46				
89	1.8				
90	0.69				
91	1.4				
92	1.6				
93	0.78				
95	2.0				
98	0.50				
99	0.70				
103	1.5				
105	0.62				

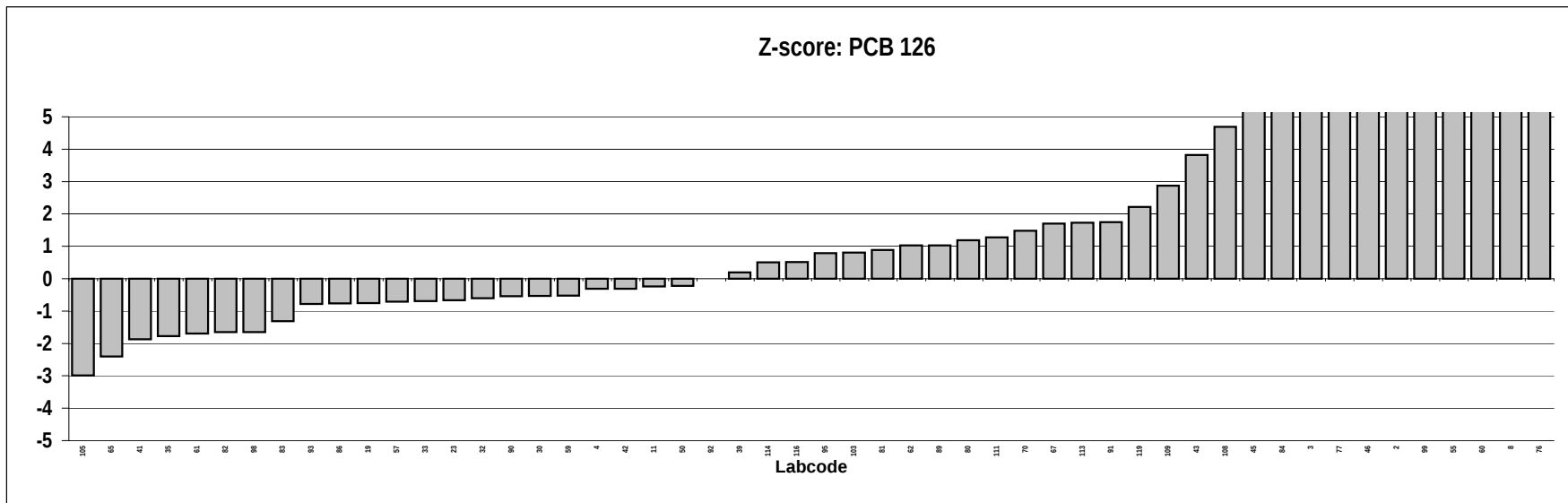
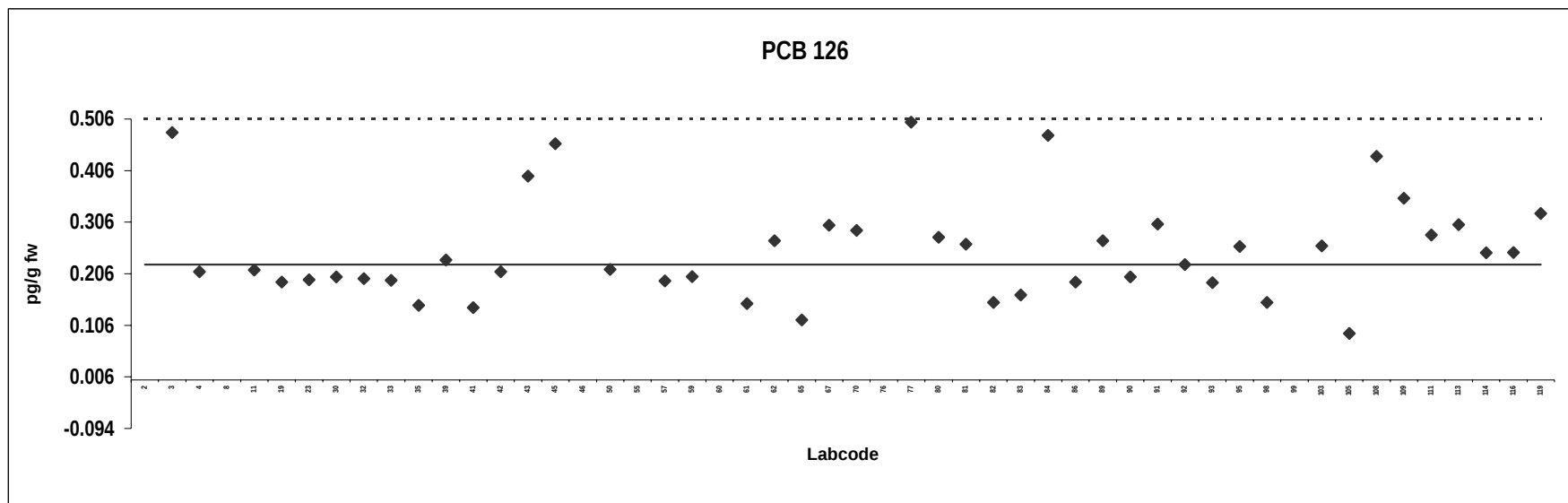
Consensus statistics	
Consensus median, pg/g	0.82
Median all values pg/g	1.0
Consensus mean, pg/g	1.0
Standard deviation, pg/g	0.44
Relative standard deviation, %	44
No. of values reported	52
No. of values removed	8
No. of reported non-detects	3



Cheese
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.58	Outlier	108	0.43	
3	0.48		109	0.35	
4	0.21		111	0.28	
8	3.6	Outlier	113	0.30	
11	0.21		114	0.25	
19	0.19	ND	116	0.25	
23	0.19		119	0.32	
30	0.20				
32	0.20				
33	0.19				
35	0.14				
39	0.23				
41	0.14				
42	0.21				
43	0.40				
45	0.46				
46	0.52	Outlier			
50	0.21				
55	1.0	Outlier,ND			
57	0.19				
59	0.20				
60	3.4	Outlier			
61	0.15				
62	0.27				
65	0.12				
67	0.30				
70	0.29	ND			
76	10	Outlier			
77	0.50	ND			
80	0.28				
81	0.26				
82	0.15				
83	0.17				
84	0.47				
86	0.19				
89	0.27				
90	0.20				
91	0.30				
92	0.22				
93	0.19				
95	0.26				
98	0.15				
99	0.79	Outlier			
103	0.26				
105	0.090				

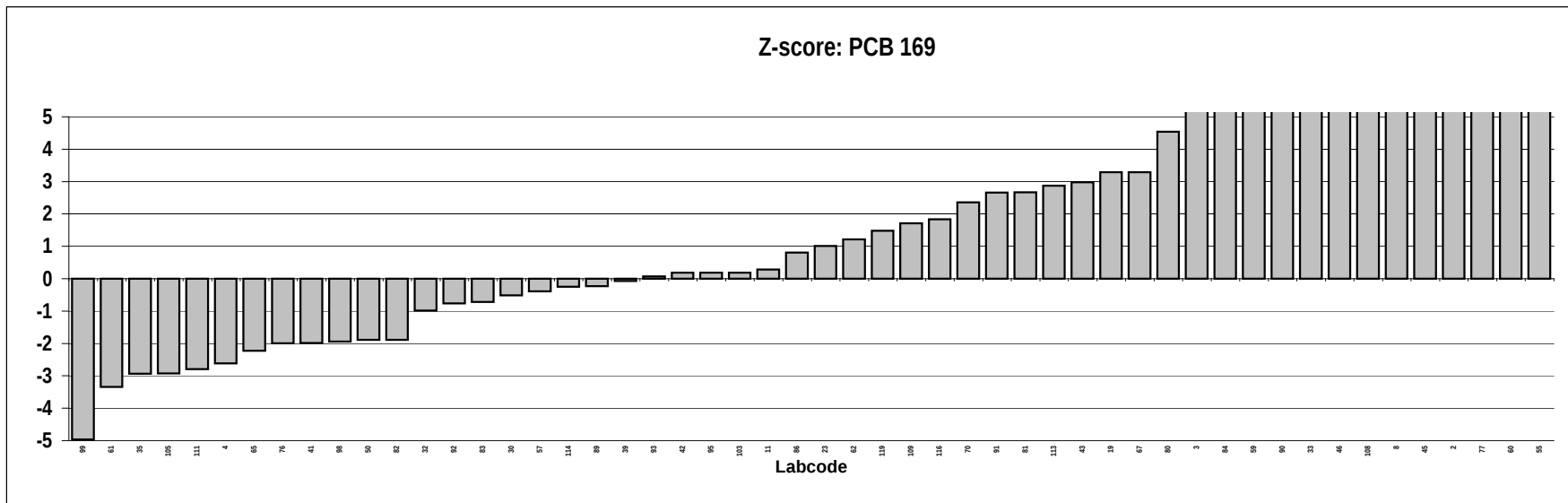
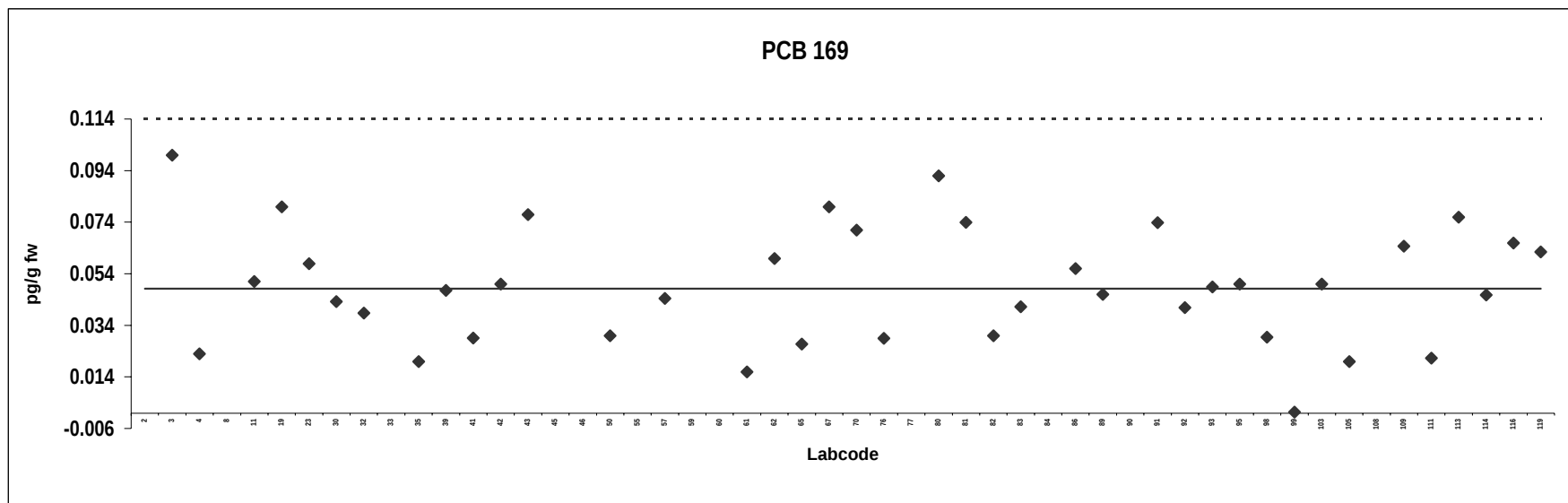
Consensus statistics	
Consensus median, pg/g	0.22
Median all values pg/g	0.25
Consensus mean, pg/g	0.25
Standard deviation, pg/g	0.099
Relative standard deviation, %	39
No. of values reported	52
No. of values removed	7
No. of reported non-detects	4



Cheese
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.39	Outlier	108	0.26	Outlier
3	0.10	ND	109	0.065	
4	0.023	ND	111	0.021	
8	0.28	Outlier	113	0.076	
11	0.051		114	0.046	
19	0.080	ND	116	0.066	
23	0.058		119	0.063	
30	0.043				
32	0.039				
33	0.15	Outlier,ND			
35	0.020				
39	0.048				
41	0.029				
42	0.050				
43	0.077				
45	0.39	Outlier			
46	0.21	Outlier			
50	0.030				
55	1.0	Outlier,ND			
57	0.044				
59	0.13	Outlier,ND			
60	0.93	Outlier			
61	0.016				
62	0.060				
65	0.027				
67	0.080				
70	0.071				
76	0.029	ND			
77	0.49	Outlier,ND			
80	0.092	ND			
81	0.074				
82	0.030				
83	0.041	ND			
84	0.13	Outlier			
86	0.056				
89	0.046				
90	0.15	Outlier			
91	0.074				
92	0.041				
93	0.049	ND			
95	0.050	ND			
98	0.030				
99	0.00036	ND			
103	0.050				
105	0.020				

Consensus statistics	
Consensus median, pg/g	0.048
Median all values pg/g	0.057
Consensus mean, pg/g	0.049
Standard deviation, pg/g	0.023
Relative standard deviation, %	46
No. of values reported	52
No. of values removed	12
No. of reported non-detects	13



Cheese
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.15	Outlier	108	0.041	Outlier
3	0.24	Outlier	109	0.26	
4	0.079		111	0.067	
8	0.80	Outlier	113	0.054	
11	0.057	ND	114	0.031	
19	0.090	ND	116	0.066	
23	0.037		119	0.063	
30	0.043				
32	0.026				
33	0.15	Outlier,ND			
35	0.045				
39	0.056				
41	0.038				
42	0.11				
43	0.050	ND			
45	0.078				
46	0.31	Outlier			
50	0.025				
55	1.0	Outlier,ND			
57	0.036				
59	0.30	Outlier,ND			
60	0.30	Outlier			
61	0.068				
62	0.080				
65	0.031				
67	0.10				
70	0.045	ND			
76	0.027	ND			
77	0.94	Outlier,ND			
80	0.12				
81	0.080				
82	0.051				
83	0.056	ND			
84	0.24	Outlier			
86	0.057				
89	0.083				
90	0.051				
91	0.077				
92	0.066				
93	0.040	ND			
95	0.050	ND			
98	0.019				
99	0.035				
103	0.070				
105	0.10	ND			

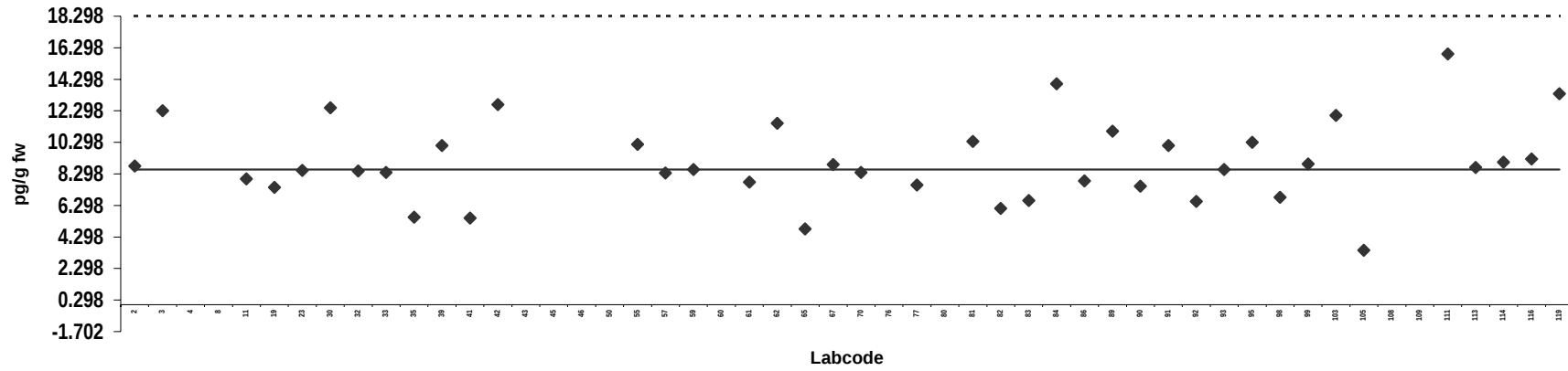
Consensus statistics	
Consensus median, pg/g	0.056
Median all values pg/g	0.066
Consensus mean, pg/g	0.059
Standard deviation, pg/g	0.025
Relative standard deviation, %	42
No. of values reported	52
No. of values removed	11
No. of reported non-detects	13

Cheese
Congener: PCB 105

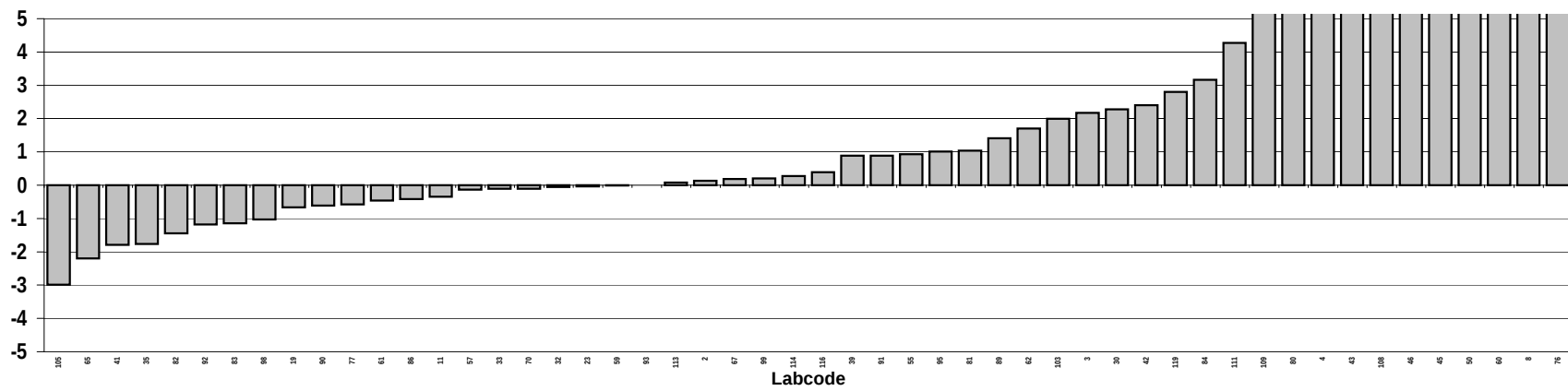
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	8.8		108	22	Outlier
3	12		109	20	Outlier
4	21	Outlier	111	16	
8	312	Outlier	113	8.7	
11	8.0		114	9.0	
19	7.4		116	9.3	
23	8.5		119	13	
30	12				
32	8.5				
33	8.4				
35	5.5				
39	10				
41	5.5				
42	13				
43	21	Outlier			
45	44	Outlier			
46	26	Outlier			
50	107	Outlier			
55	10				
57	8.3				
59	8.6				
60	153	Outlier			
61	7.8				
62	12				
65	4.8				
67	8.9				
70	8.4				
76	544	Outlier			
77	7.6				
80	21	Outlier			
81	10				
82	6.1				
83	6.6				
84	14				
86	7.9				
89	11				
90	7.5				
91	10				
92	6.5				
93	8.6				
95	10				
98	6.8				
99	8.9				
103	12				
105	3.5				

Consensus statistics	
Consensus median, pg/g	8.6
Median all values pg/g	9.1
Consensus mean, pg/g	9.0
Standard deviation, pg/g	2.6
Relative standard deviation, %	28
No. of values reported	52
No. of values removed	11
No. of reported non-detects	0

PCB 105



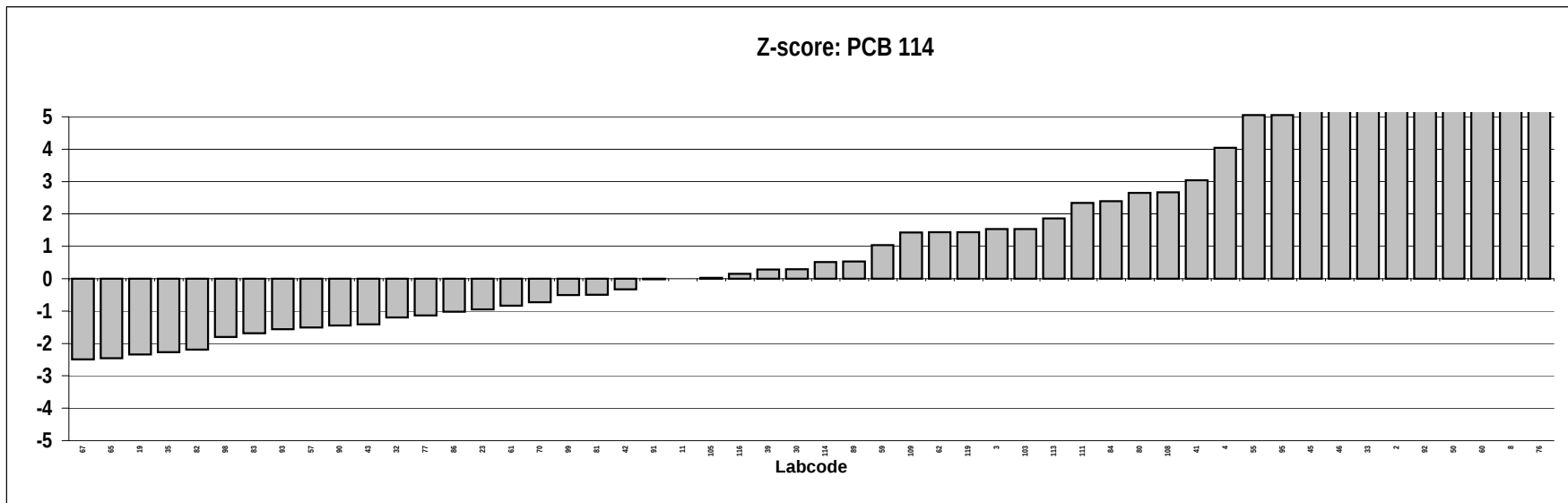
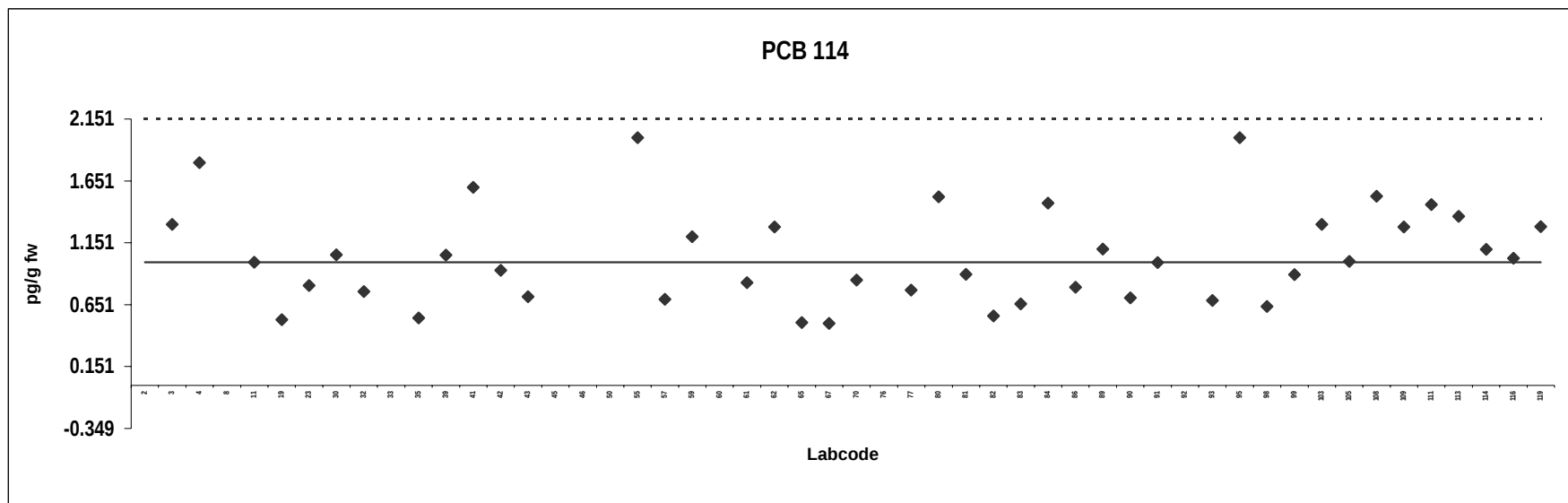
Z-score: PCB 105



