2019

REPORT

Interlaboratory Comparison on POPs in Food

The twentieth round of an international study

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NIPH

Norwegian Institute of Public Health

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Summary

The 20th round of the Interlaboratory Comparison on POPs in Food was conducted in 2019 by the Norwegian Institute of Public Health (NIPH). The study included the determination of the 2,3,7,8-chlorinated dibenzo-*p*-dioxins (PCDDs) and dibenzofurans (PCDFs), as well as dioxin-like non-ortho and mono-ortho chlorinated biphenyls (PCBs) in three different food items. Additionally, the participating laboratories could determine the concentrations of six indicator PCBs, polybrominated diphenyl ethers (PBDEs) and hexabromocyclododecanes (HBCDs) in the same food samples.

For the first time a fourth matrix was added, designated for the determination of the following poly- and perfluoroalkyl substances (PFASs): Perfluorooctanesulfonate (PFOS), perfluorohexanesulfonate (PFHxS), perfluorooctanoate (PFOA), perfluorononanoate (PFNA), perfluorodecanoate (PFDA) and perfluoroundecanoate (PFUnDA).

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, as well as for PFASs, in regular foodstuffs.

With respect to PCDDs/PCDFs, non-ortho PCBs, mono-ortho PCBs, indicator PCBs, PBDEs and α-HBCD, the 2019-round of the study was performed on unfortified homogenates of veal, herring and brown meat from crab (hereafter referred to as Brown meat). An unfortified homogenate of perch was offered for the determination of PFASs.

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 73 laboratories worldwide in January, and results were returned from 72 of these.

A draft report was made available on our webpage www.fhi.no/ILC in July 2019, and the deadline for commenting on the published results was set to September 15th 2019.

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 are also presented.

For the first time, we will also present the results of PFOS, PFHxS, PFOA, PFNA, PFDA and PFUnDA in a sample of Perch.

The consensus concentration (assigned value) for each analyte in the four 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, and this second median was called consensus value.

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 (consensus value) and consensus mean as well as standard deviation (SD) were calculated from the remaining data.

When calculating the results for PFASs in the sample of Perch, we adopted the same approach as we used for the indicator PCBs and PBDEs. However, as the number of reported results were much lower for PFAS than for the other groups of analytes, outliers would contribute to a larger degree. Therefor we have chosen to remove low outliers, as well as high outliers, from the PFAS data set.

Toxic equivalents (TEQs) were calculated from the consensus medians of individual congeners using the toxic equivalency factors derived by WHO 2006 (from 2012: $WHO_{2006}TEQs$ as opposed to $WHO_{1998}TEQs$ as in the reports published before 2012).

Z-scores for the PCDD/PCDF TEQs were calculated for each laboratory using ±20 % of the consensus TEQs as a value for target standard deviation ($\sigma=0.2$), on both fresh weight and lipid weight basis. 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 of Veal, Herring and Brown meat ($\sigma=0.2$) (both on a fresh weight and a lipid weight basis). The z-scores for PFASs were calculated in the same way, but on fresh weight base only.

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.

The sample of Brown meat was the sample in this study with the highest total TEQ (2.3 pg TE/g fw, $WHO_{2006}TEFs$). For this sample, Z-scores within ±1 were obtained by 82 % of the participating laboratories, and Z-scores within ±2 were achieved by 93 % of the participants (Z scores within ±1 and ±2, corresponding to a trueness of ±20 % and ±40 %, respectively). The Brown meat -sample was closely followed by the Herring-sample, with a consensus total TEQ of 2.1 pg TE/g fw ($WHO_{2006}TEFs$). For this sample 86 % of the participants achieved Z-scores within ±1, and an impressing 98 % achieved Z-scores within ±2!

For the sample of Veal, which on beforehand was assumed to be the sample with lowest level of contamination (total TEQ=0.082 pg TE/g, $WHO_{2006}TEFs$, fresh weight), Z-scores within ±1 were obtained by 33 % of the reporting participants on fresh weight basis, and Z-scores within ±2 was achieved by 53 % of the participants. This clearly mirrors the high number of non-detects reported for the PCDD/PCDFs, and the variation in the reported limits of detection reported by the participants.