Cheese
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.3	Outlier,ND	108	1.5	
3	1.3		109	1.3	
4	1.8		111	1.5	
8	24	Outlier	113	1.4	
11	1.0		114	1.1	
19	0.53		116	1.0	
23	0.81		119	1.3	
30	1.1				
32	0.76				
33	2.9	Outlier,ND			
35	0.54				
39	1.1				
41	1.6	ND			
42	0.93				
43	0.72				
45	2.5	Outlier			
46	2.6	Outlier			
50	7.8	Outlier			
55	2.0	ND			
57	0.70				
59	1.2				
60	11	Outlier			
61	0.83				
62	1.3				
65	0.51				
67	0.50	ND			
70	0.85				
76	29	Outlier			
77	0.77	ND			
80	1.5				
81	0.90				
82	0.56				
83	0.66				
84	1.5				
86	0.79				
89	1.1				
90	0.71				
91	0.99				
92	5.4	Outlier			
93	0.68				
95	2.0	ND			
98	0.64				
99	0.89				
103	1.3				
105	1.0	ND			

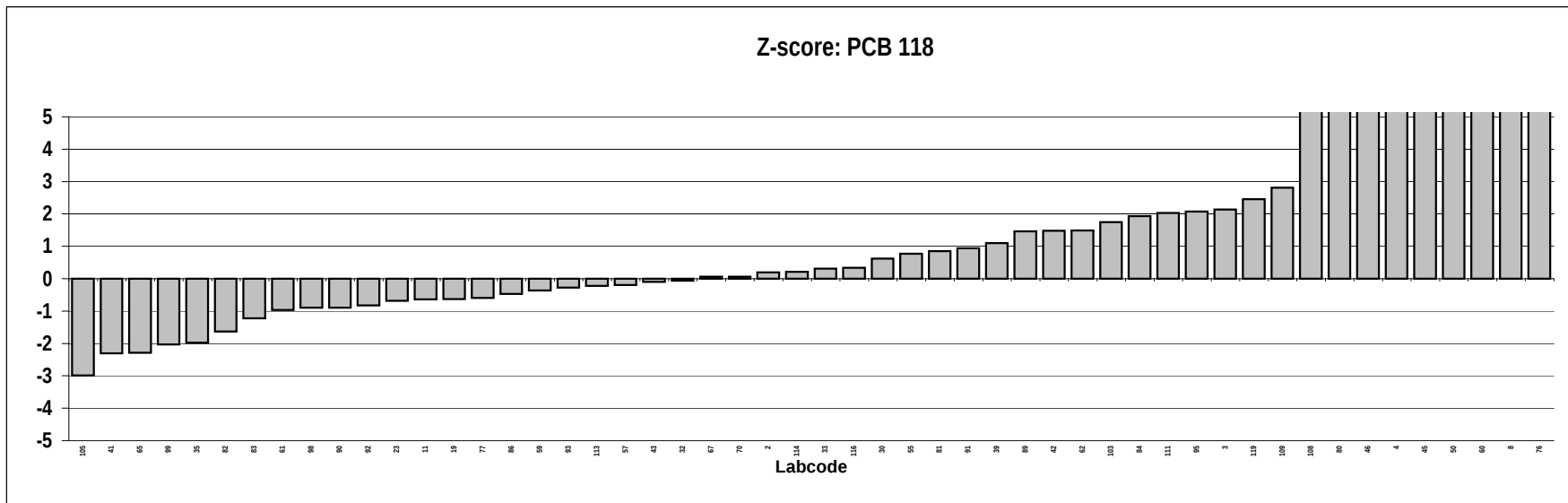
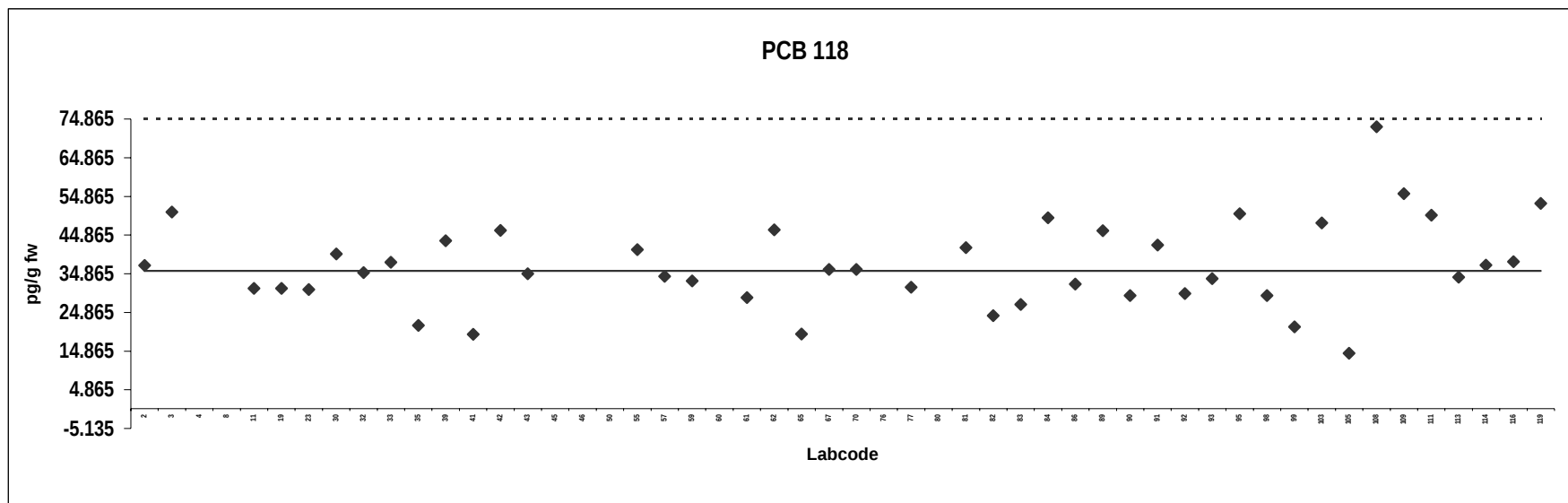
Consensus statistics	
Consensus median, pg/g	1.0
Median all values pg/g	1.1
Consensus mean, pg/g	1.0
Standard deviation, pg/g	0.39
Relative standard deviation, %	38
No. of values reported	52
No. of values removed	9
No. of reported non-detects	8



Cheese
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	37		108	73	
3	51		109	56	
4	105	Outlier	111	50	
8	1190	Outlier	113	34	
11	31		114	37	
19	31		116	38	
23	31		119	53	
30	40				
32	35				
33	38				
35	22				
39	43				
41	19				
42	46				
43	35				
45	111	Outlier			
46	98	Outlier			
50	273	Outlier			
55	41				
57	34				
59	33				
60	370	Outlier			
61	29				
62	46				
65	19				
67	36				
70	36				
76	1888	Outlier			
77	31				
80	84	Outlier			
81	42				
82	24				
83	27				
84	49				
86	32				
89	46				
90	29				
91	42				
92	30				
93	34				
95	50				
98	29				
99	21				
103	48				
105	14				

Consensus statistics	
Consensus median, pg/g	36
Median all values pg/g	37
Consensus mean, pg/g	37
Standard deviation, pg/g	11
Relative standard deviation, %	30
No. of values reported	52
No. of values removed	8
No. of reported non-detects	0

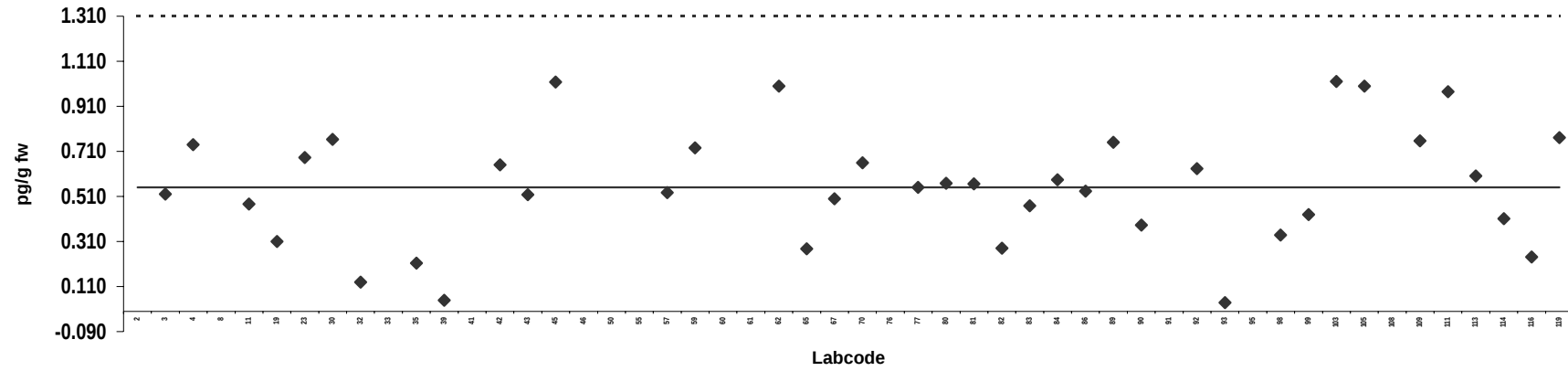


Cheese
Congener: PCB 123

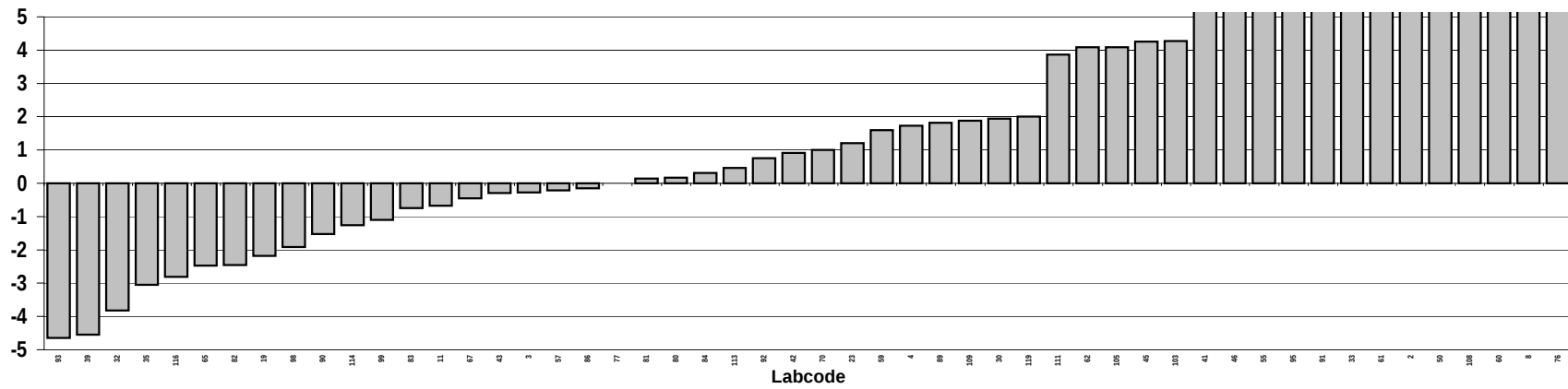
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.3	Outlier,ND	108	9.3	Outlier
3	0.52	ND	109	0.76	
4	0.74		111	0.98	
8	17	Outlier	113	0.60	
11	0.48		114	0.41	
19	0.31		116	0.24	
23	0.68		119	0.77	
30	0.76				
32	0.13				
33	2.9	Outlier,ND			
35	0.21				
39	0.050	ND			
41	1.8	Outlier,ND			
42	0.65				
43	0.52				
45	1.0				
46	1.9	Outlier			
50	8.6	Outlier			
55	2.0	Outlier,ND			
57	0.53				
59	0.73				
60	13	Outlier			
61	3.1	Outlier			
62	1.0				
65	0.28				
67	0.50	ND			
70	0.66				
76	36	Outlier			
77	0.55	ND			
80	0.57				
81	0.57				
82	0.28				
83	0.47				
84	0.58				
86	0.53				
89	0.75				
90	0.38				
91	2.9	Outlier			
92	0.63	ND			
93	0.039	ND			
95	2.0	Outlier,ND			
98	0.34				
99	0.43	ND			
103	1.0				
105	1.0	ND			

Consensus statistics	
Consensus median, pg/g	0.55
Median all values pg/g	0.66
Consensus mean, pg/g	0.56
Standard deviation, pg/g	0.26
Relative standard deviation, %	47
No. of values reported	52
No. of values removed	13
No. of reported non-detects	13

PCB 123



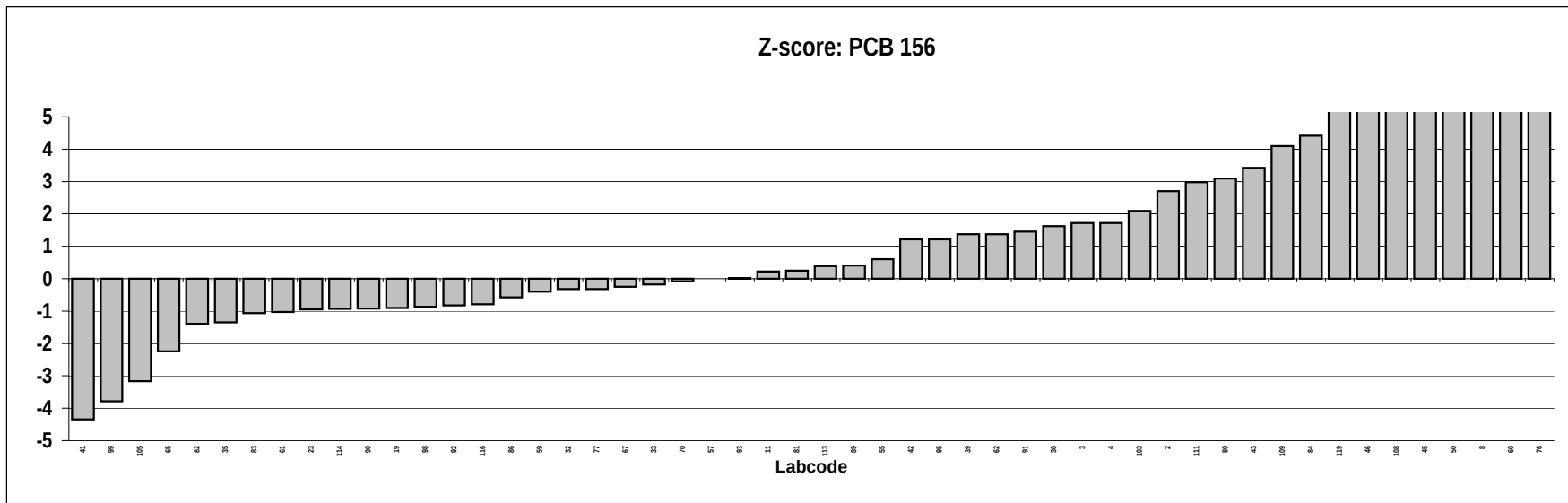
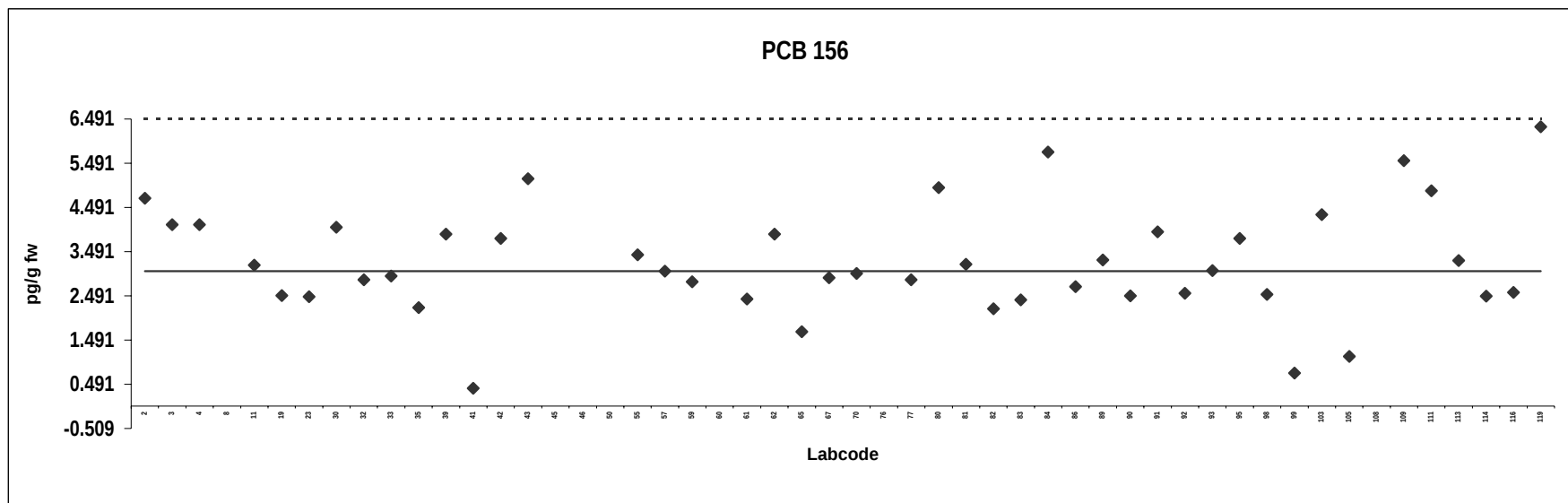
Z-score: PCB 123



Cheese
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4.7		108	12	Outlier
3	4.1		109	5.5	
4	4.1		111	4.9	
8	45	Outlier	113	3.3	
11	3.2		114	2.5	
19	2.5		116	2.6	
23	2.5		119	6.3	
30	4.0				
32	2.9				
33	2.9	ND			
35	2.2				
39	3.9				
41	0.40	ND			
42	3.8				
43	5.1				
45	18	Outlier			
46	8.4	Outlier			
50	44	Outlier			
55	3.4				
57	3.1				
59	2.8				
60	100	Outlier			
61	2.4				
62	3.9				
65	1.7				
67	2.9				
70	3.0				
76	265	Outlier			
77	2.9				
80	4.9				
81	3.2				
82	2.2				
83	2.4				
84	5.7				
86	2.7				
89	3.3				
90	2.5				
91	3.9				
92	2.5				
93	3.1				
95	3.8				
98	2.5				
99	0.74				
103	4.3				
105	1.1				

Consensus statistics	
Consensus median, pg/g	3.1
Median all values pg/g	3.2
Consensus mean, pg/g	3.3
Standard deviation, pg/g	1.2
Relative standard deviation, %	38
No. of values reported	52
No. of values removed	7
No. of reported non-detects	2

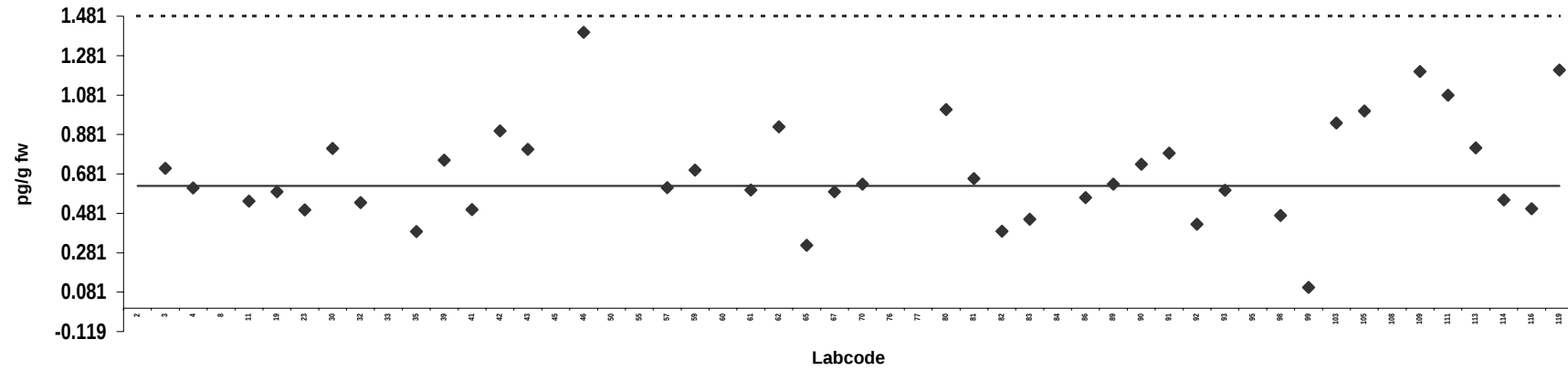


Cheese
Congener: PCB 157

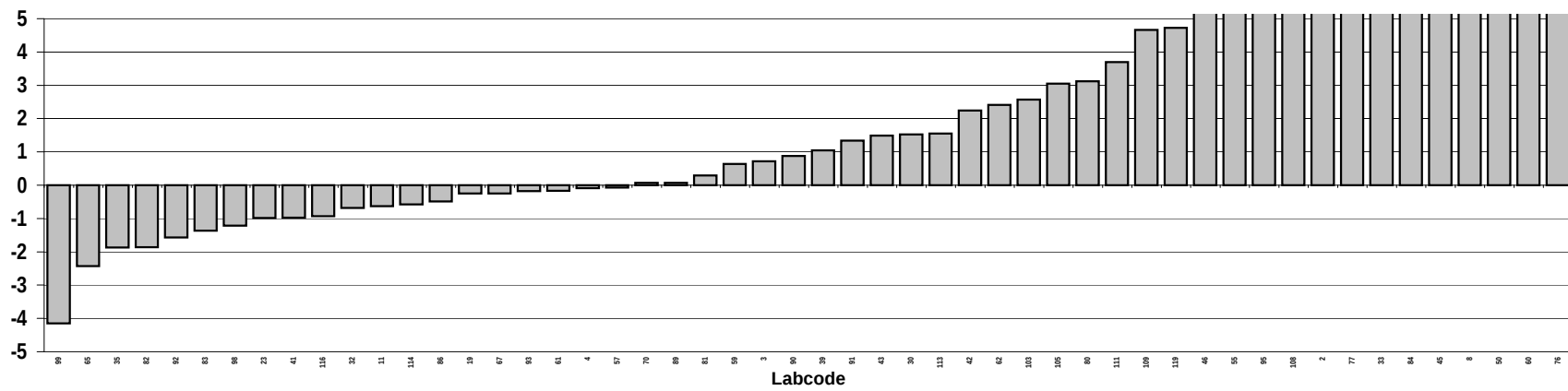
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	2.7	Outlier,ND	108	2.5	Outlier
3	0.71		109	1.2	
4	0.61		111	1.1	
8	9.4	Outlier	113	0.81	
11	0.54		114	0.55	
19	0.59		116	0.51	
23	0.50		119	1.2	
30	0.81				
32	0.54				
33	2.9	Outlier,ND			
35	0.39				
39	0.75				
41	0.50	ND			
42	0.90				
43	0.81				
45	3.8	Outlier			
46	1.4				
50	14	Outlier			
55	2.0	Outlier,ND			
57	0.61				
59	0.70				
60	16	Outlier			
61	0.60				
62	0.92				
65	0.32				
67	0.59				
70	0.63				
76	54	Outlier			
77	2.9	Outlier			
80	1.0				
81	0.66				
82	0.39				
83	0.45				
84	3.0	Outlier			
86	0.56				
89	0.63				
90	0.73				
91	0.79				
92	0.43	ND			
93	0.60				
95	2.0	Outlier,ND			
98	0.47				
99	0.11	ND			
103	0.94				
105	1.0	ND			

Consensus statistics	
Consensus median, pg/g	0.62
Median all values pg/g	0.74
Consensus mean, pg/g	0.69
Standard deviation, pg/g	0.26
Relative standard deviation, %	38
No. of values reported	52
No. of values removed	12
No. of reported non-detects	8

PCB 157



Z-score: PCB 157

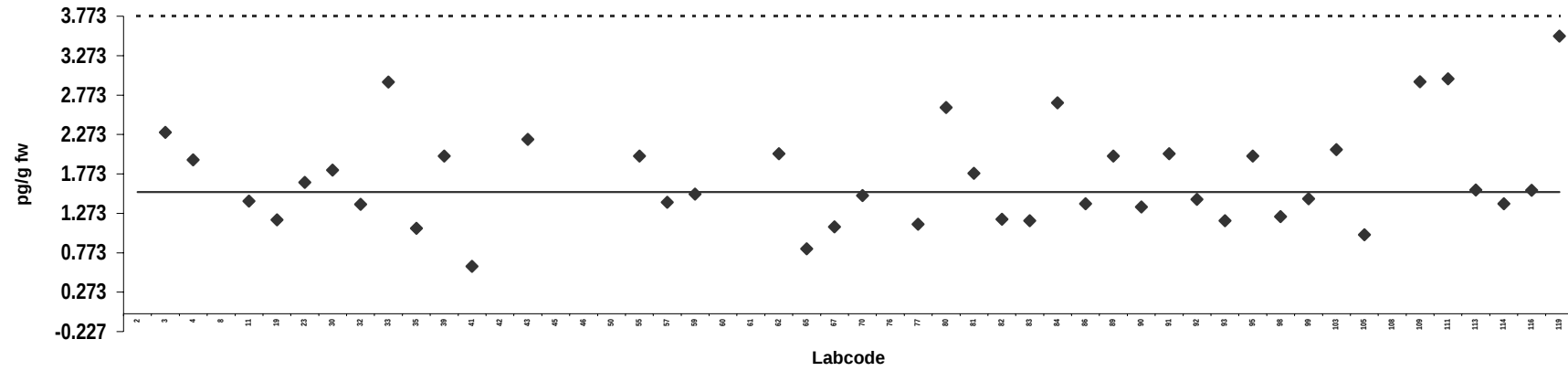


Cheese
Congener: PCB 167

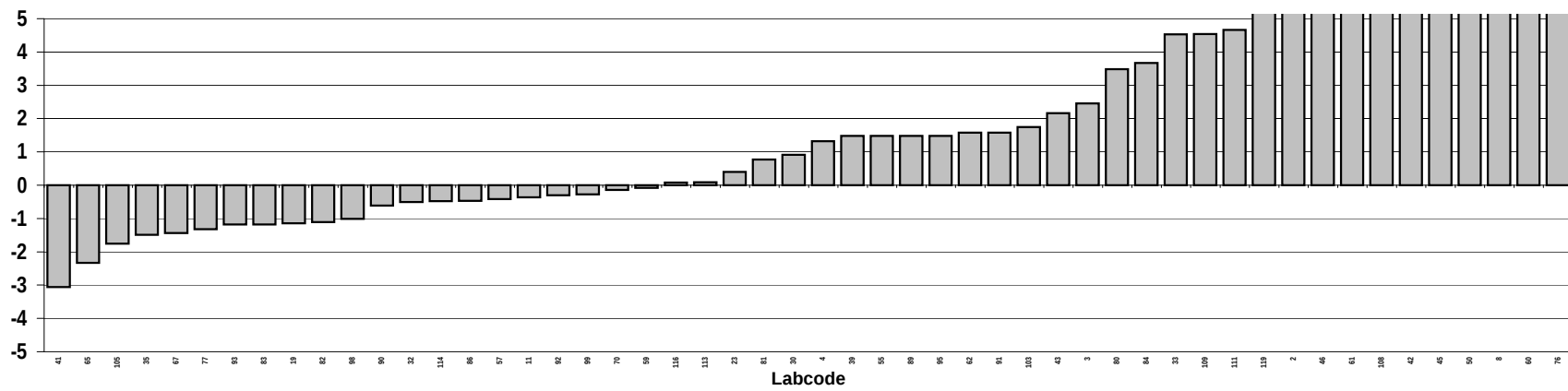
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	3.9	Outlier	108	5.8	Outlier
3	2.3		109	2.9	
4	2.0		111	3.0	
8	28	Outlier	113	1.6	
11	1.4		114	1.4	
19	1.2		116	1.6	
23	1.7		119	3.5	
30	1.8				
32	1.4				
33	2.9	ND			
35	1.1				
39	2.0				
41	0.60	ND			
42	6.6	Outlier			
43	2.2				
45	8.9	Outlier			
46	3.9	Outlier			
50	26	Outlier			
55	2.0	ND			
57	1.4				
59	1.5				
60	53	Outlier			
61	4.7	Outlier			
62	2.0				
65	0.82				
67	1.1				
70	1.5				
76	148	Outlier			
77	1.1				
80	2.6				
81	1.8				
82	1.2				
83	1.2				
84	2.7				
86	1.4				
89	2.0				
90	1.4				
91	2.0				
92	1.5				
93	1.2				
95	2.0	ND			
98	1.2				
99	1.5				
103	2.1				
105	1.0	ND			

Consensus statistics	
Consensus median, pg/g	1.5
Median all values pg/g	1.9
Consensus mean, pg/g	1.7
Standard deviation, pg/g	0.64
Relative standard deviation, %	37
No. of values reported	52
No. of values removed	10
No. of reported non-detects	5

PCB 167



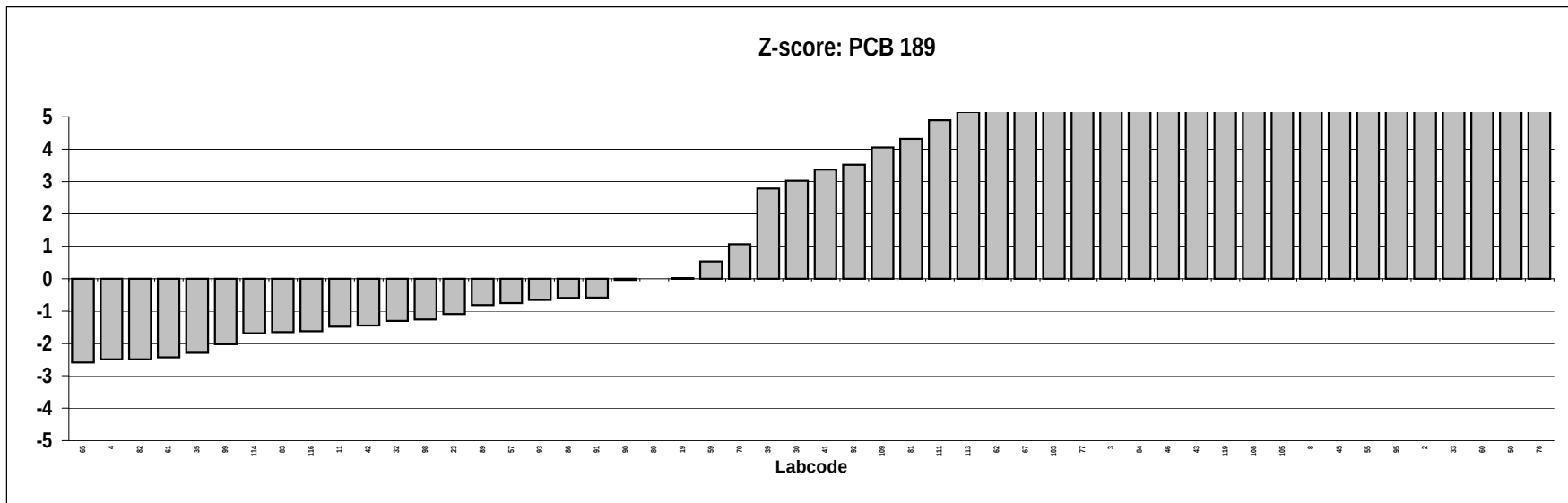
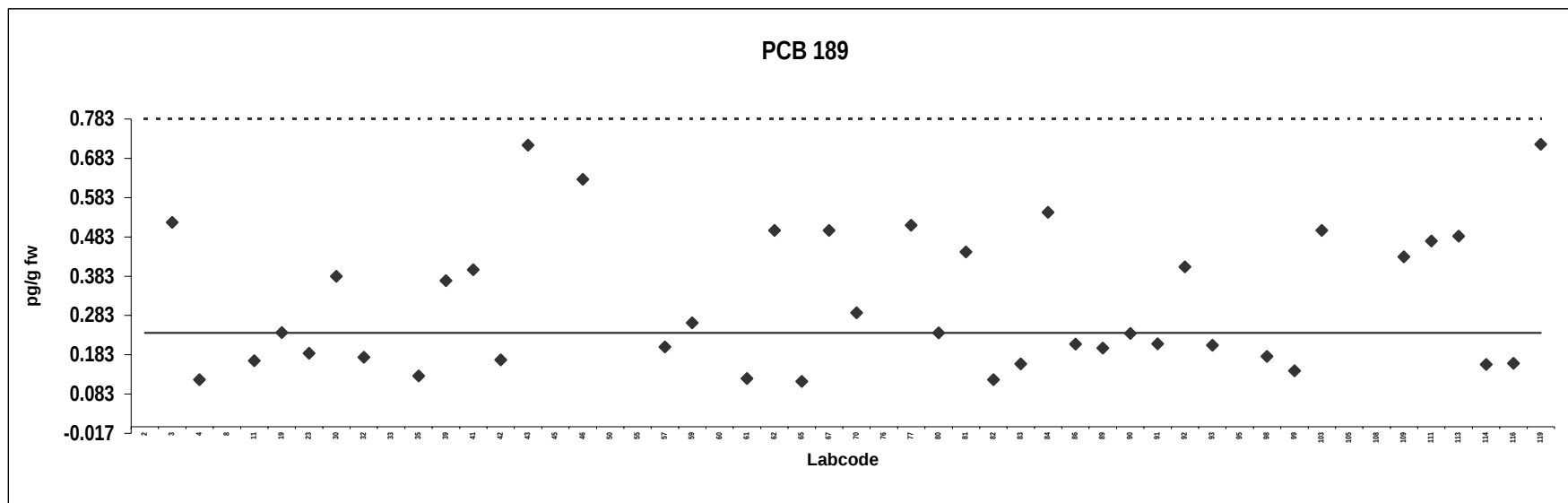
Z-score: PCB 167



Cheese
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	2.7	Outlier,ND	108	0.90	Outlier
3	0.52	ND	109	0.43	
4	0.12		111	0.47	
8	1.1	Outlier	113	0.49	ND
11	0.17	ND	114	0.16	
19	0.24	ND	116	0.16	
23	0.19	ND	119	0.72	
30	0.38				
32	0.18				
33	2.9	Outlier,ND			
35	0.13				
39	0.37				
41	0.40	ND			
42	0.17				
43	0.72				
45	1.3	Outlier			
46	0.63				
50	9.1	Outlier			
55	2.0	Outlier,ND			
57	0.20				
59	0.26				
60	6.1	Outlier			
61	0.12				
62	0.50	ND			
65	0.12				
67	0.50	ND			
70	0.29				
76	23	Outlier			
77	0.51	ND			
80	0.24				
81	0.45				
82	0.12				
83	0.16				
84	0.55				
86	0.21				
89	0.20				
90	0.24				
91	0.21				
92	0.41	ND			
93	0.21				
95	2.0	Outlier,ND			
98	0.18				
99	0.14	ND			
103	0.50	ND			
105	1.0	Outlier,ND			

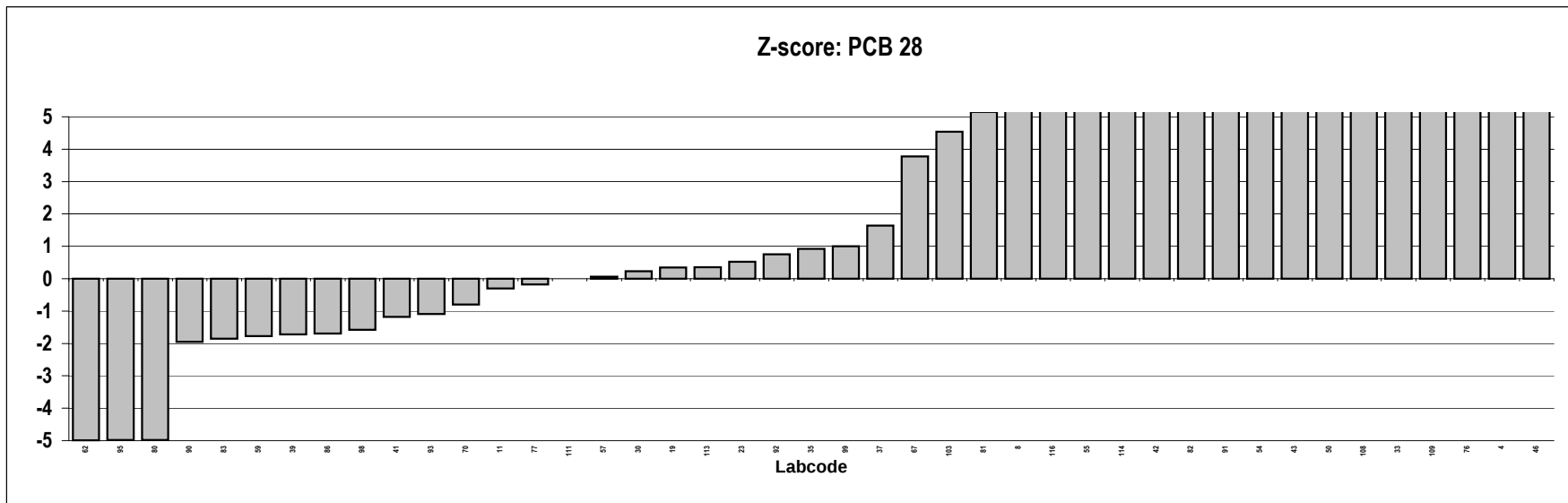
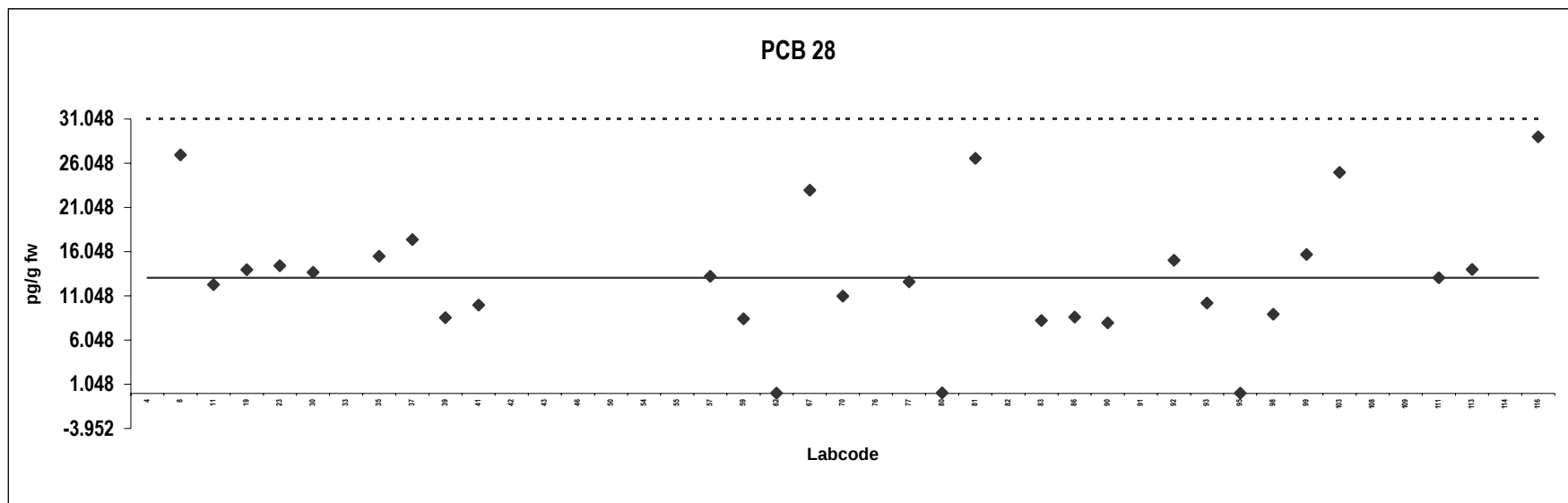
Consensus statistics	
Consensus median, pg/g	0.24
Median all values pg/g	0.39
Consensus mean, pg/g	0.32
Standard deviation, pg/g	0.18
Relative standard deviation, %	56
No. of values reported	52
No. of values removed	11
No. of reported non-detects	17



Cheese
Congener: PCB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	181	Outlier			
8	27				
11	12				
19	14	ND			
23	14				
30	14				
33	104	Outlier			
35	16				
37	17				
39	8.6				
41	10				
42	35	Outlier			
43	51	Outlier			
46	228	Outlier			
50	60	Outlier			
54	50	Outlier			
55	33	Outlier			
57	13				
59	8.4				
62	0.029				
67	23				
70	11				
76	153	Outlier			
77	13				
80	0.058				
81	27				
82	36	Outlier			
83	8.3	ND			
86	8.7				
90	8.0				
91	37	Outlier			
92	15				
93	10				
95	0.040				
98	9.0				
99	16				
103	25				
108	62	Outlier			
109	138	Outlier			
111	13				
113	14				
114	34	Outlier			
116	29				

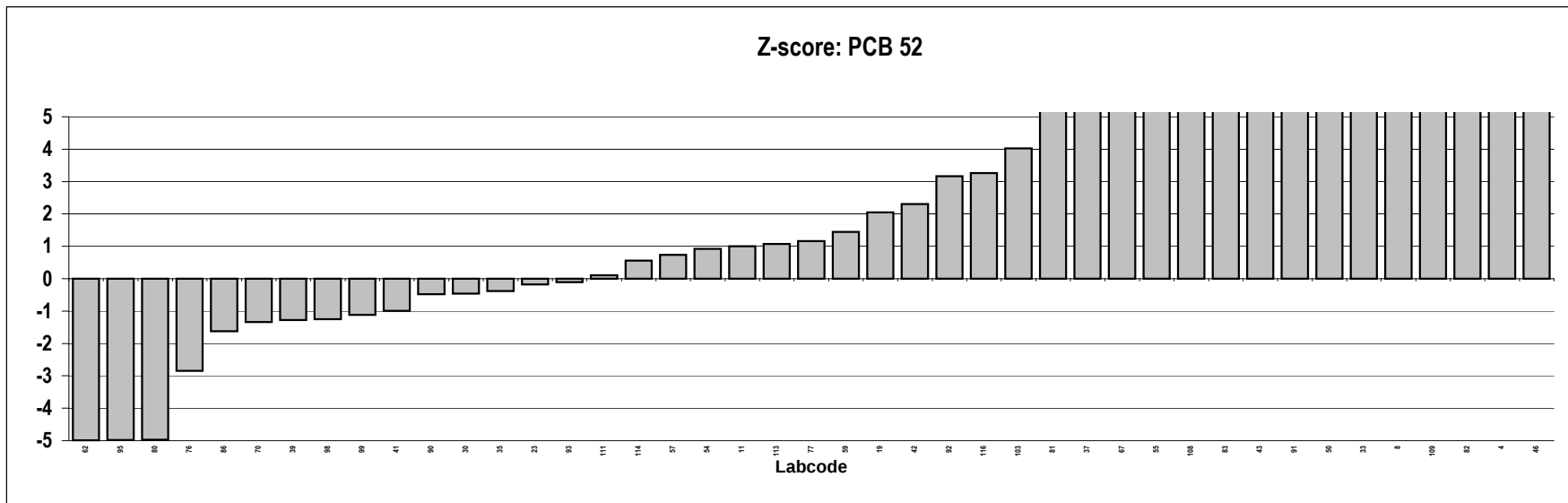
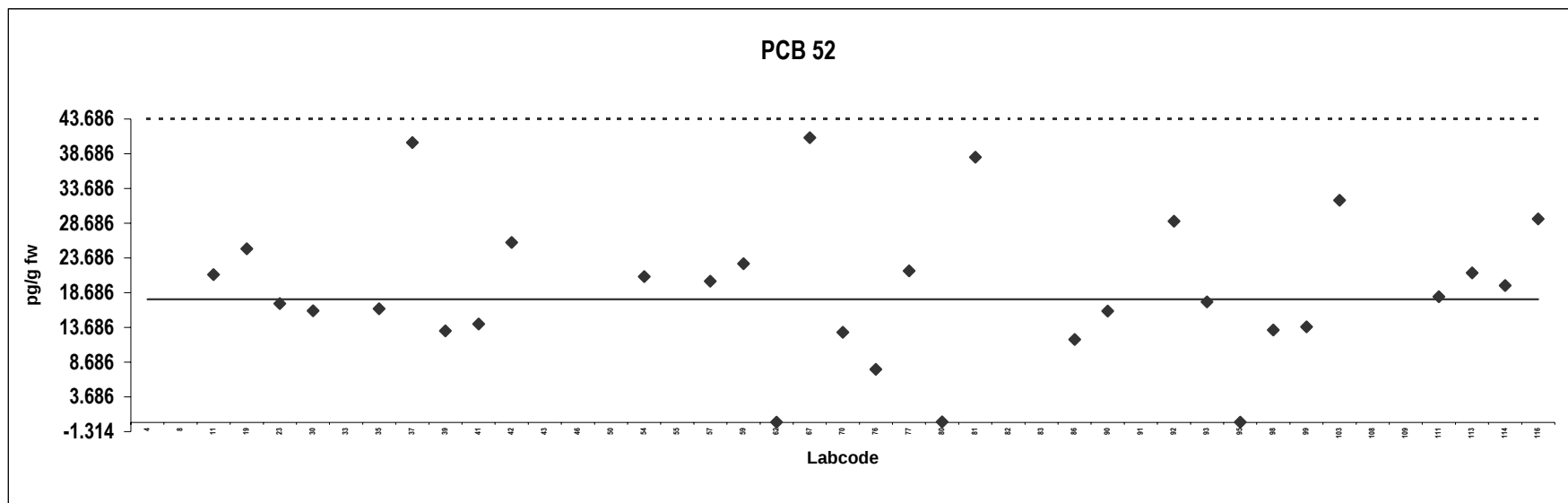
Consensus statistics	
Consensus median, pg/g	13
Median all values pg/g	16
Consensus mean, pg/g	13
Standard deviation, pg/g	7.5
Relative standard deviation, %	57
No. of values reported	43
No. of values removed	14
No. of reported non-detects	2