The relative standard deviation (RSD) calculated for the total TEQ after removal of outliers was 15-23 % for the two samples that had the highest levels of contamination (Herring and Brown meat , respectively). For the lower contaminated Veal-sample, the corresponding RSD was 115 %. Considering the levels of contamination in the three food samples in this study, it may be concluded that the abilities and performance of laboratories worldwide in determining dioxin-like compounds is generally good.

For the food samples, 43-56 laboratories reported results for the six indicator PCBs. The total consensus concentrations on fresh weight basis for six indicator PCBs were 300 pg/g (10 %) in Veal, 12201 pg/g (16 %) in Herring and 5837 pg/g (13 %) in Brown meat, with total RSDs given in parentheses.

16-27 laboratories reported concentrations for all seven of the tetra- to hepta-PBDEs and 14-21 laboratories reported concentrations for PBDE-209. The consensus concentrations of the sum of the PBDEs with PBDE-209 excluded, were on fresh weight basis 6.0 (23 %), 513 (18 %) and 102 (12 %) pg/g in Veal, Herring and Brown meat, respectively, with total RSDs given in parentheses. The consensus concentrations for PBDE-209 were 12 (n=14, RSD=52 %), 11 (n=21, RSD=111 %) and 14 (n=17, RSD=54 %) pg/g fresh weight in Veal, Herring and Brown meat, respectively.

The consensus concentrations calculated for HBCDs are indicative, as only a few laboratories reported results (n=3-6).

9-10 laboratories reported results for the different PFASs in the samples of Perch. The sample was on beforehand known to be heavily contaminated with PFOS (consensus concentration 125393 pg/g fw). 80 % of the participants obtained a Z-score ±2 for PFOS, and 60 % obtained Z-scores ≤1. For PFDA (consensus median 705 pg/g fw), 55 % of the participants obtained z-scores ≤1, and for PFUnDA (consensus concentration was 951 pg/g fw) 56 % obtained z-scores ≤1.

The consensus values for PFHxS, PFOA and PFNA are indicative due to few reported results (many non-detects).

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. For the same reasons, the European Union introduced levels of legislation in 2014 for the indicator PCBs as well. For PFASs, new provisional tolerable weekly intakes for PFOS and PFOA were published by EFSA in 2018. 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 20th round of a world-wide interlaboratory comparison study on dioxin-like compounds, eight PBDEs, six indicator PCBs and HBCD in food, organized by the Department of Environmental Exposure and Epidemiology, at the Norwegian Institute of Public Health (NIPH), Oslo, Norway. New in 2019 was the addition of a food sample designated for the determination of six selected PFASs.

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

The exercise took place from January 2019, when the samples were shipped to the laboratories for analysis, until the reporting deadline in April 2019, 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, 2019.

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 72 laboratories that submitted results, and thereby contributed to the study results, are presented in Table 1.

Table 1. Participants that reported results in the 20th round of the Interlaboratory Comparison on POP's in Food 2019

ALPA Chimies Micropolluants Saint Julien-Les-Metz, France	**ALS Czech Republic** Pardubice, Czech Republic
ALS Environmental - Burlington Burlington, Ontario, Canada	**AsureQuality Ltd – Wellington** Lower Hutt, New Zealand
Arkansas Laboratory (ARKL) **Office of Regulatory Affairs** Jefferson, Arkansas, United States of America	**Australian Ultra Trace Laboratory** **National Measurement Institute - North Ryde** Sydney, Australia
BioDetection Systems B.V. Amsterdam, The Netherlands	**Canadian Food Inspection Agency (CFIA)** Calgary, Alberta, Canada
CARSO-LSEHL Vénissieux, France	**Central Lab of Residue Analysis of Pesticides and Heavy Metals in Foods** Giza, Egypt

Chemisches und Veterinäruntersuchungsamt (CVUA) Freiburg Freiburg, Germany	**China Academy of Inspection and Quarantine Beijing, China**
China National Center for Food Safety Risk Assessment Beijing, China	**Chinese Academy of Sciences Center for Eco-Environmental Sciences** Beijing, China
Concept Life Sciences Manchester, United Kingdom	**CVUA MEL** Münster , Germany
Danish Veterinary and Food Administration Ringsted , Denmark	**Dioxin laboratory of Comprehensive test center of Chinese Academy of Inspection and Quarantine** Hangzhou, Beijing, China
Environmental Laboratory – IQS Barcelona, Spain	**Eurofins ANATECH** SÃO PAULO, Brasil
Eurofins GfA Lab Service GmbH Hamburg, Germany	**Eurofins Laboratorium Zeeuws Vlaanderen** Graauw, The Netherlands
Fera Science Ltd. York, United Kingdom	**Government Laboratory Additives, Contaminants and Composition Section** Hong Kong, China
Havforskningsinstituttet Bergen, Norway	**Health Canada Health Products and Food Branch** Ottawa, Canada
Health Canada Burnaby, British Columbia, Canada Ottawa, Canada	**Hessisches Landeslabor** Wiesbaden, Germany
Hubei Provincial Centre for Disease Control and Prevention Institute of Health Inspection and Testing Wuhan, Hubei Province, China	**Hyper Quantum Technologies, Ltd.** Food Authenticity & Safety Testing Center Kaohsiung City, Taiwan, China
Institute for Agro-food Standards and Testing Technology Shanghai Academy of Agricultural Sciences Shanghai, China	**Institute of Quality Standard & Testing Technology for Agro-Products** The Chinese Academy of Agricultural Sciences Beijing, China
Istituto Zooprofilattico Sperimentale Lombardia Emilia Romagna-Bologna Chemical Department Bologna Bologna, Italy	**Japan Food Research Laboratories** Nagayama Tama-city, Tokyo, Japan
La Drôme Laboratoire Valence, France	**Laboratory of SGS Bulgaria Ltd** Varna, Bulgaria
Laboratory of Vendee (LEAV) la Roche sur Yon, France	**Landesamt für Umweltschutz Sachsen-Anhalt** Halle/Saale, Germany
mas | münster analytical solutions gmbh Münster, Germany, Germany	**Mass Spectrometry and Dioxin Analysis Laboratory NSCR "Demokritos"** Athens, Greece
Maxxam Analytics International Corporation Mississauga, Canada	**MICROPOLLUANTS TECHNOLOGIE SA** Saint Julien-Les-Metz, France
National Cheng Kung University Research Center for Environmental Trace Toxic Substances Tainan, China	**National Food Agency (Livsmedelsverket)** Uppsala, Sweden

National Institute for Health and Welfare **Environmental Health Unit** **Chemical Risks team** Kuopio, Finland	**National Institute of Food and Drug Safety** Ministry of Food and Drug Safety Food contaminants division Cheongju-si, Repulic of Korea
Niedersächsisches Landesamt für Verbraucherschutz **und Lebensmittelsicherheit** **Lebensmittel-und Veterinärinstitut Oldenburg** Oldenburg, Germany	**NILU (Norwegian Institute for Air Research)** Kjeller, Norway
Nofalab Schiedam , The Netherlands	**Pacific Rim Laboratories Inc.** Surrey BC, Canada
POP Lab **Shenzhen Center for Disease Control & Prevention** Shenzhen, Guangdong, China	**SGS Belgium NV** Antwerpen, Belgium
SGS Institut Fresenius GmbH **Bayreuth, Germany**	**SGS Taiwan Ltd.** New Taipei City, Taiwan (R.O.C.)
Shanghai Municipal Center for Disease Control and **Prevention (1)** Shanghai, China	**Shanghai Municipal Center for Disease Control and** **Prevention (2)** Shanghai, China
SIA Analysis Laboratory Edirne, Turkey	**SIA Analysis Laboratory Izmir Branch Office** Izmir, Turkey
Sintef Industri Avd. for Bioteknologi og Nanomedisin Trondheim, Norway	**Sun Dream Environmental Technology Corporation** **Food Hygiene Laboratory** Taichung City, China
Super Micro Mass Research & Technology Center Cheng Shiu University Niaosong District, Kaohsiung City, Taiwan	**SYNLAB Analytics & Services Germany GmbH** Standort Jena Jena, Germany
Taiwan Agricultural Chemicals and Toxic Substances **Research Institute** Council of Agriculture, Executive Yuan Taichung, Taiwan, China	**The State Laboratory - Ireland** Celbridge, Kildare, Ireland
TLR International Laboratories Rotterdam, The Netherlands	**Umeå University** **Department of Chemistry** **Trace Analysis Platform** Umeå, Sweden
Wellington Laboratories Inc. Guelph, Ontario, Canada	**WESSLING GmbH** **Altenberge, Germany**
Worthies Engineering Consultants Corp. **Environmental & Ultra Trace Testing Lab** Taichung, Taiwan	**Yangtze Delta Region Institute of Tsinghua University** Zhejiang, China
Super Micro Mass Research & Technology Center Cheng Shiu University Niaosong District, Kaohsiung City, Taiwan	**SYNLAB Analytics & Services Germany GmbH** Standort Jena Jena, Germany