Cheese
Congener: PCB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	265	Outlier			
8	146	Outlier			
11	21				
19	25	ND			
23	17				
30	16				
33	104	Outlier			
35	16				
37	40				
39	13				
41	14				
42	26				
43	53	Outlier			
46	684	Outlier			
50	100	Outlier			
54	21				
55	44	Outlier			
57	20				
59	23				
62	0.031				
67	41				
70	13				
76	7.7				
77	22				
80	0.099				
81	38				
82	220	Outlier			
83	52	Outlier			
86	12				
90	16				
91	67	Outlier			
92	29				
93	17				
95	0.058				
98	13				
99	14				
103	32				
108	46	Outlier			
109	181	Outlier			
111	18				
113	22				
114	20				
116	29				

Consensus statistics	
Consensus median, pg/g	18
Median all values pg/g	22
Consensus mean, pg/g	19
Standard deviation, pg/g	10
Relative standard deviation, %	54
No. of values reported	43
No. of values removed	12
No. of reported non-detects	1

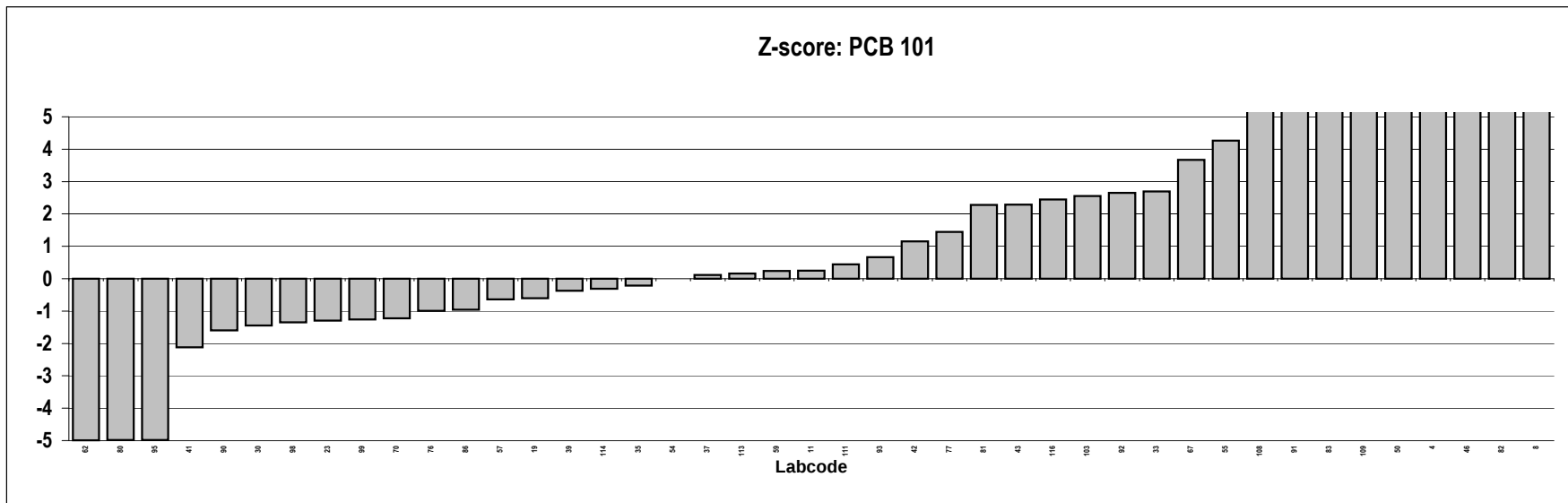
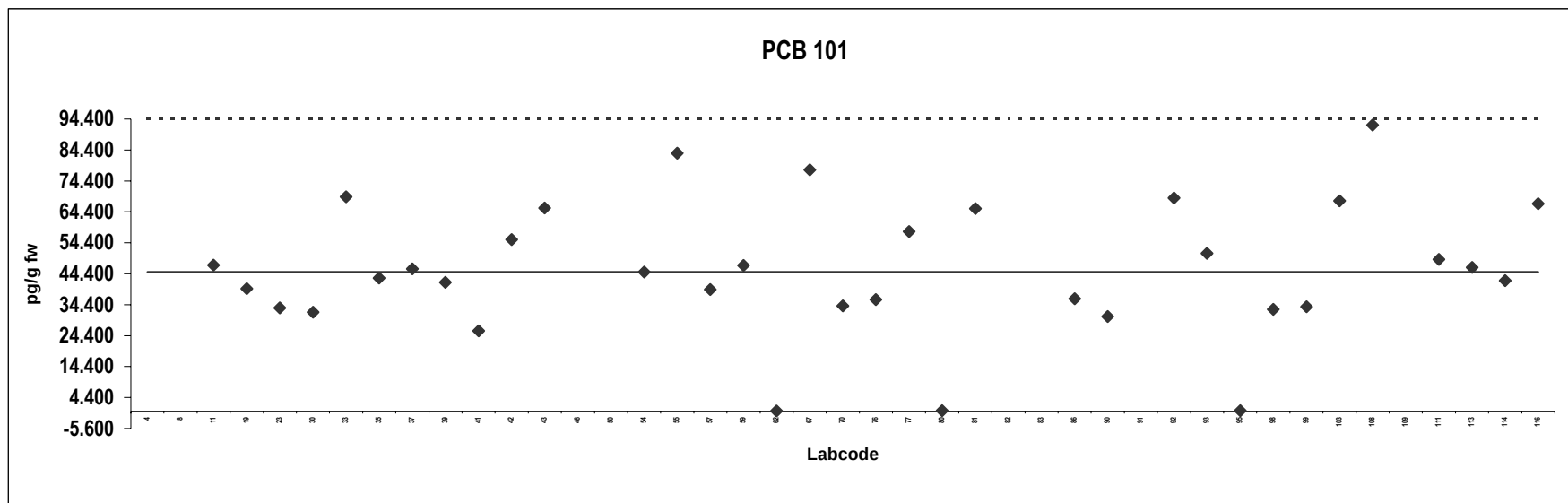


Cheese

Congener: PCB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	265	Outlier			
8	1633	Outlier			
11	47				
19	40				
23	33				
30	32				
33	69				
35	43				
37	46				
39	42				
41	26				
42	55				
43	66				
46	293	Outlier			
50	253	Outlier			
54	45				
55	83				
57	39				
59	47				
62	0.070				
67	78				
70	34				
76	36				
77	58				
80	0.14				
81	66				
82	863	Outlier			
83	101	Outlier			
86	36				
90	31				
91	96	Outlier			
92	69				
93	51				
95	0.16				
98	33				
99	34				
103	68				
108	92				
109	177	Outlier			
111	49				
113	46				
114	42				
116	67				

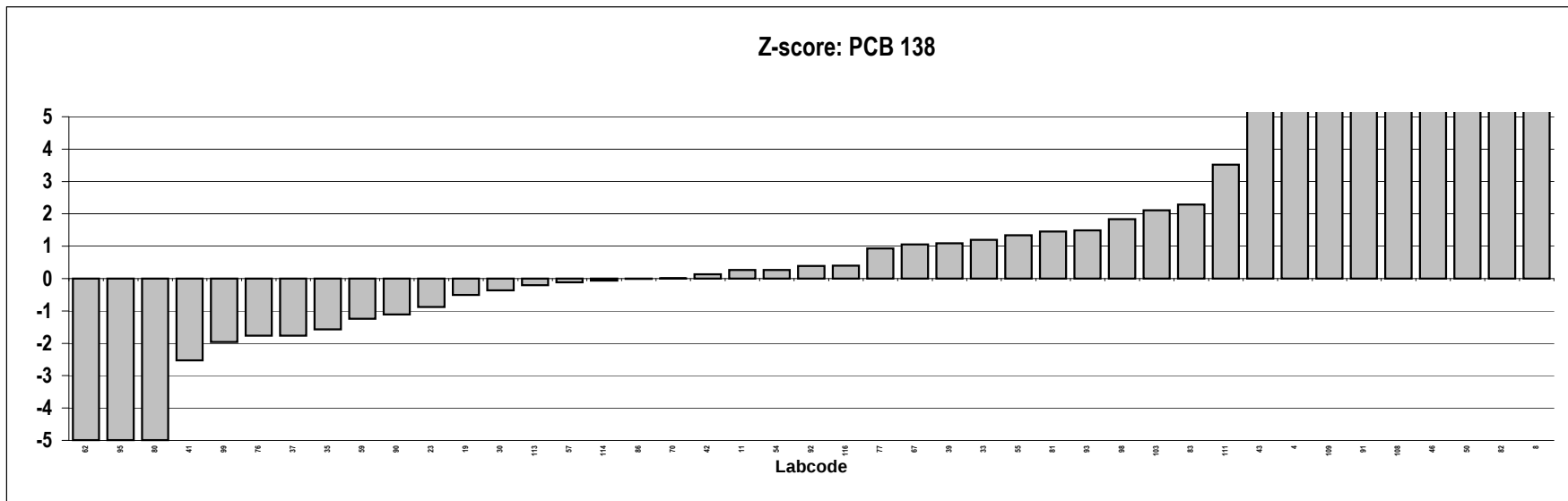
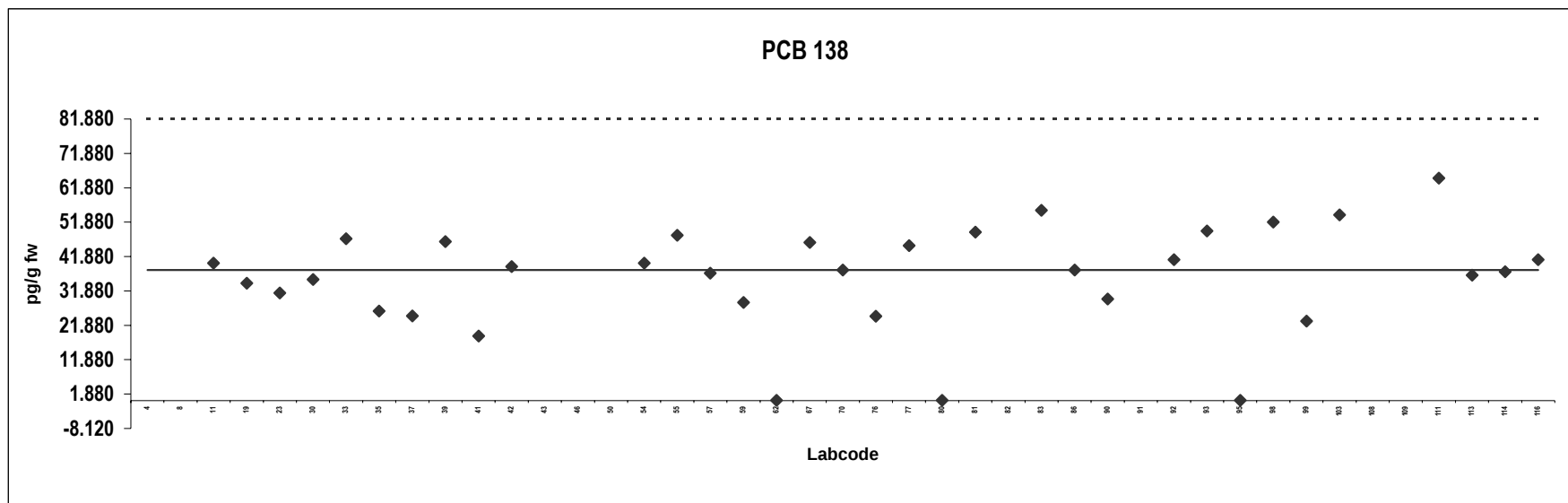
Consensus statistics	
Consensus median, pg/g	45
Median all values pg/g	47
Consensus mean, pg/g	46
Standard deviation, pg/g	21
Relative standard deviation, %	47
No. of values reported	43
No. of values removed	8
No. of reported non-detects	0



Cheese
Congener: PCB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	97	Outlier			
8	1197	Outlier			
11	40				
19	34				
23	31				
30	35				
33	47				
35	26				
37	25				
39	46				
41	19				
42	39				
43	93	Outlier			
46	161	Outlier			
50	665	Outlier			
54	40				
55	48				
57	37				
59	29				
62	0.054				
67	46				
70	38				
76	25				
77	45				
80	0.081				
81	49				
82	912	Outlier			
83	55				
86	38				
90	30				
91	107	Outlier			
92	41				
93	49				
95	0.069				
98	52				
99	23				
103	54				
108	142	Outlier			
109	103	Outlier			
111	65				
113	36				
114	37				
116	41				

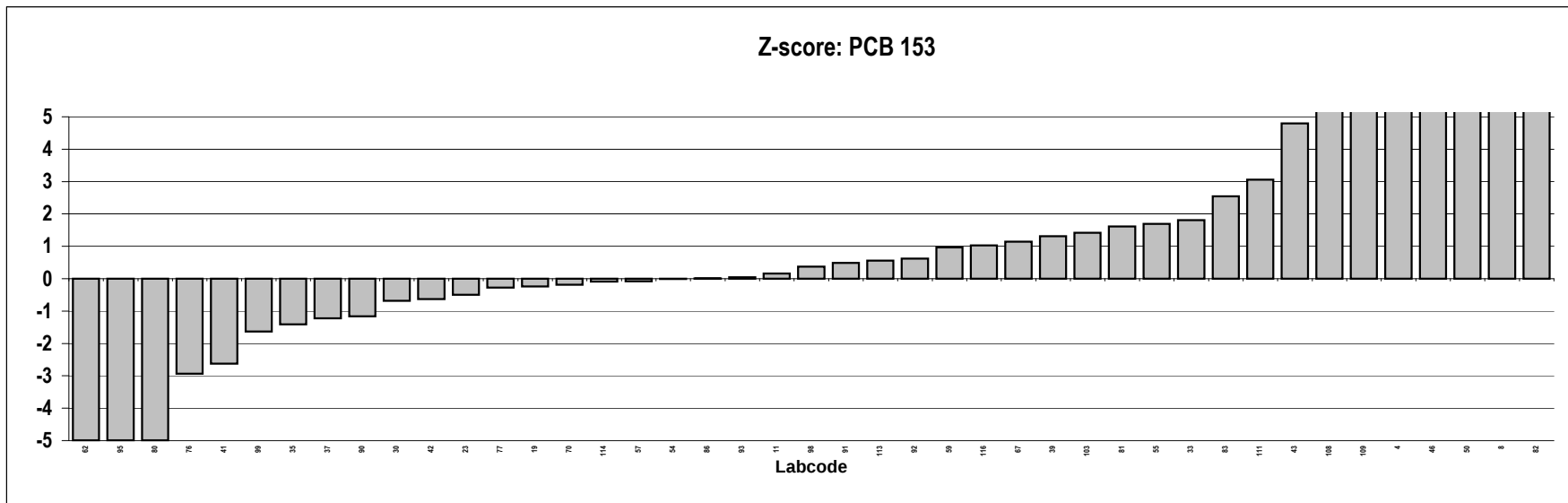
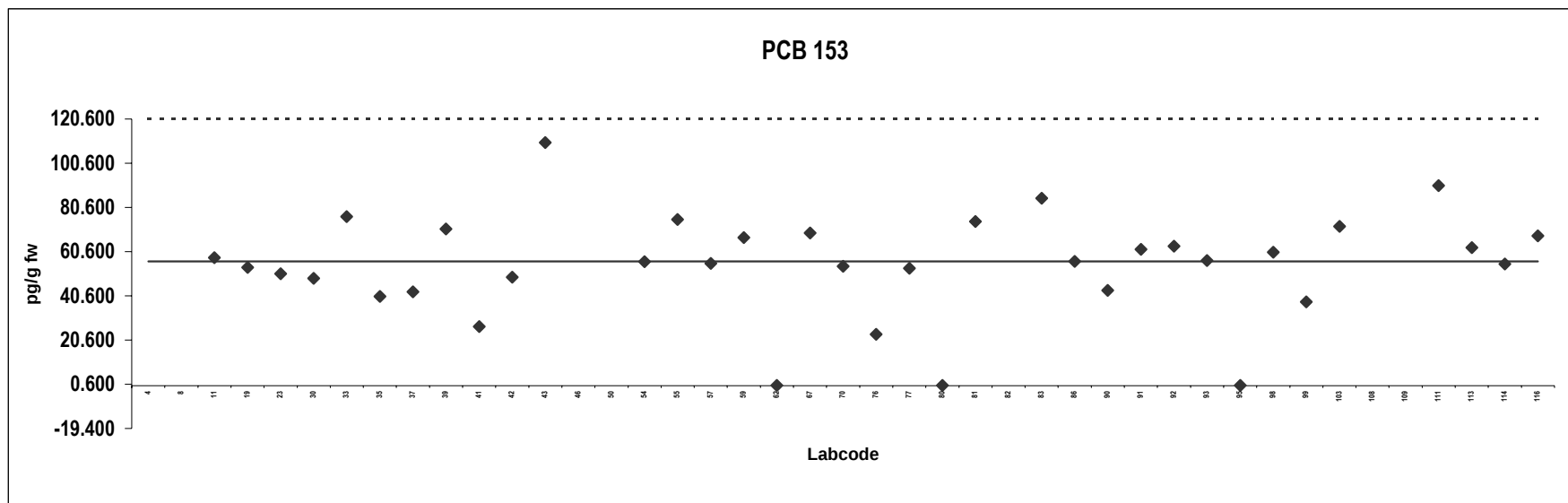
Consensus statistics	
Consensus median, pg/g	38
Median all values pg/g	41
Consensus mean, pg/g	36
Standard deviation, pg/g	15
Relative standard deviation, %	42
No. of values reported	43
No. of values removed	9
No. of reported non-detects	0



Cheese
Congener: PCB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	175	Outlier			
8	987	Outlier			
11	58				
19	53				
23	51				
30	49				
33	76				
35	40				
37	42				
39	71				
41	27				
42	49				
43	110				
46	225	Outlier			
50	889	Outlier			
54	56				
55	75				
57	55				
59	67				
62	0.075				
67	69				
70	54				
76	23				
77	53				
80	0.13				
81	74				
82	1429	Outlier			
83	85				
86	56				
90	43				
91	62				
92	63				
93	57				
95	0.11				
98	60				
99	38				
103	72				
108	130	Outlier			
109	147	Outlier			
111	91				
113	62				
114	55				
116	68				

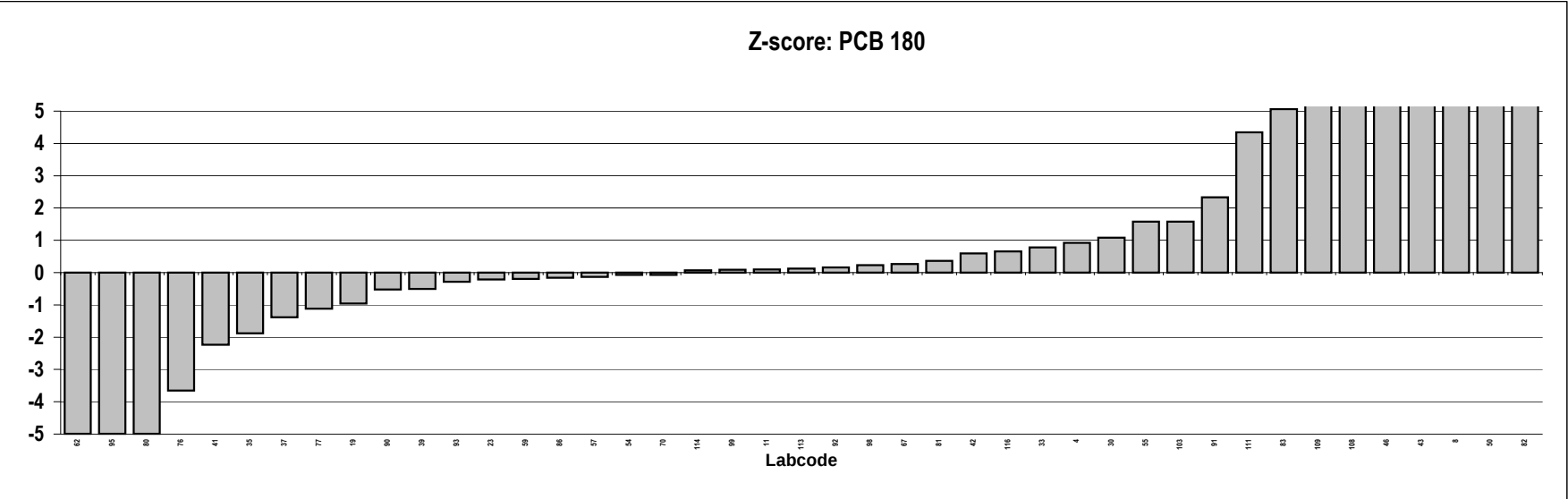
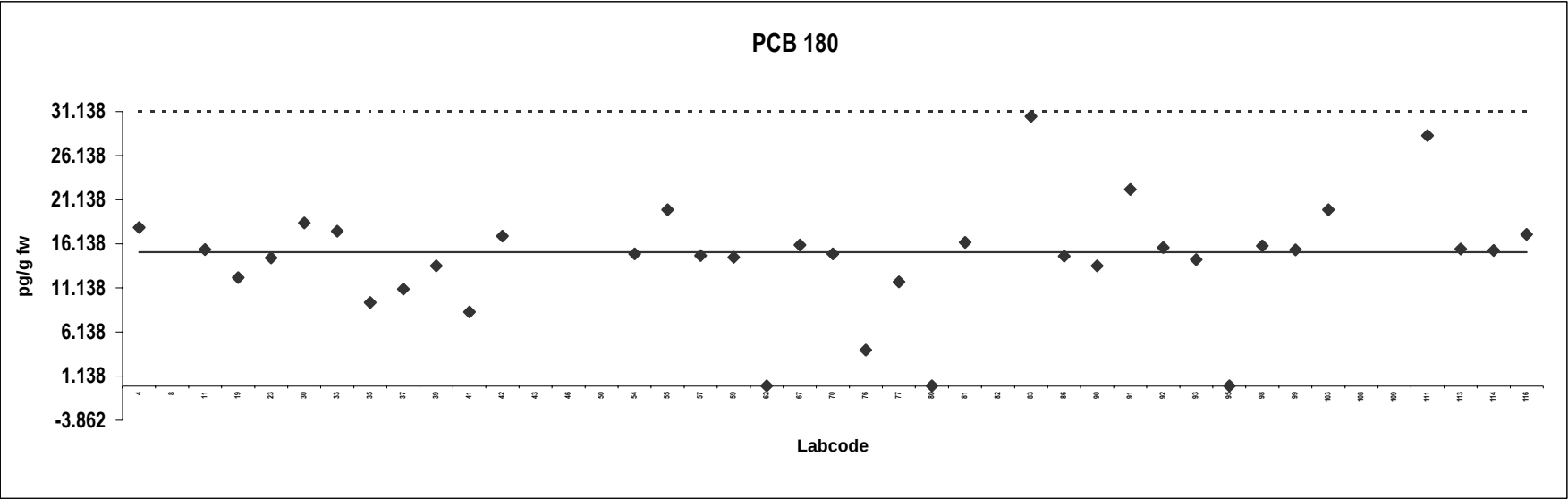
Consensus statistics	
Consensus median, pg/g	56
Median all values pg/g	60
Consensus mean, pg/g	55
Standard deviation, pg/g	24
Relative standard deviation, %	43
No. of values reported	43
No. of values removed	7
No. of reported non-detects	0



Cheese
Congener: PCB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	18				
8	143	Outlier			
11	16				
19	12				
23	15				
30	19				
33	18				
35	9.5				
37	11				
39	14				
41	8.4				
42	17				
43	59	Outlier			
46	54	Outlier			
50	296	Outlier			
54	15	ND			
55	20	ND			
57	15				
59	15				
62	0.018				
67	16				
70	15				
76	4.1				
77	12				
80	0.028				
81	16				
82	656	Outlier			
83	31				
86	15				
90	14				
91	22				
92	16				
93	14				
95	0.023				
98	16				
99	15				
103	20				
108	53	Outlier			
109	35	Outlier			
111	28				
113	16				
114	15				
116	17				

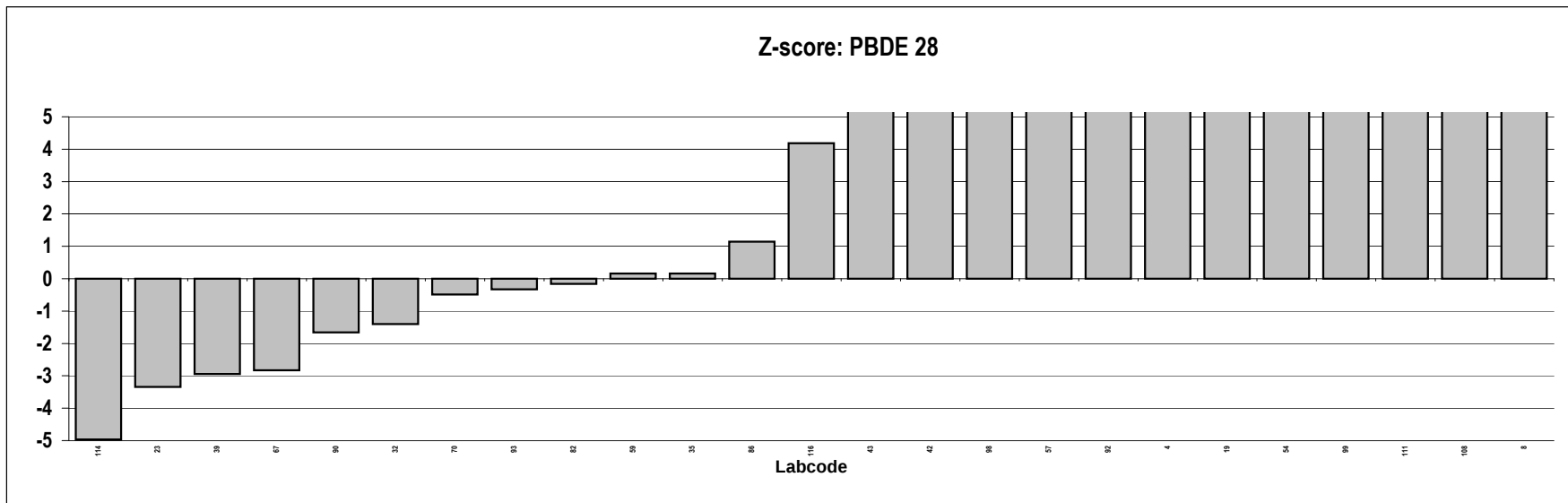
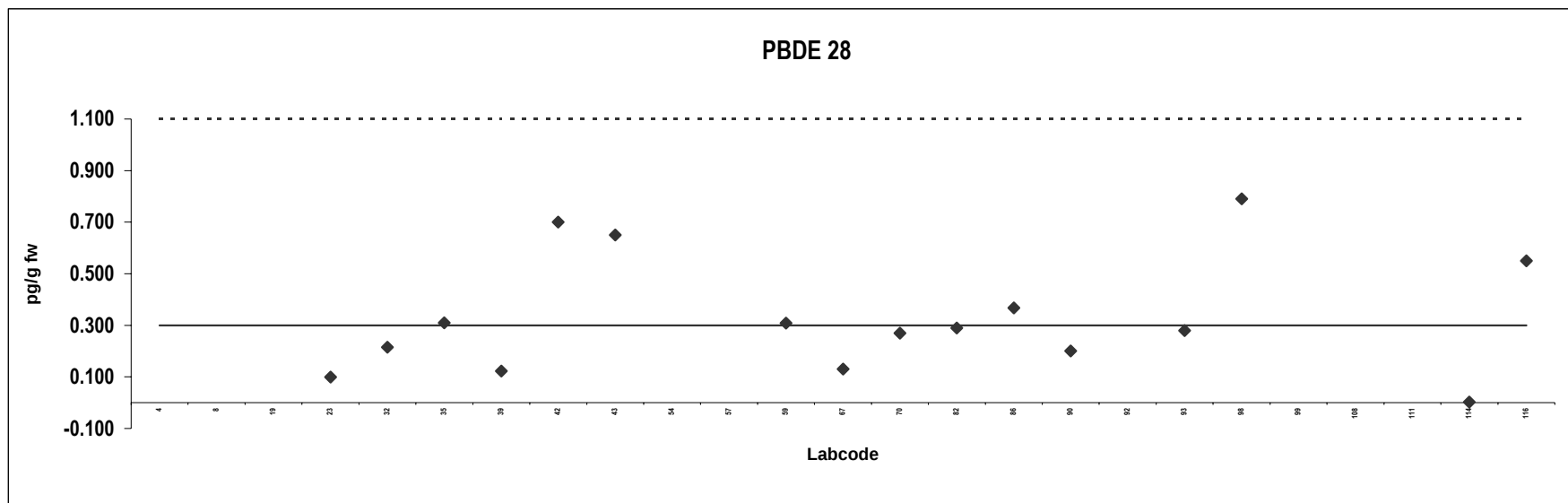
Consensus statistics	
Consensus median, pg/g	15
Median all values pg/g	16
Consensus mean, pg/g	15
Standard deviation, pg/g	6.5
Relative standard deviation, %	45
No. of values reported	43
No. of values removed	7
No. of reported non-detects	2



Cheese
Congener: PBDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	1.5	Outlier			
8	160	Outlier			
19	2.0	Outlier			
23	0.10	ND			
32	0.22				
35	0.31				
39	0.12				
42	0.70				
43	0.65				
54	2.5	Outlier,ND			
57	1.3	Outlier			
59	0.31				
67	0.13				
70	0.27				
82	0.29				
86	0.37	ND			
90	0.20	ND			
92	1.3	Outlier			
93	0.28				
98	0.79				
99	2.8	Outlier			
108	15	Outlier,ND			
111	4.0	Outlier,ND			
114	0.0020	ND			
116	0.55				

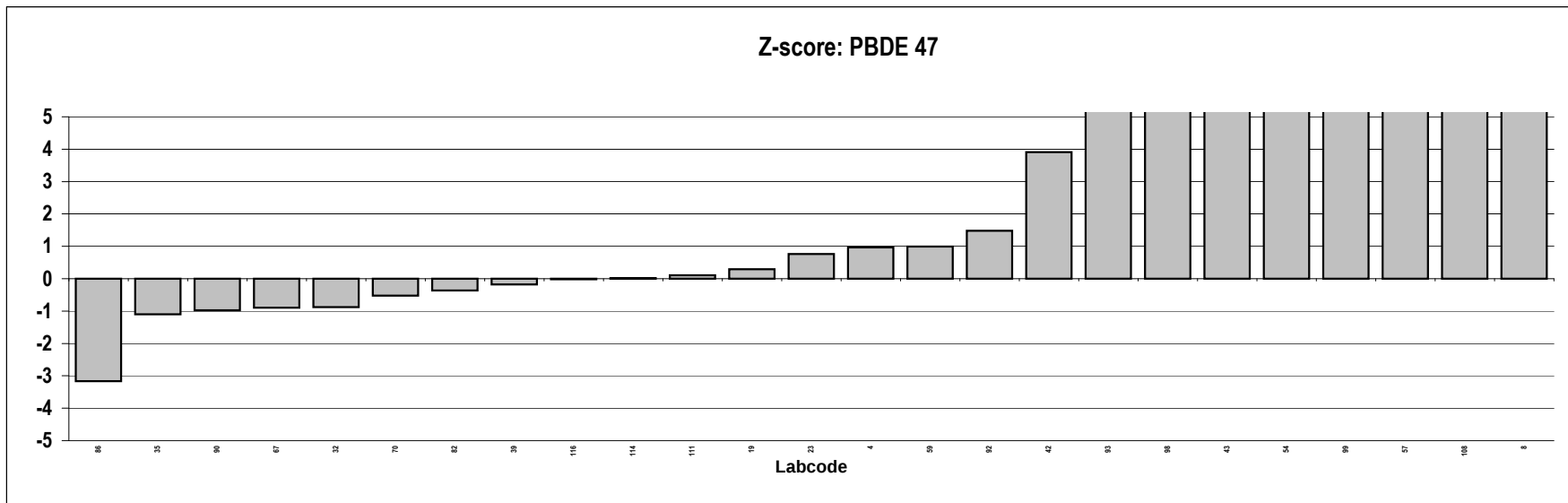
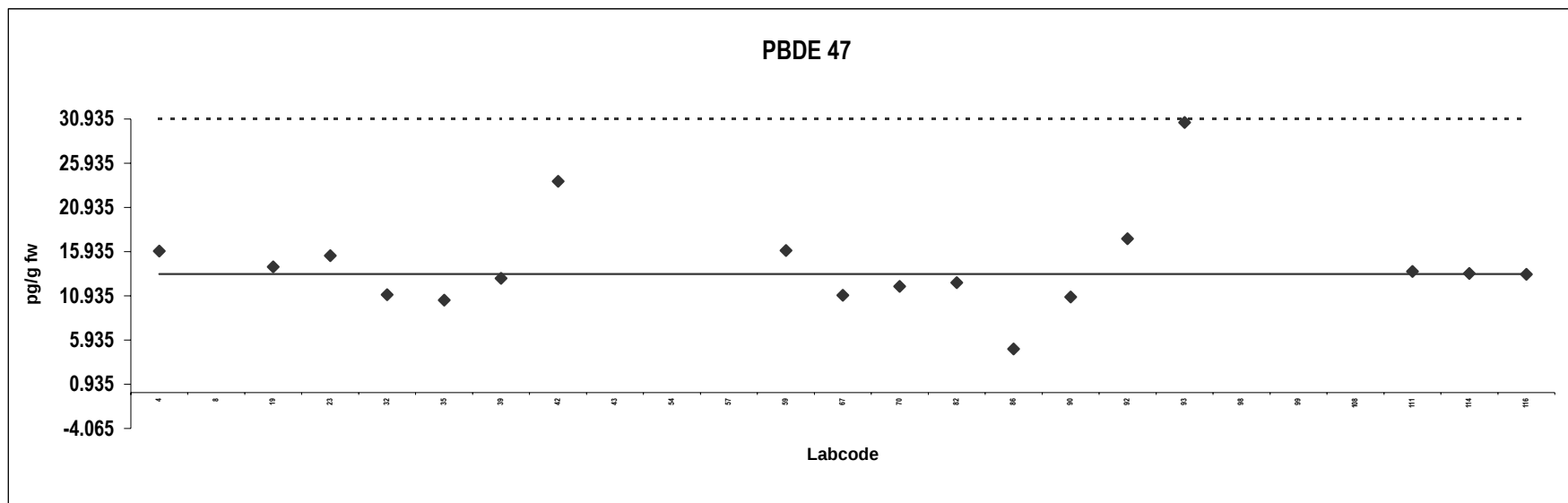
Consensus statistics	
Consensus median, pg/g	0.30
Median all values pg/g	0.55
Consensus mean, pg/g	0.33
Standard deviation, pg/g	0.23
Relative standard deviation, %	69
No. of values reported	25
No. of values removed	9
No. of reported non-detects	7



Cheese
Congener: PBDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	16				
8	4364	Outlier			
19	14				
23	15				
32	11				
35	10				
39	13				
42	24				
43	35	Outlier			
54	49	Outlier			
57	57	Outlier			
59	16				
67	11				
70	12				
82	12				
86	4.9				
90	11				
92	17				
93	31				
98	33	Outlier			
99	56	Outlier			
108	329	Outlier			
111	14				
114	13				
116	13				

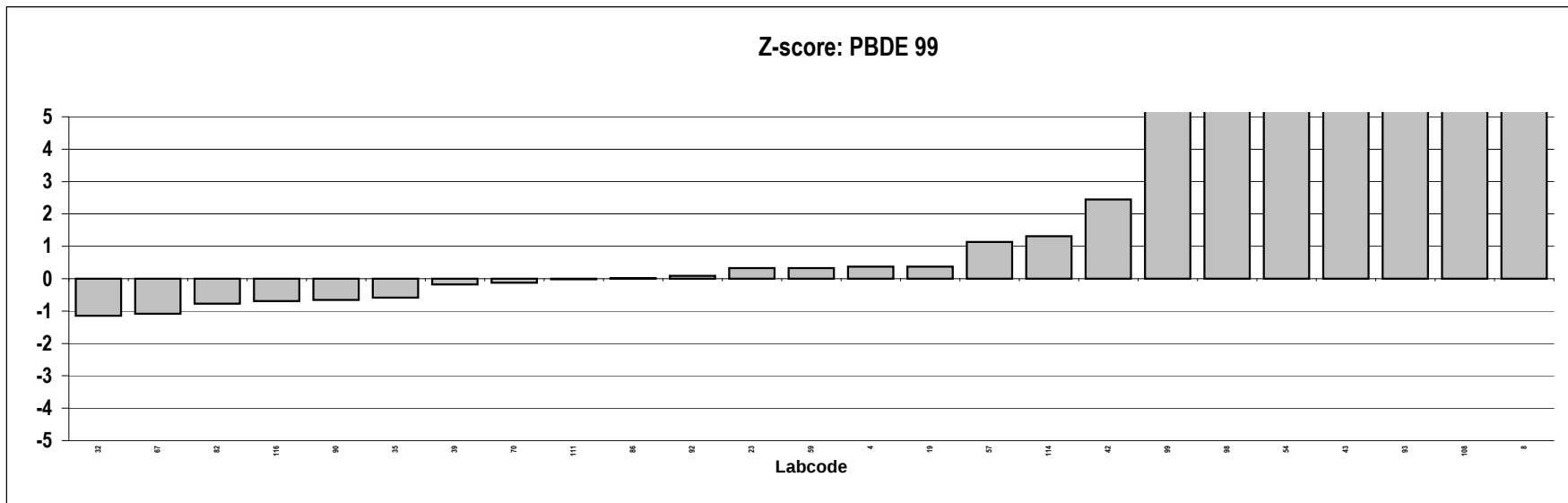
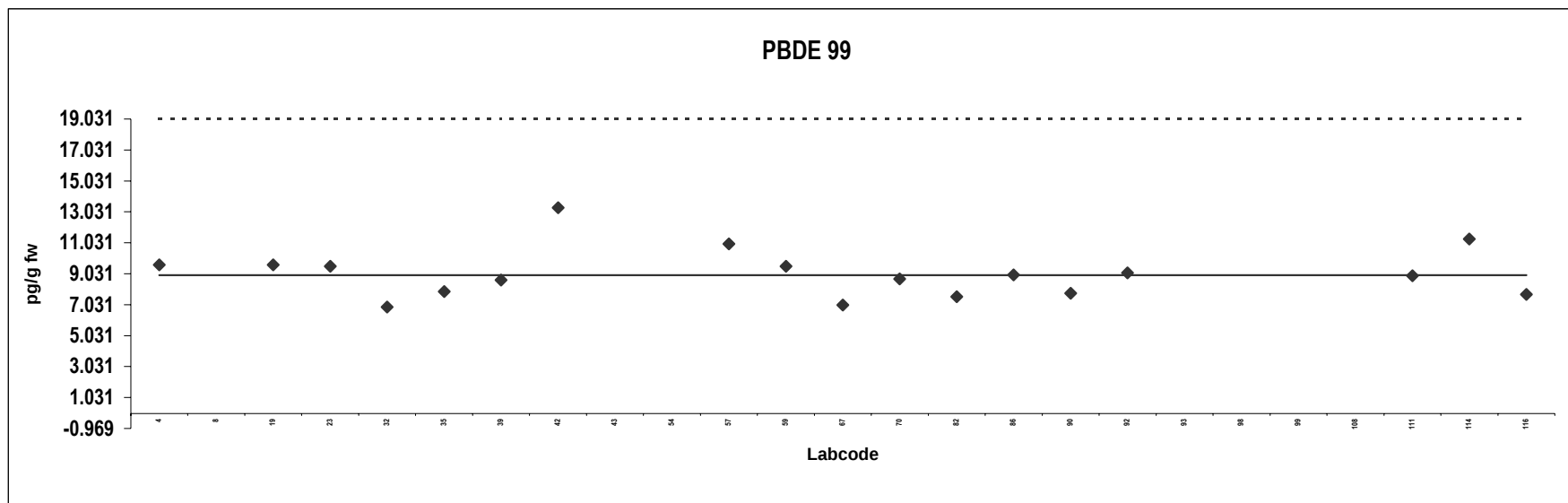
Consensus statistics	
Consensus median, pg/g	13
Median all values pg/g	15
Consensus mean, pg/g	14
Standard deviation, pg/g	5.5
Relative standard deviation, %	38
No. of values reported	25
No. of values removed	7
No. of reported non-detects	0



Cheese
Congener: PBDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	9.6				
8	1070	Outlier			
19	9.6				
23	9.5				
32	6.9				
35	7.9				
39	8.6				
42	13				
43	28	Outlier			
54	25	Outlier			
57	11				
59	9.5				
67	7.0				
70	8.7				
82	7.6				
86	9.0				
90	7.8				
92	9.1				
93	32	Outlier			
98	22	Outlier			
99	21	Outlier			
108	404	Outlier			
111	8.9				
114	11				
116	7.7				

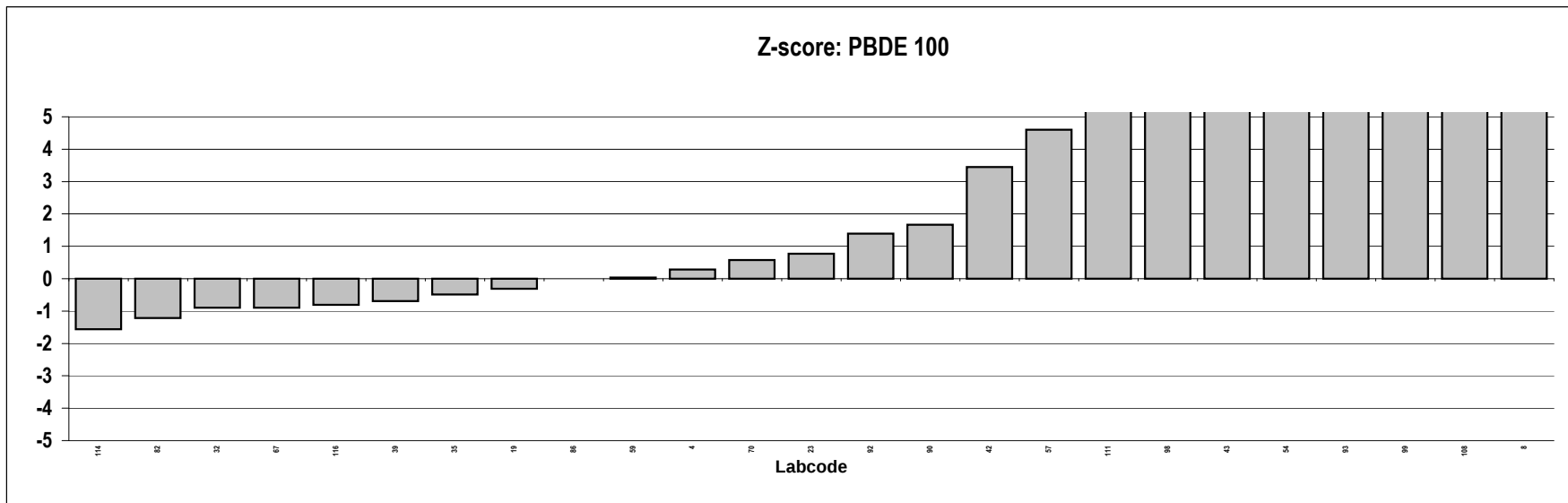
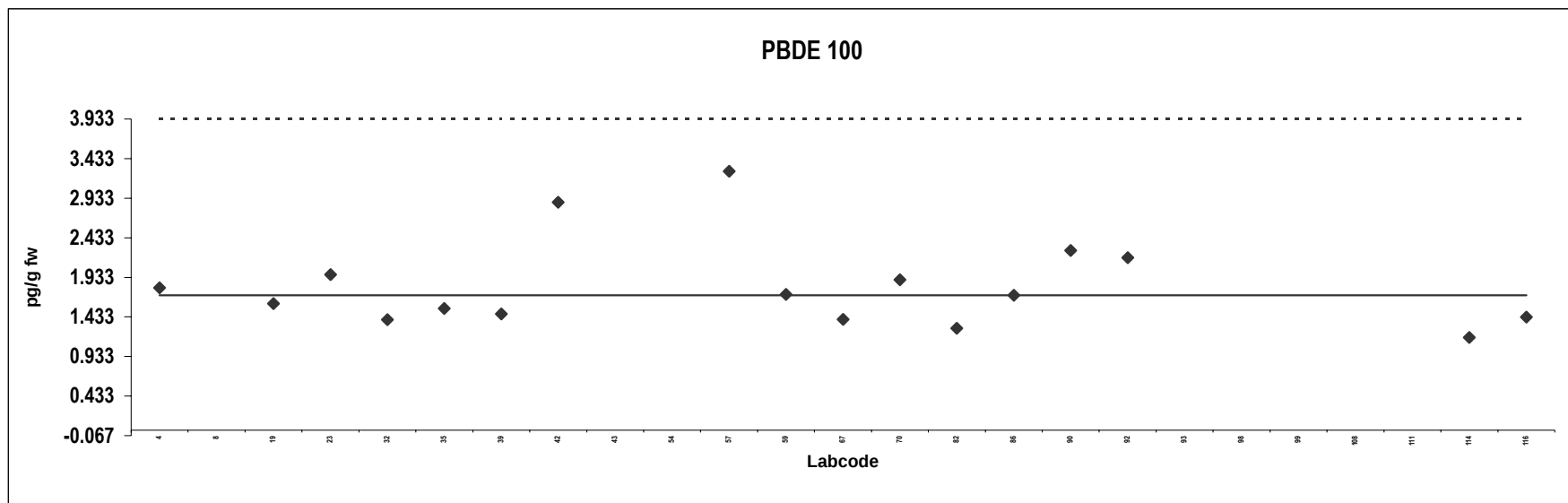
Consensus statistics	
Consensus median, pg/g	8.9
Median all values pg/g	9.5
Consensus mean, pg/g	9.0
Standard deviation, pg/g	1.6
Relative standard deviation, %	18
No. of values reported	25
No. of values removed	7
No. of reported non-detects	0