Design and practical implementation

Study design and reporting of results: PCDDs/PCDFs, non-ortho substituded PCBs, mono-ortho substituted PCBs, indicator PCBs, PBDEs and HBCDs

As in the previous rounds of this interlaboratory comparison study, the test material chosen represented naturally contaminated food items. 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 desired, 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 Veal, Herring and Brown meat.

The laboratories were to report the concentration of each detected congener (e.g. S/N ≥3) in the food items on fresh weight basis, as well as the limit of detection (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 percentage 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/μl for tetra:penta-hexa-hepta:octa chlorinated dibenzo-p-dioxins/-dibenzo furans respectively)

2) Four non-ortho PCBs (10 pg/μl)

3) Eight mono-ortho PCBs (100 pg/μl)

4) Eight PBDEs (100 pg/μl)

5) Six indicator PCBs (100 pg/μl)

6) α-HBCD (500 pg/μl)

The test materials consisted of homogenates of Veal, Herring and Brown meat from Crab. The laboratories could choose to analyze one, two or all three food samples.

Study design and reporting of results: PFASs

For the 20th round of the Norwegian POPs in Food-study, we also offered a food sample for the determination of the following PFASs: PFOS, PFHxS, PFOA, PFNA, PFDA and PFUnDA. The sample material consisted of Perch caught in an area well known to be contaminated by PFOS. As for the other matrices, the Perch sample was not fortified.

The laboratories' own methods for sample preparation and instrumental analysis, as well as their own quantification standards should be used for the analysis of the sample.

The laboratories were to report the concentration of each detected congener (e.g. S/N ≥3) in the Perch on fresh weight basis as well as the limit of detection (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.

Confidentiality

Each participating laboratory was given an exclusive laboratory code by the 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 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 web page www.fhi.no/ilc in July 2019.

Collection, preparation, and distribution of samples

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

- Veal (~100 g)
- Herring (~100 g)
- Brown meat from Crab (~60 g)
- Perch (~25 g)

The test materials were produced from natural products and were not fortified with standards.

The Veal was purchased from "Lierkalv", a Norwegian producer of veal from sucling calves in the south-east of Norway. The Herring was caught in the Baltic sea and shipped to NIPH from the National Food Agency in Sweden. The Brown meat was brown meat from Norwegian Brown Crab, and bought from Hitramat in mid-Norway. The Perch was caught in a lake known to be contaminated by PFOS in the east of Norway.

The Veal arrived as fresh, minced meat in parcels of 500 g. The parcels were pooled and homogenaized thoroughly in a large, industrial food grinder.

The Herring from the Baltic sea arrived as filets. All the filtes were pooled, grinded and homogenized thoroughly.

The Brown meat arrived as packets of frozen material from the same production batch. At arrival to the Norwegian Institute of Public Health the packets were defrosted, pooled and homogenized until the bulk sample was homogeneous.

The Perch arrived as whole, frozen fishes. The fishes were filleted before they were pooled and homogenized.

Sub-samples of at least 100 g of Veal (Veal-2019), 100 g of Herring (Herring-2019), 60 g of Brown meat (Brown meat -2018) and 25 g of Perch (Perch-2019) 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 (assigned value) 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. The same approach was used for the calculation of the PFASs.

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

For PFASs, the number of participants were limited compared to the other groups of analytes. Therefore, when identifying low outliers, they were removed from the data set as well as the high outliers.

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 that were removed prior to consensus calculation are marked accordingly in the tables presenting the individual results.