Cheese
Congener: PBDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	1.8				
8	993	Outlier			
19	1.6				
23	2.0				
32	1.4				
35	1.5				
39	1.5				
42	2.9				
43	5.4	Outlier			
54	5.7	Outlier			
57	3.3				
59	1.7				
67	1.4				
70	1.9				
82	1.3				
86	1.7				
90	2.3				
92	2.2				
93	6.6	Outlier			
98	5.3	Outlier			
99	7.1	Outlier			
108	74	Outlier			
111	4.0	Outlier,ND			
114	1.2				
116	1.4				

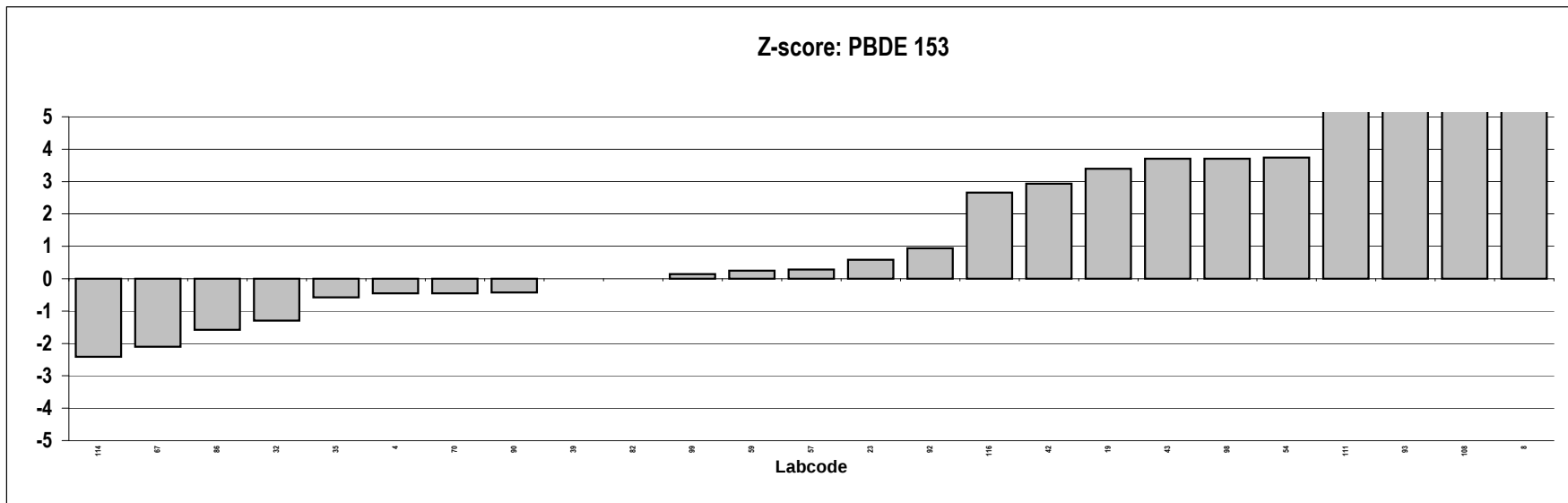
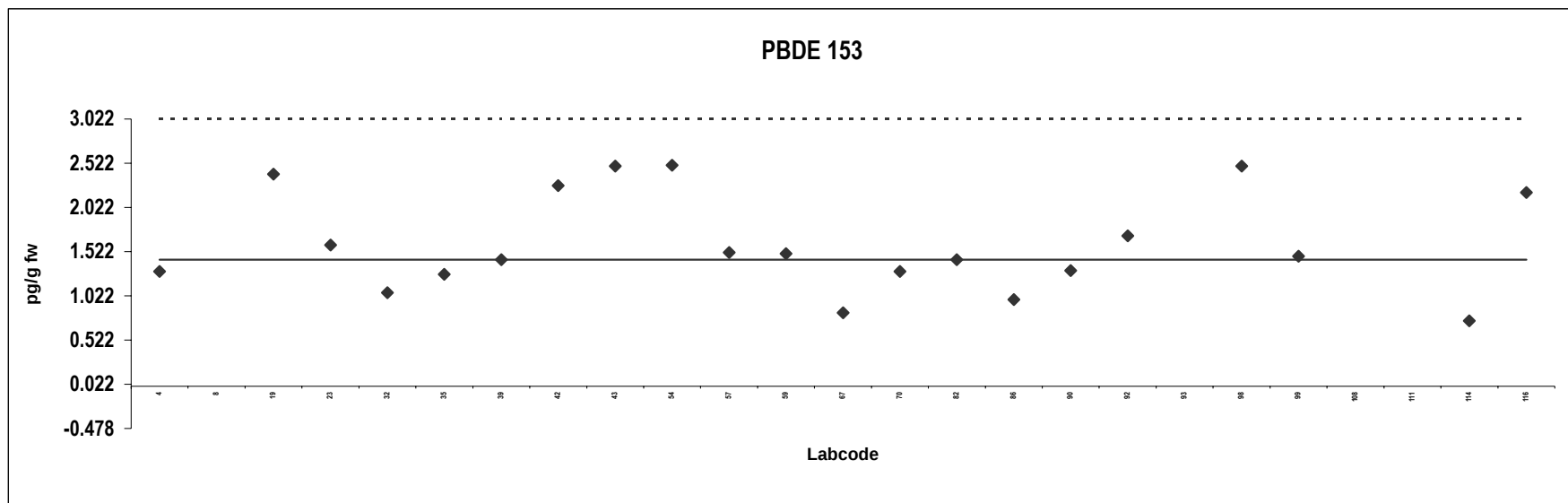
Consensus statistics	
Consensus median, pg/g	1.7
Median all values pg/g	2.0
Consensus mean, pg/g	1.8
Standard deviation, pg/g	0.56
Relative standard deviation, %	31
No. of values reported	25
No. of values removed	8
No. of reported non-detects	1



Cheese
Congener: PBDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	1.3				
8	383	Outlier			
19	2.4	ND			
23	1.6				
32	1.1				
35	1.3				
39	1.4				
42	2.3				
43	2.5				
54	2.5	ND			
57	1.5				
59	1.5				
67	0.83				
70	1.3				
82	1.4				
86	0.98				
90	1.3				
92	1.7				
93	5.4	Outlier			
98	2.5				
99	1.5				
108	40	Outlier			
111	4.0	Outlier,ND			
114	0.74				
116	2.2				

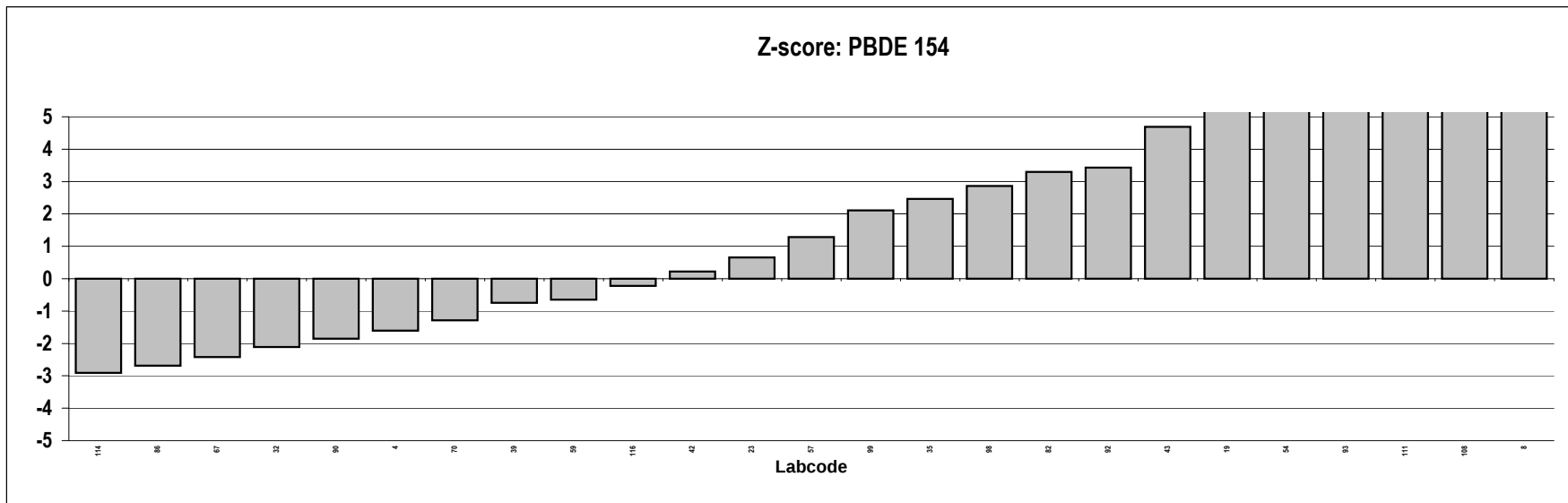
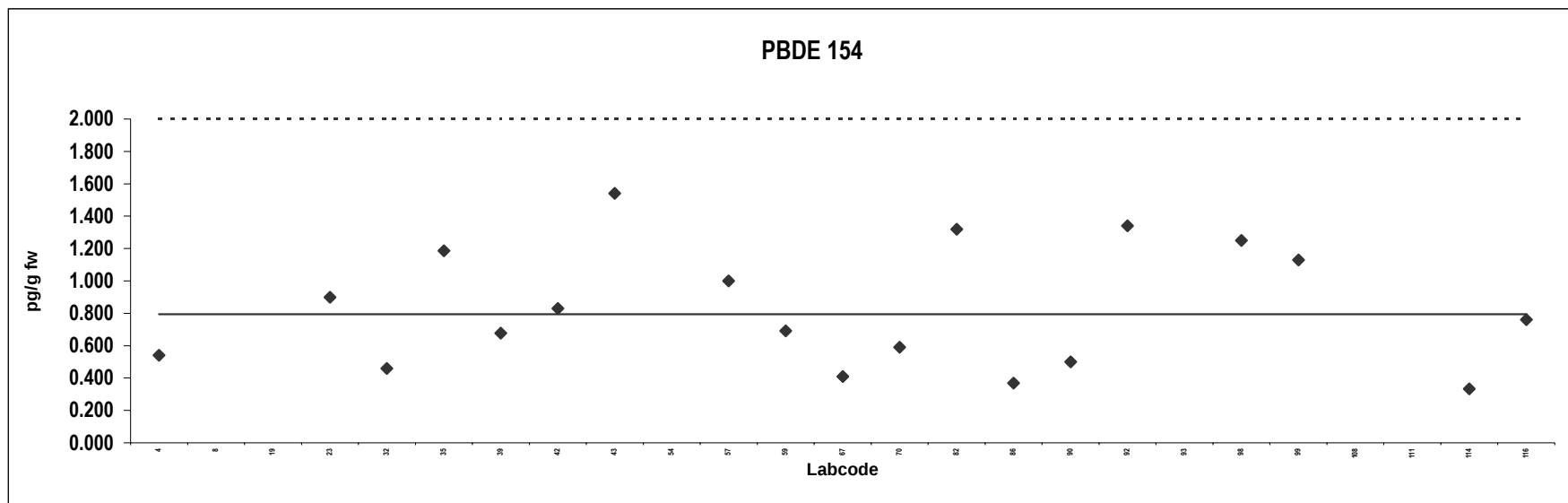
Consensus statistics	
Consensus median, pg/g	1.4
Median all values pg/g	1.5
Consensus mean, pg/g	1.6
Standard deviation, pg/g	0.56
Relative standard deviation, %	35
No. of values reported	25
No. of values removed	4
No. of reported non-detects	3



Cheese
Congener: PBDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	0.54				
8	993	Outlier			
19	2.4	Outlier,ND			
23	0.90				
32	0.46				
35	1.2				
39	0.68				
42	0.83				
43	1.5				
54	2.5	Outlier,ND			
57	1.0	ND			
59	0.69				
67	0.41				
70	0.59				
82	1.3				
86	0.37	ND			
90	0.50	ND			
92	1.3				
93	3.4	Outlier			
98	1.3				
99	1.1				
108	34	Outlier			
111	4.0	Outlier,ND			
114	0.33				
116	0.76				

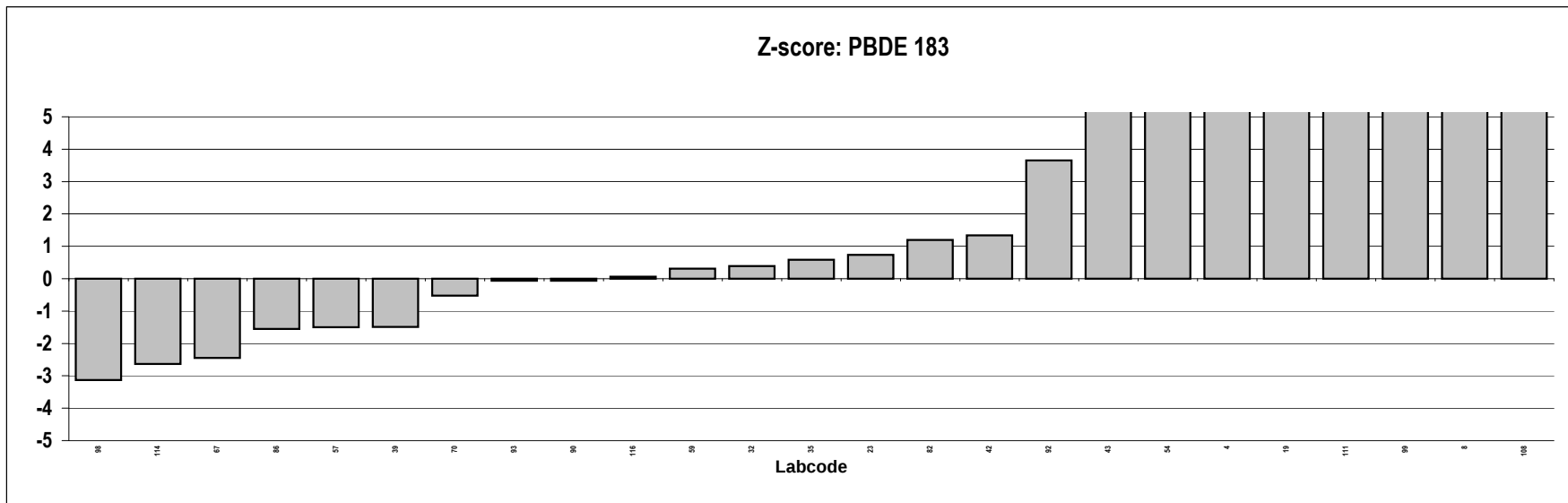
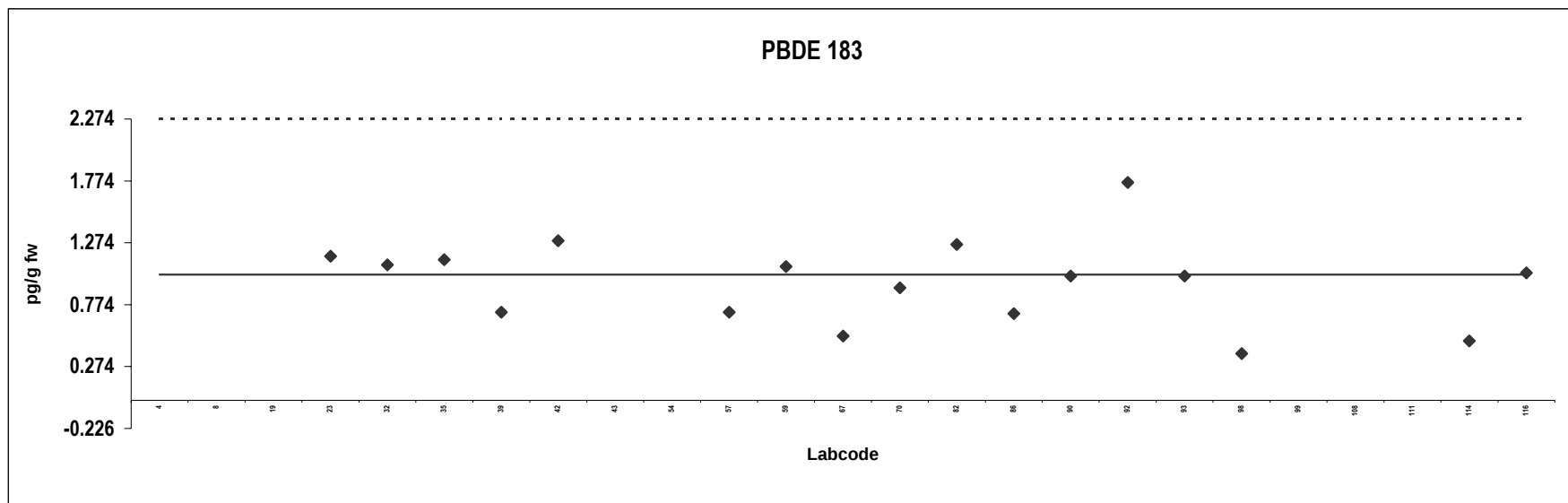
Consensus statistics	
Consensus median, pg/g	0.80
Median all values pg/g	1.0
Consensus mean, pg/g	0.83
Standard deviation, pg/g	0.37
Relative standard deviation, %	45
No. of values reported	25
No. of values removed	6
No. of reported non-detects	6



Cheese
Congener: PBDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	3.7	Outlier,ND			
8	7.7	Outlier			
19	4.0	Outlier,ND			
23	1.2				
32	1.1				
35	1.1				
39	0.71				
42	1.3				
43	2.5	Outlier			
54	2.5	Outlier,ND			
57	0.71				
59	1.1				
67	0.52				
70	0.91				
82	1.3				
86	0.70				
90	1.0				
92	1.8				
93	1.0				
98	0.38	ND			
99	5.9	Outlier			
108	15	Outlier,ND			
111	4.0	Outlier,ND			
114	0.48				
116	1.0				

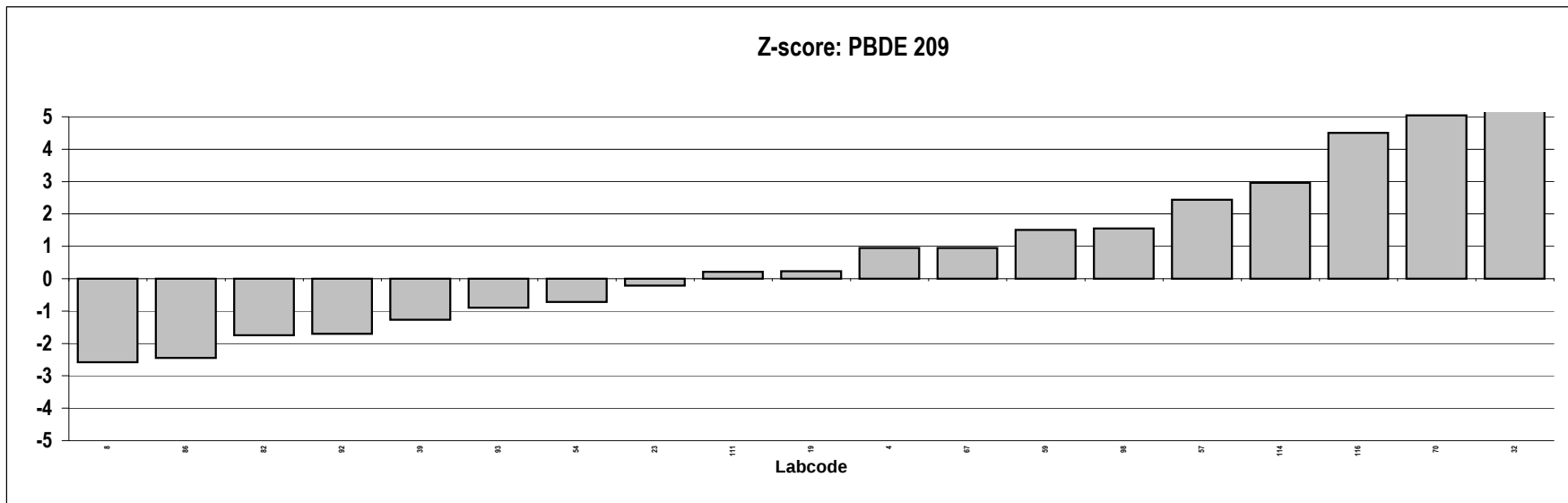
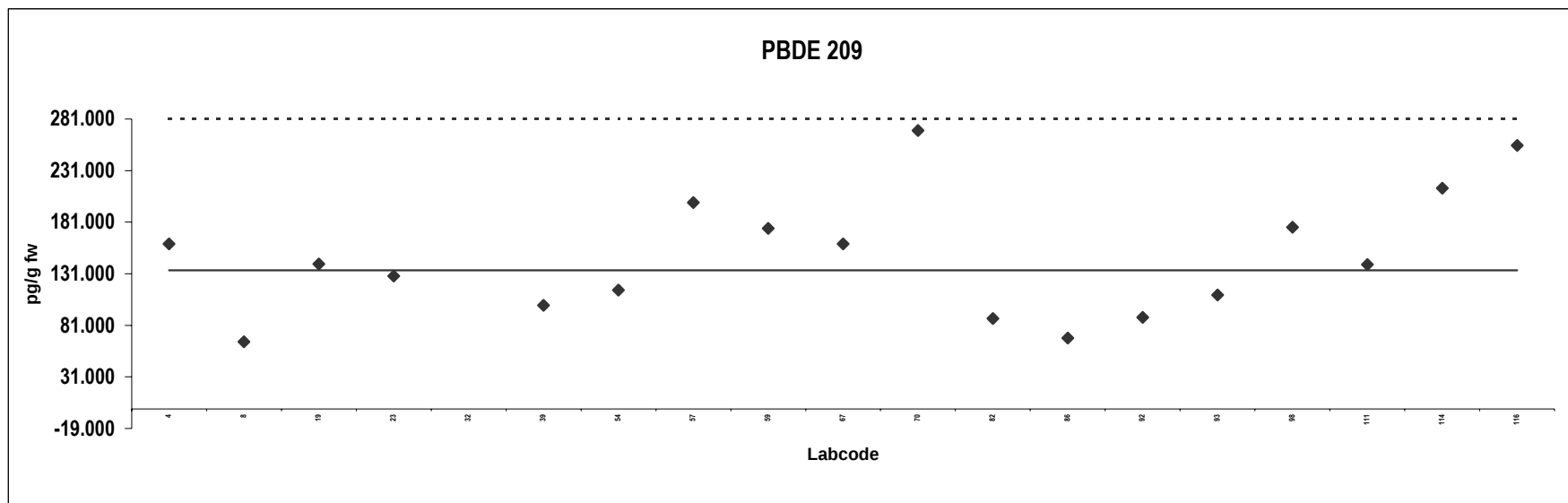
Consensus statistics	
Consensus median, pg/g	1.0
Median all values pg/g	1.1
Consensus mean, pg/g	0.96
Standard deviation, pg/g	0.34
Relative standard deviation, %	36
No. of values reported	25
No. of values removed	8
No. of reported non-detects	6



Cheese
Congener: PBDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
4	160	ND			
8	65				
19	141				
23	129				
32	349	Outlier			
39	100				
54	115				
57	200	ND			
59	175				
67	160				
70	270				
82	88				
86	69				
92	89				
93	110				
98	176				
111	140				
114	214				
116	255				

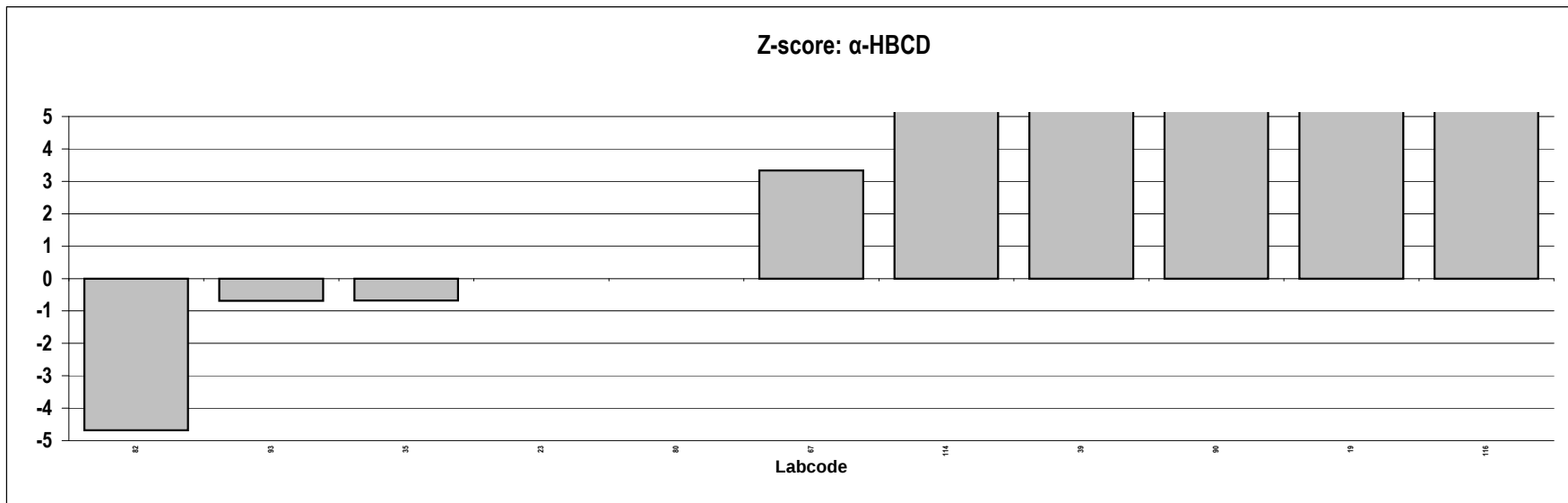
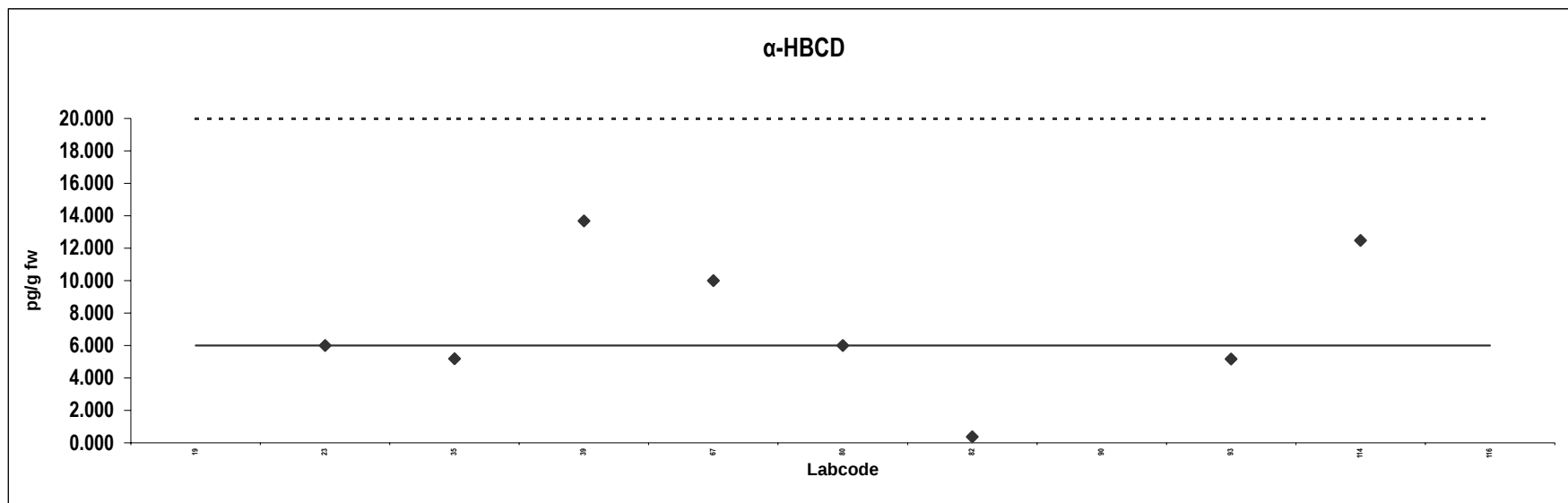
Consensus statistics	
Consensus median, pg/g	134
Median all values pg/g	141
Consensus mean, pg/g	147
Standard deviation, pg/g	60
Relative standard deviation, %	41
No. of values reported	19
No. of values removed	1
No. of reported non-detects	2



Cheese
Congener: α -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
19	25	Outlier,ND			
23	6.0				
35	5.2				
39	14				
67	10	ND			
80	6.0				
82	0.38	ND			
90	23	Outlier,ND			
93	5.2				
114	12				
116	103	Outlier			

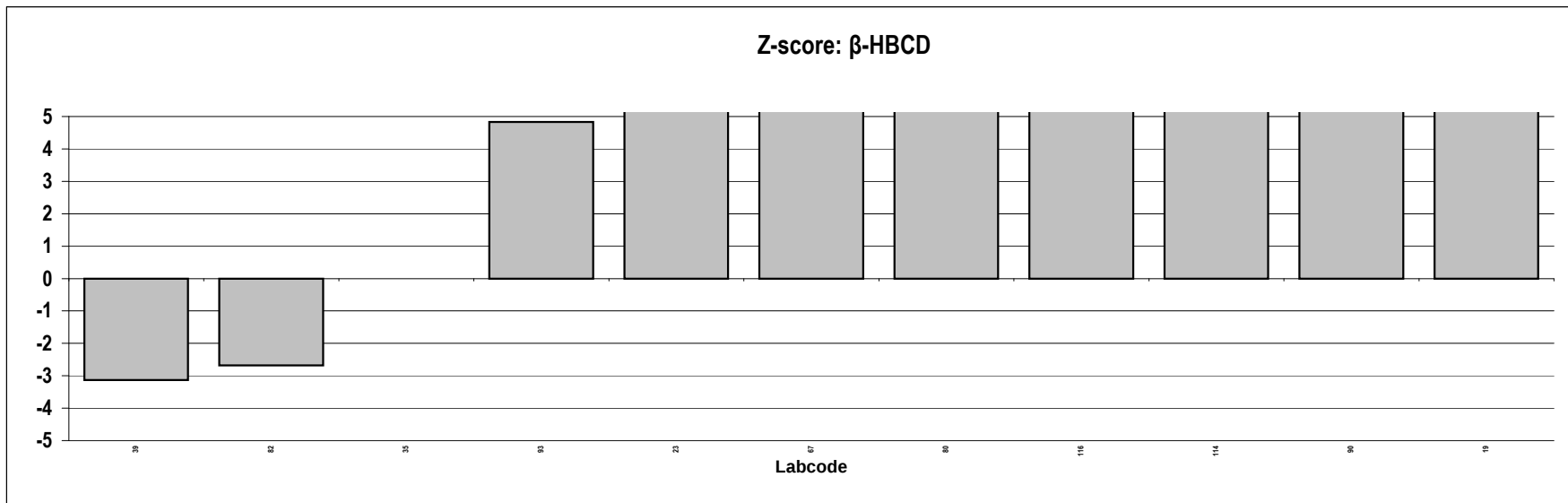
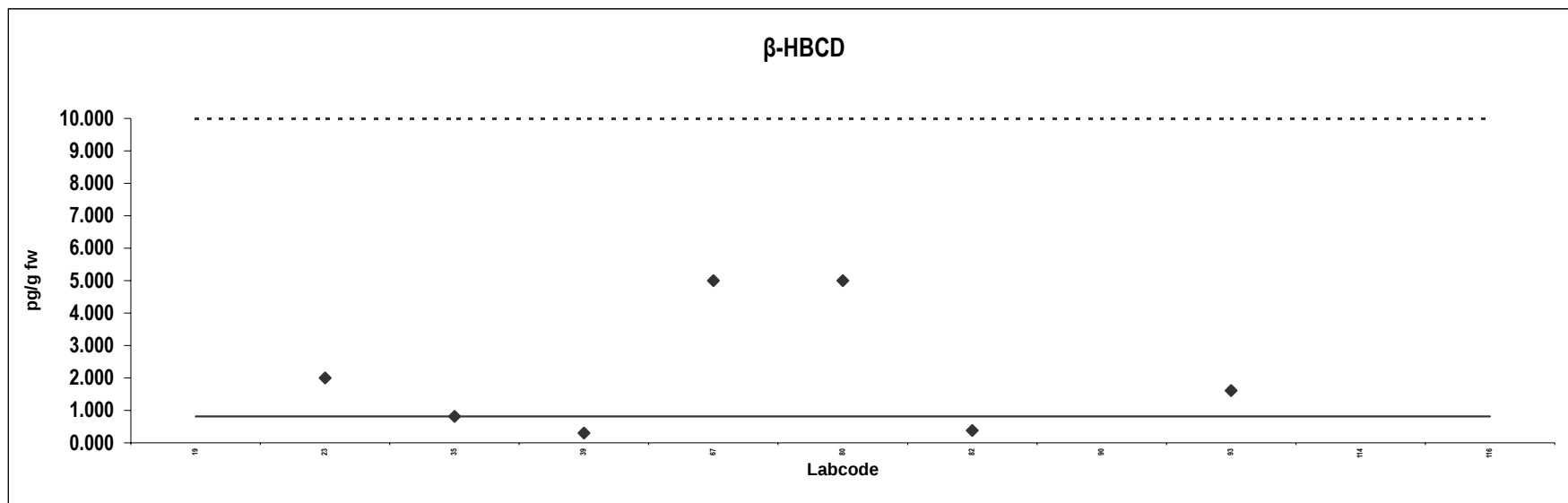
Consensus statistics	
Consensus median, pg/g	6.0
Median all values pg/g	10
Consensus mean, pg/g	7.4
Standard deviation, pg/g	4.4
Relative standard deviation, %	60
No. of values reported	11
No. of values removed	3
No. of reported non-detects	4



Cheese
Congener: β -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
19	25	Outlier,ND			
23	2.0	ND			
35	0.82				
39	0.31	ND			
67	5.0	ND			
80	5.0	ND			
82	0.38	ND			
90	23	Outlier,ND			
93	1.6	ND			
114	16	Outlier			
116	15	Outlier,ND			

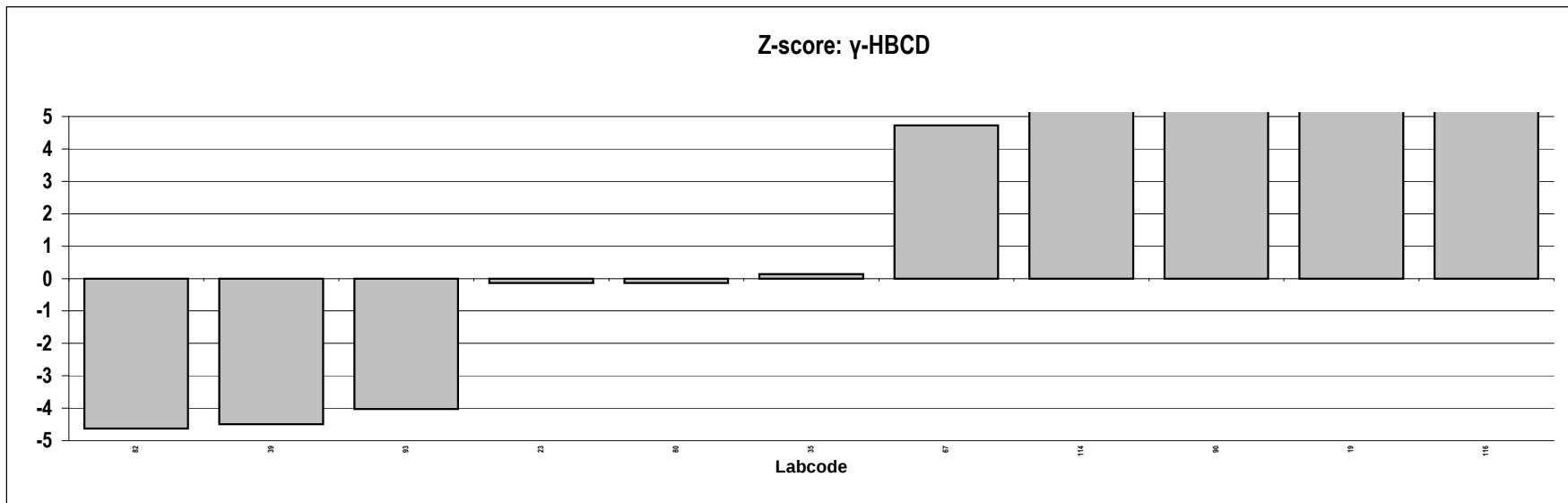
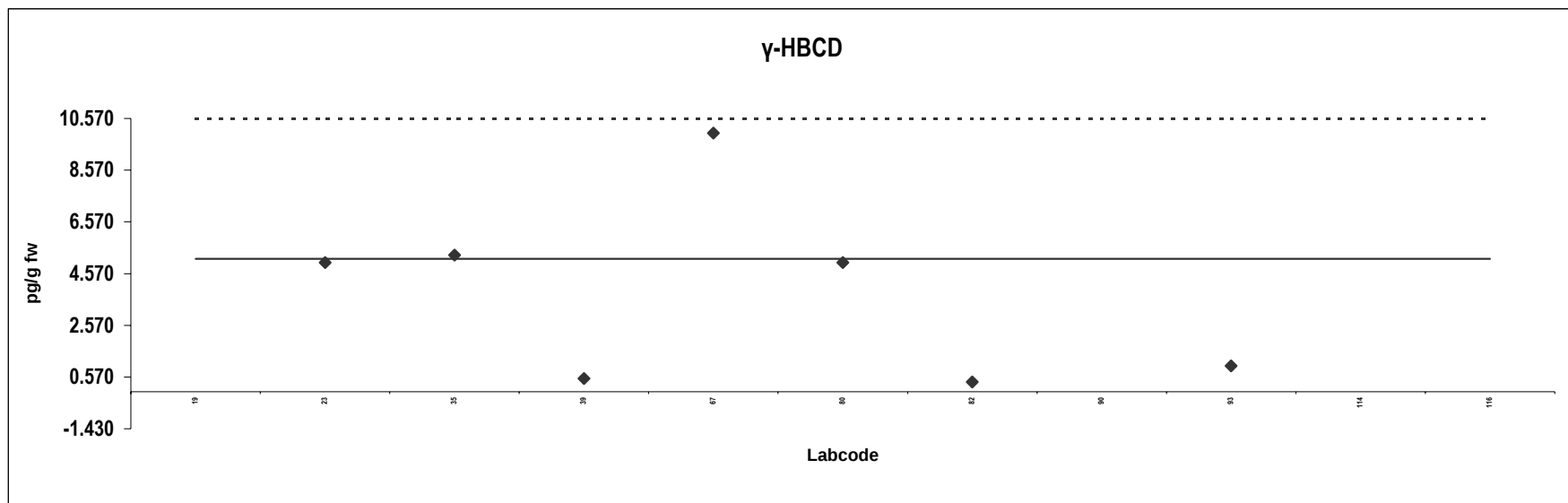
Consensus statistics	
Consensus median, pg/g	0.82
Median all values pg/g	5.0
Consensus mean, pg/g	2.2
Standard deviation, pg/g	2.0
Relative standard deviation, %	94
No. of values reported	11
No. of values removed	4
No. of reported non-detects	9



Cheese
Congener: γ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
19	25	Outlier,ND			
23	5.0				
35	5.3				
39	0.52	ND			
67	10	ND			
80	5.0	ND			
82	0.38	ND			
90	23	Outlier,ND			
93	1.0	ND			
114	19	Outlier			
116	40	Outlier,ND			

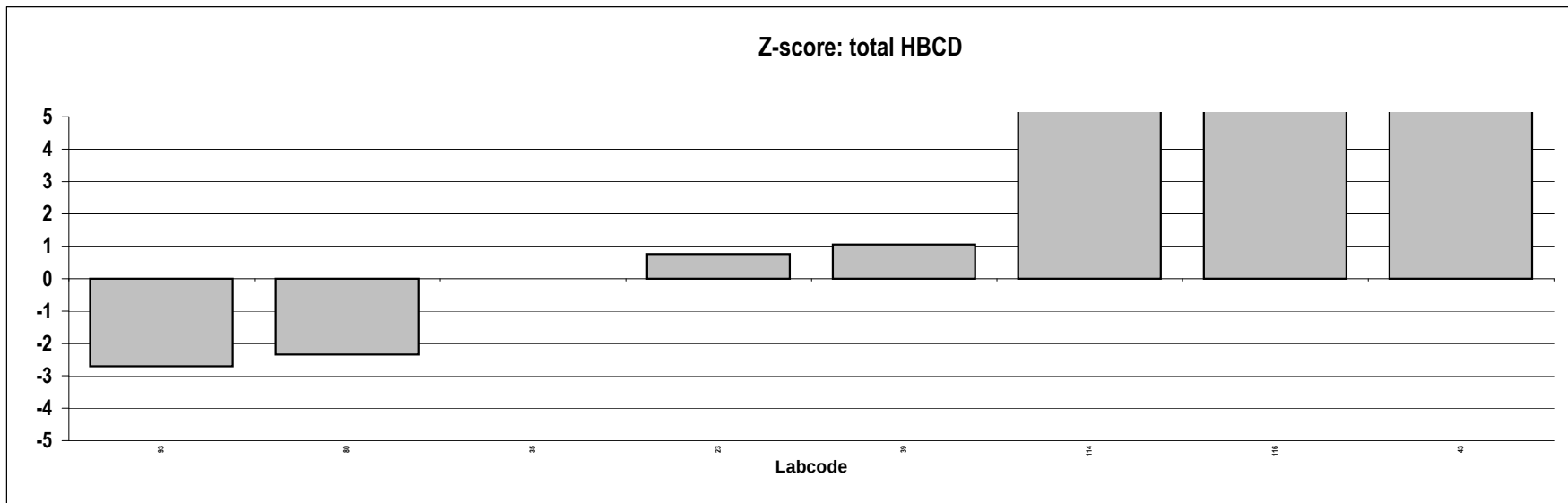
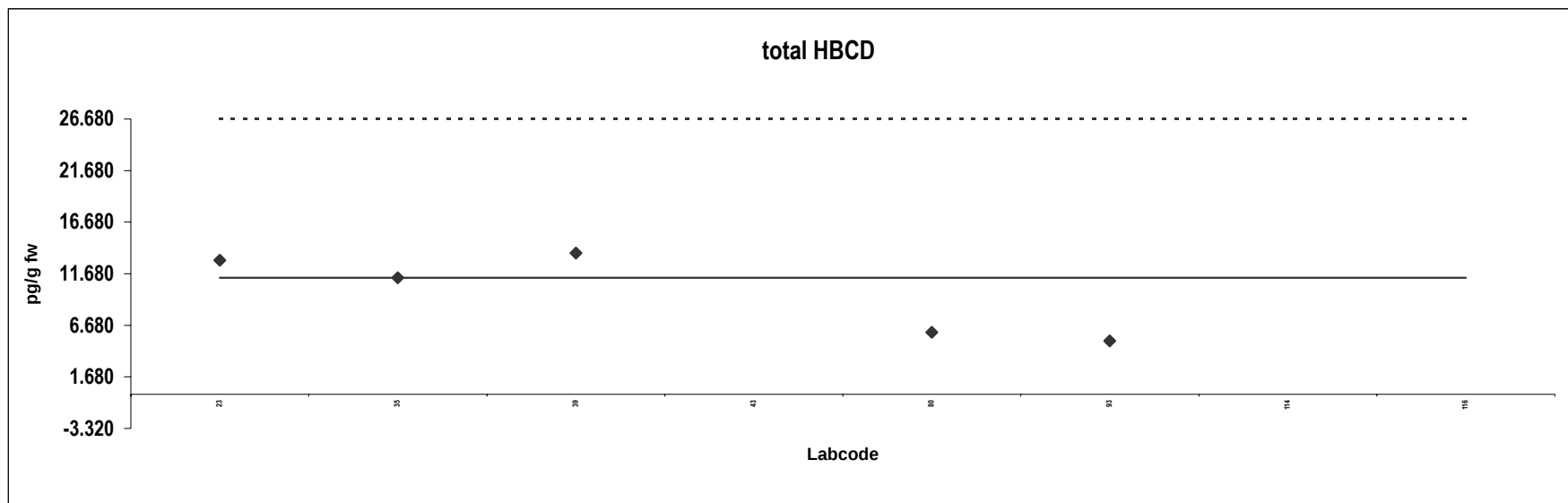
Consensus statistics	
Consensus median, pg/g	5.1
Median all values pg/g	5.3
Consensus mean, pg/g	3.9
Standard deviation, pg/g	3.5
Relative standard deviation, %	90
No. of values reported	11
No. of values removed	4
No. of reported non-detects	8