For the standard solutions, outliers were defined as those values outside ±50 % of the median of all reported values and 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 ±2*SD.

TEQs were calculated from the consensus medians for PCDDs/PCDFs, non-ortho PCBs, and mono-ortho PCBs, using the toxic equivalency factors derived by WHO in 1998 and 2006. 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 (WHO$_{2006}$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); σ = target value for standard deviation. A σ of 0.2 multiplied by the consensus value was used, i.e. Z-scores between +1 and -1 reflect a deviation of ±20 % from the consensus value.

The final report and certificate

The draft of the final report was prepared by the coordinators and published electronically in July 2019.

The final report will be made available to the participants in pdf format at www.fhi.no/ILC.

A certificate of participation, stating the participant's laboratory code, will be sent to each participating laboratory who has contributed to the results by the end of 2019.

Coordination

The study was initiated and carried out by the Dept. of Environmental Exposure and Epidemiology, Norwegian Institute of Public Health, Oslo, Norway. Members of the coordination committee were:

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Results

Presentation in the report

Seventy-two laboratories worldwide submitted their results within the deadline and the results are presented in the following chapters. All participating laboratories will be able to compare their own performance, congener by congener, with the other laboratories. Since variations in performances are based on several factors, it is recommended that each laboratory carefully evaluate the factors that, favorably or unfavorably, may have contributed to its performance.

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

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 TEQ_{2006}-values.

Individual results reported by the laboratories for each congener are given for Veal, Herring and Brown meat in Appendix 2, 3 and 4. The results for PFAS in the sample of Perch will be presented in Appendix 5, and results of the lipid determinations are presented in Appendix 6.

Summarizing comments on results

PCDDs/PCDFs

Analyte solution-2019
Concentrations of PCDDs/PCDFs were reported by 61 laboratories. The average RSD for the 17 congeners was 6,9 % ranging from 5.8 % for 1,2,3,7,8,9-HxCDF to 9.3 % for 1,2,3,4,6,7,8,9-OCDD. The calculation of Z-scores for the TEQs (target 12.5 pg TEQ/μL based on TEF_{2006}-values) of the PCDD/PCDF standard solution showed that 98 % of the laboratories were within the range of ±20 % of the consensus value. This clearly demonstrates that the calibration solutions used by the laboratories generally are of high quality.

Veal-2019
For the sample of Veal, PCDD/PCDF results from 50 laboratories were received. From these results, the calculated consensus TEQ (PCDD/PCDF TEQ based on WHO_{2006}-TEFs) was 0.022 pg TE/g fresh weight and 0.27 pg TE/g lipid weight.

The average RSD was 50 %, ranging from 32-71 % for 1,2,3,4,6,7,8-HpCDD and 1,2,3,4,7,8,9-HpCDF respectively. Z-scores within ±1 were obtained by 33 % of the laboratories and 53 % of the laboratories had Z-scores within ±2 (fresh weight basis).

Herring-2019
PCDD/PCDF concentrations in the Herring sample were reported by 63 laboratories. The consensus TEQ was 0.94 pg TEQ/g fresh weight, and 13 pg TEQ/g lipid weight

(PCDD/PCDF TEQ based on WHO$_{2006}$TEFs). The average RSD was 31 % ranging from 18-67 % (2,3,4,7,8-PeCDF and 1,2,3,4,6,7,8,9-OCDF respectively). Z-scores were within ±1 for 88 % of the laboratories and within ±2 for 95 % of the laboratories (fresh weight basis).

Brown meat -2019

PCDD/PCDF concentrations in the sample of Brown meat were determined by 56 laboratories. The consensus TEQ for PCDD/PCDF based on WHO$_{2006}$TEFs was 1.3 pg TEQ/g fresh weight and 16 pg TEQ/g lipid weight (PCDD/PCDF TEQ based on WHO$_{2006}$TEFs). The average RSD was 27 % ranging from 17-56 % (2,3,4,7,8-PeCDF and 1,2,3,7,8,9-HxCDF respectively). Z-scores for PCDD/PCDF TEQ within ±1 were obtained by 86 % of the laboratories and 95 % had Z-scores within ±2 (fresh weight basis).

Dioxin-like PCBs

Analyte solution-2019

The 12 dioxin-like PCBs in the analyte solution were analyzed and reported by 60-62 laboratories. The RSDs for the different congeners were ranging from 5.4 % for PCB-189 to 7.6 % for PCB-114, with an average of 6.5 %.

Veal-2019

Dioxin-like PCB concentrations in the sample of Veal were reported from 50 laboratories. The concentrations of the 12 congeners varied between 0.053 pg/g fresh weight (PCB-81) and 59 pg/g fresh weight (PCB-118). The average RSD for concentrations of individual dioxin-like PCB congeners was 25 % ranging from 15 % for PCB-118 to 42 % for PCB-123.

The dioxin-like PCBs contribute 73 % to the total TEQ (WHO TEF$_{2006}$) in the sample with PCB-126 as the main contributor (68 %).

Herring-2019

Of the participating laboratories, 63 measured and reported dioxin-like PCB concentrations in the Herring sample. The concentrations ranged from 0.55 pg/g fresh weight for PCB-81 to 1426 pg/g fresh weight for PCB-118. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 22 % ranging from 13 % for PCB-189 to 43 % for PCB-123.

The dioxin-like PCBs contribute to about 55 % of the total TEQ in the sample with PCB-126 as the main contributor (47 %).

Brown meat -2019

Dioxin-like PCBs in Brown meat were reported by 54 laboratories. Levels were ranging from 1.7 pg/g fresh weigh for PCB-81 to 924 pg/g fresh weight for PCB-118. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 20 % ranging from 13 % for PCB-156 to 33 % for PCB-126.

The contribution of the dioxin-like PCBs to the total TEQ was about 42 % with PCB-126 as the main contributor (36 % of total TEQ).

Total TEQ

The total TEQ for the sample of Veal was 0.082 pg TEQ/g fresh weight and 1.0 pg TEQ/g lipid weight (WHO TEF$_{2006}$). The total TEQ of the Herring-sample was 2.1 pg TEQ/g fresh weight and 30 pg TEQ/g lipid weight, and the Brown meat contained 2.3 pg TEQ/g on fresh weight basis and 28 pg TEQ/g lipid weight basis.

The RSDs for total TEQs on fresh weight basis calculated from the RSD of individual congeners were 13 % for the sample of Veal, 8.4 % for Herring and 8.5 % for Brown meat.