Cheese
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
23	13				
35	11				
39	14				
43	520	Outlier			
80	6.0				
93	5.2				
114	47	Outlier			
116	103	Outlier			

Consensus statistics	
Consensus median, pg/g	11
Median all values pg/g	13
Consensus mean, pg/g	9.8
Standard deviation, pg/g	4.0
Relative standard deviation, %	40
No. of values reported	8
No. of values removed	3
No. of reported non-detects	0



Appendix 5:

Presentation of results
for lipid determination

Lipid determination for Beef

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
3	13	outlier	93	12	outlier			
4	14		95	15				
7	13		98	12				
8	12		99	11				
11	14		101	14				
15	15		103	13				
17	15		105	13				
19	14		107	6.6				
20	14		108	15				
22	12		109	13				
23	13		110	13				
26	7.3		111	13				
27	12		113	15				
30	13		114	11				
32	12		116	13	outlier			
33	13	outlier	117	17				
35	14		118	12				
36	13		119	14				
39	12							
41	12							
42	13							
43	13							
45	11							
46	16							
47	13							
50	11	outlier						
53	19							
54	14							
55	15							
57	13							
59	13							
61	13							
62	13							
65	5.7							
67	14							
70	13							
80	13							
81	14							
82	12							
83	11	outlier						
84	17							
85	13							
86	13							
90	12							
91	13							
92	12							

Mean	Standard deviation	Relative standard deviation	Median
13	1.1	8.3	13

Lipid determination for Salmon

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
1	8.1		84	9.4				
3	8.1		86	7.7				
4	8.9		90	6.8				
6	8.6		91	8.0				
7	8.5		92	7.9				
8	8.3		93	8.1				
11	8.4		95	6.8				
16	6.4		98	7.9				
17	7.8		103	14	outlier			
19	8.8		105	7.2				
22	7.3		106	9.0				
23	8.6		107	4.0				
24	7.7		108	9.7				
27	7.7		109	7.6				
29	8.3		110	8.1				
30	8.0		111	7.9				
31	1.8	outlier	113	8.5				
32	7.6		114	7.7				
33	8.2		115	9.5				
35	8.3		116	8.0				
36	8.1		117	15	outlier			
37	2.6	outlier	118	7.6				
39	7.8		119	8.3				
41	7.2							
42	5.1							
43	7.5							
44	8.1							
45	6.3							
46	8.5							
47	8.7							
50	2.4	outlier						
54	7.6							
55	8.5							
56	7.1							
57	8.4							
59	8.1							
61	5.5							
62	14	outlier						
65	2.0	outlier						
67	9.4							
70	7.9							
76	6.1							
80	7.9							
81	8.0							
82	7.8							
83	6.7							

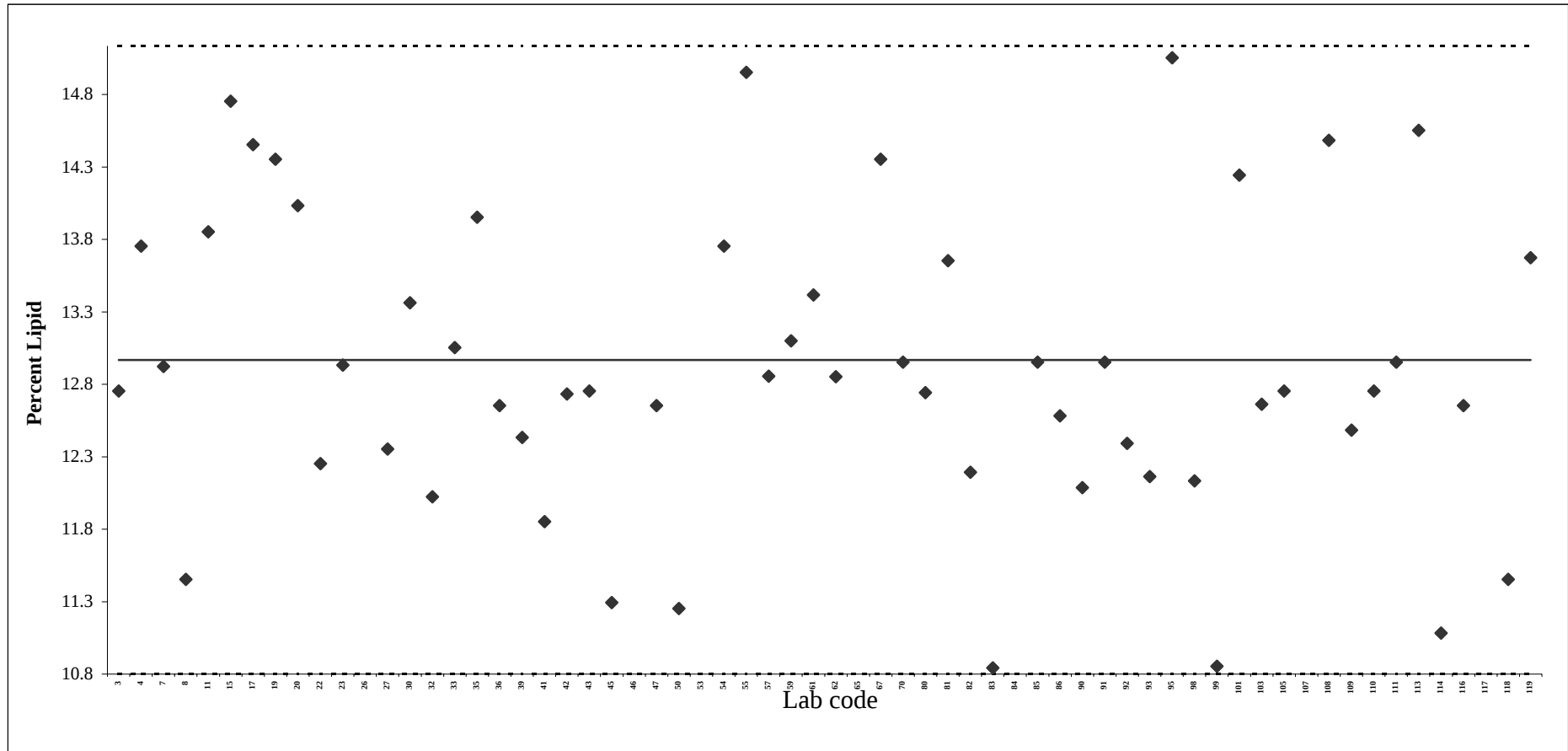
Mean	Standard deviation	Relative standard deviation	Median
7.8	1.0	13	8.0

Lipid determination for Cheese

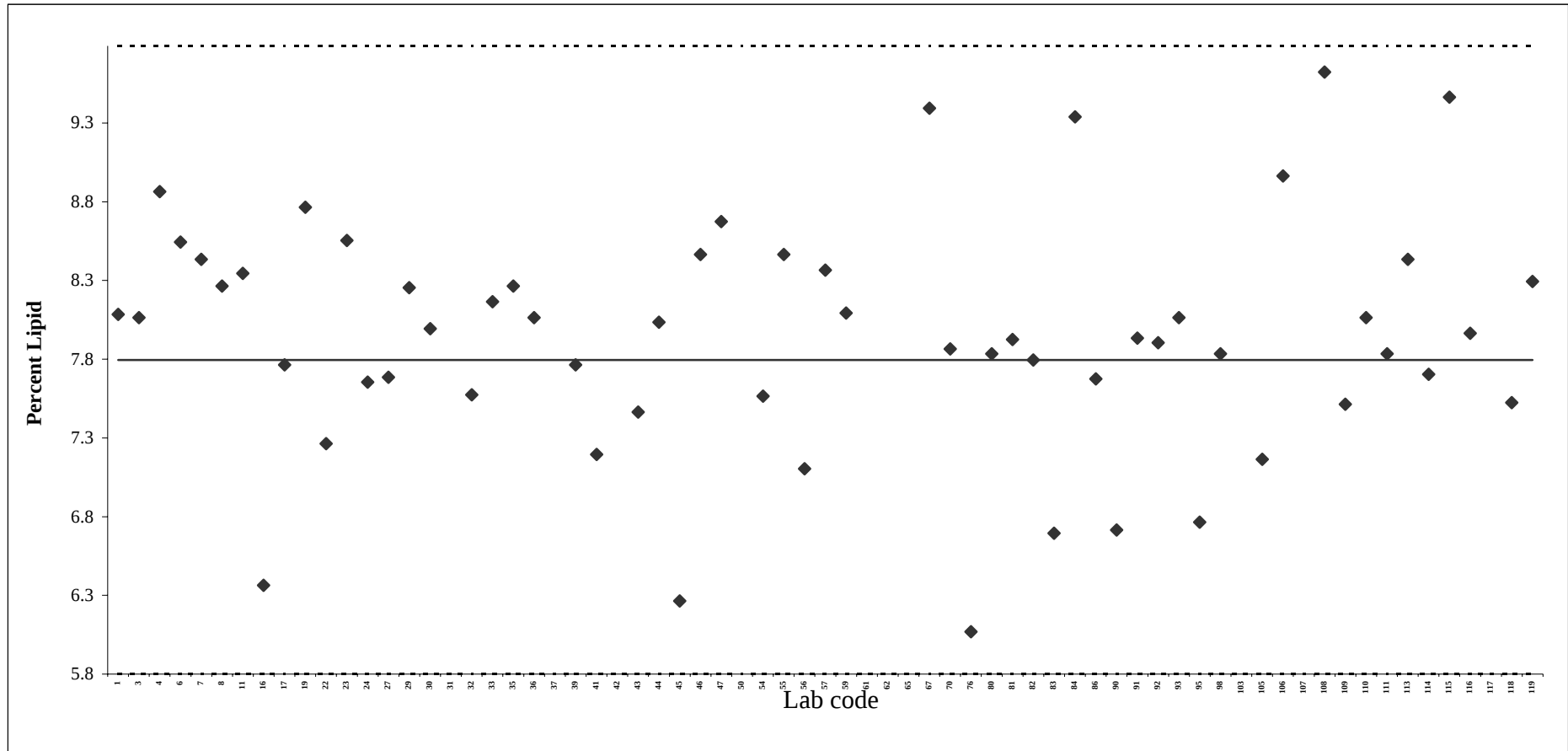
Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
2	27	outlier	108	29				
3	26		109	26				
4	27		111	26				
8	23		113	29				
11	22		114	26				
19	29		116	26				
23	28		119	28				
30	25							
32	15							
33	26							
35	16							
37	10							
39	24							
41	16							
42	23							
43	27							
45	23							
46	31							
50	23							
54	17							
55	26							
57	26							
59	26							
61	34							
62	26							
65	22							
67	30							
70	26							
76	27							
77	32							
80	27							
81	26							
82	25							
83	25							
84	27							
86	24							
89	27							
90	23							
91	27							
92	29							
93	24							
95	26							
98	25							
99	20							
103	25	outlier						
105	7.7							

Mean	Standard deviation	Relative standard deviation	Median
25	3.7	14	26

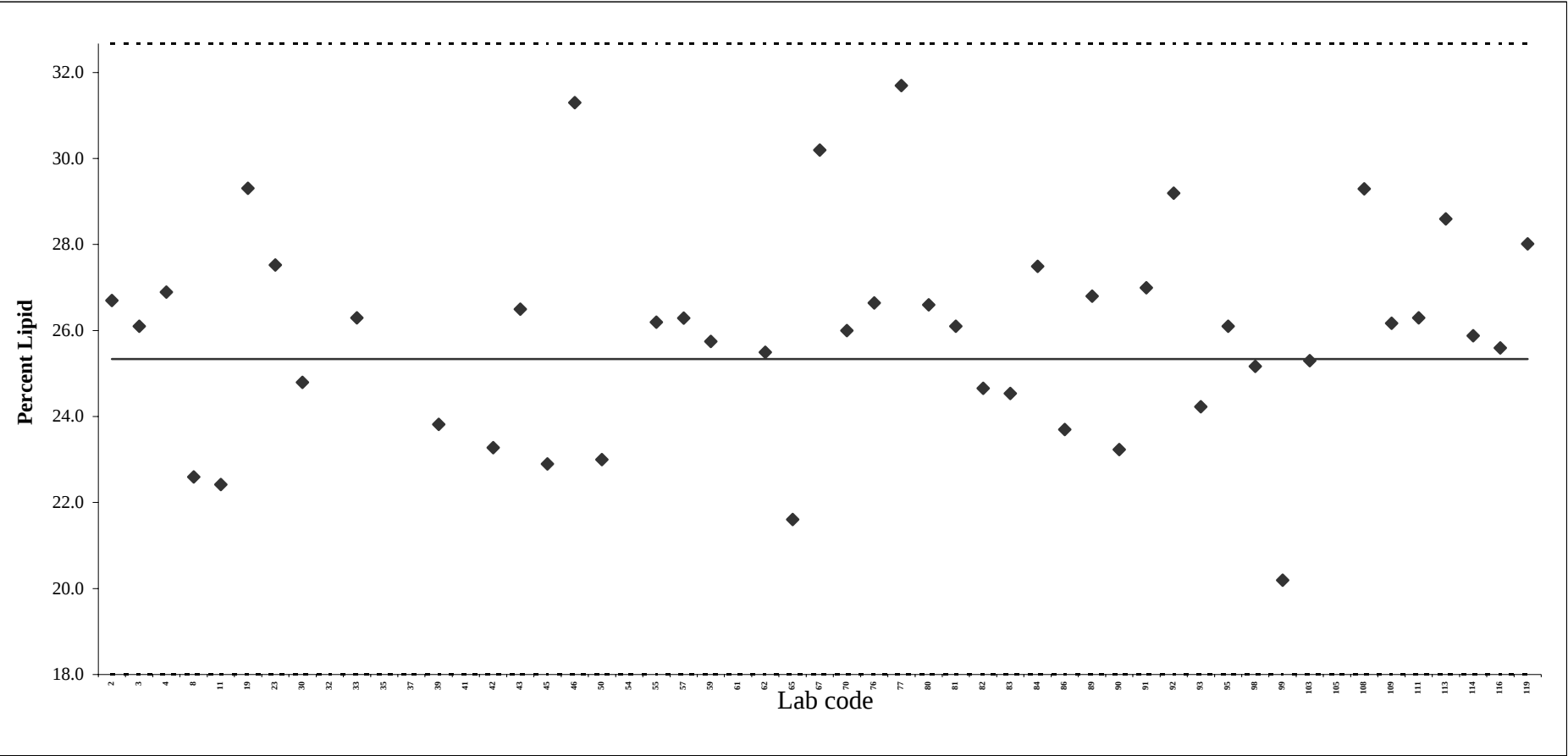
Lipid determination; Beef



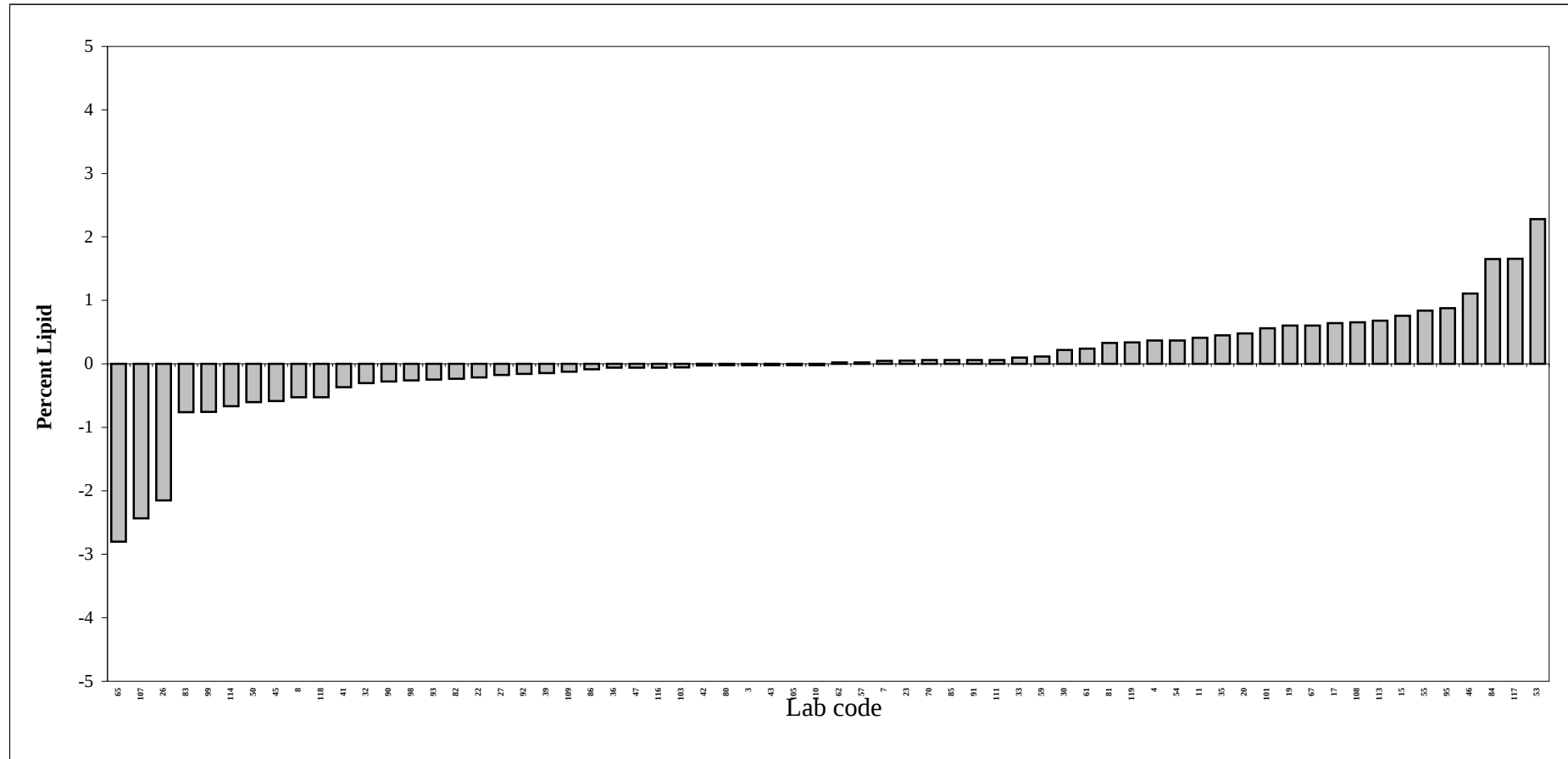
Lipid determination; Salmon



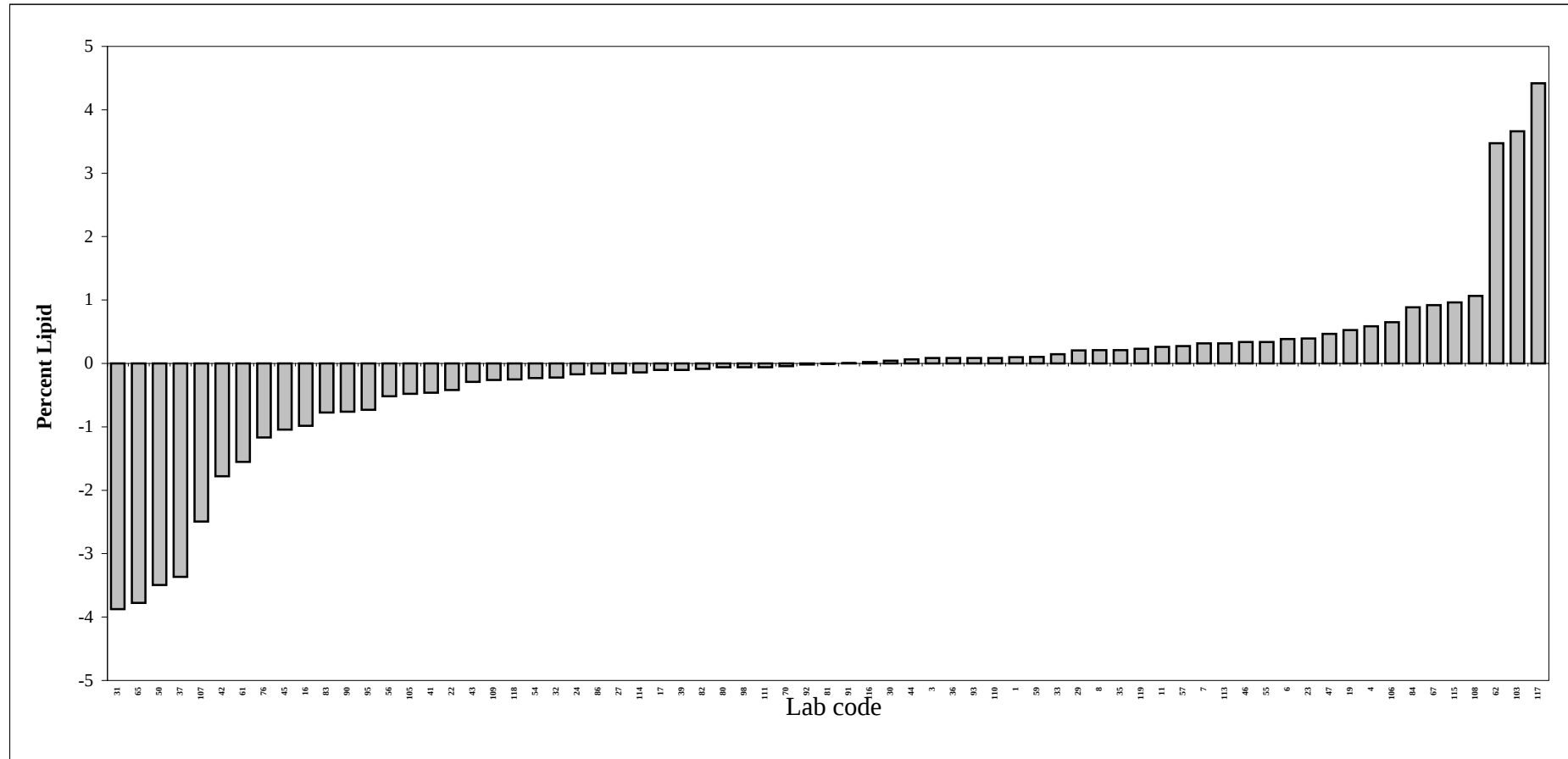
Lipid determination; Cheese



Z-score lipid determination; Beef



Z-score lipid determination; Salmon



Z-score lipid determination; Cheese