In Figure 1 the percentage contribution to the TEQ-values for the three groups of compounds is depicted based on WHO TEF$_{2006}$ and WHO TEF$_{1998}$, respectively. For the selection of food-items included in this study the dioxin-like PCBs contributed from 42 % to 73 % to the total TEQ (using WHO TEF$_{2006}$), 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 percentage contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using both the WHO$_{2006}$ TEFs and WHO$_{1998}$ TEFs, in the three food samples.
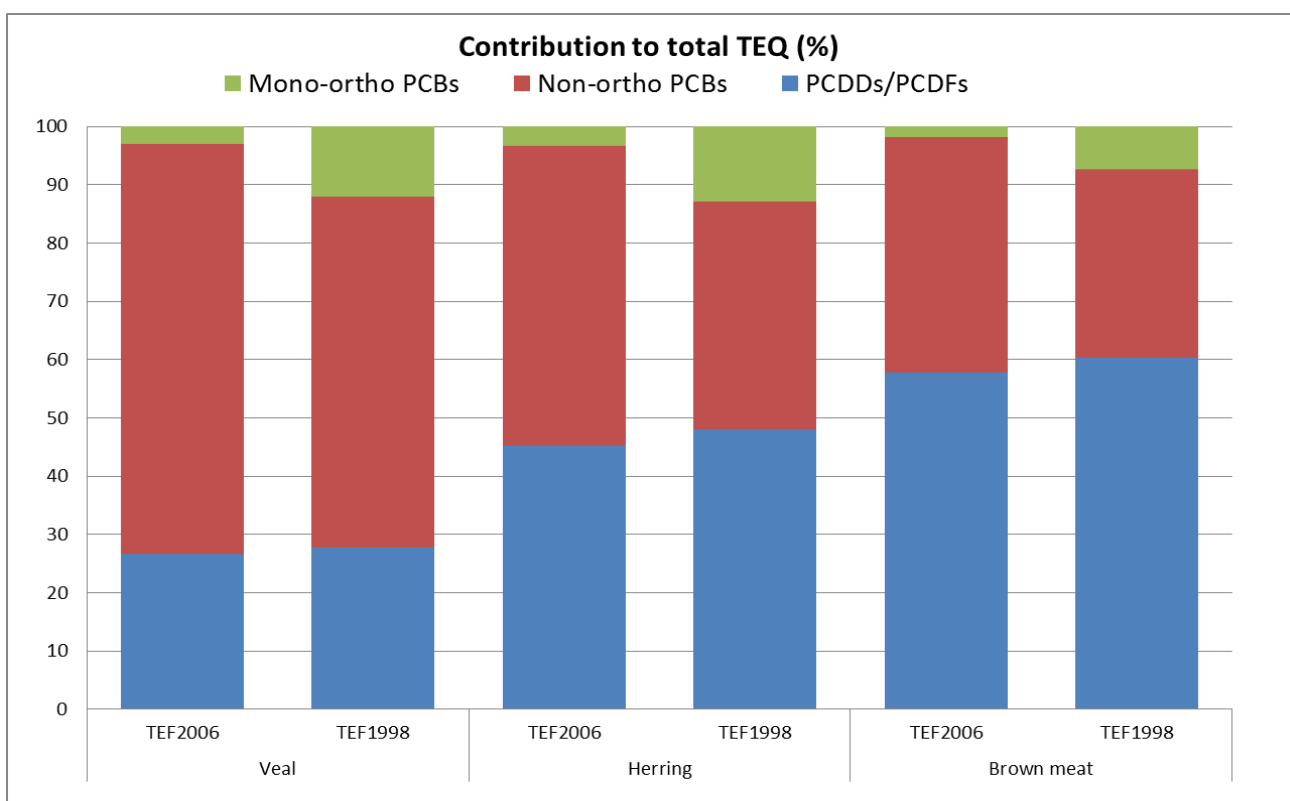
Indicator PCBs

Analyte solution-2019

52 laboratories reported indicator PCBs in the analyte solution. The average RSD was 8.1 % ranging from 6.6 to 9.3 % (outliers removed).

Veal-2019

For the sample of Veal, results for indicator PCBs were received from 44 laboratories. The consensus concentrations varied between 23 pg/g fresh weight (PCB-52) and 107 pg/g fresh weight (PCB-153). The RSDs were ranging from 18 to 31 % for PCB-153 and PCB-28 respectively, with an average of 24 % for all indicator PCBs. The consensus median for the sum of indicator PCBs was 300 pg/g fresh weight.

Herring-2019

Within the deadline, 56 laboratories reported results for indicator PCBs in the Herring sample. The consensus concentrations ranged from 234 pg/g fresh weight (PCB-28) to 5136 pg/g fresh weight (PCB-153) with a consensus median for the sum of indicator PCBs of 12201 pg/g fresh weight. The average RSD was 31 %, ranging from 29 to 33 % for PCB-52 and PCB-28 respectively.

Brown meat -2019

Results were obtained from 47 laboratories. The concentrations of indicator PCBs in Brown meat ranged from 40 pg/g fresh weight (PCB-52) to 3061 pg/g (PCB-153) and the consensus median for the sum was 5837 pg/g fresh weight. The average RSD was 30 %, ranging from 22 to 34 % for PCB-153 and PCB-52 respectively.

PBDEs

Analyte solution-2019

The tri- to hepta-PBDE standard solution was analyzed by 23 laboratories and 19 laboratories reported values for PBDE-209. The RSDs were between 5.1-11 % for all congeners.

Veal-2019

The PBDE concentrations in Veal were reported by 17 laboratories, except for PBDE-209 for which 14 results were received. The consensus concentrations were in the range of 0.15 pg/g fresh weight for PBDE-28 to 2.7 pg/g fresh weight for PBDE-47. The consensus concentration for PBDE-209 was 12 pg/g fresh weight. The sum of tri- to hepta-PBDEs was 5.6 pg/g fresh weight. The range of RSDs on fresh weight basis was 35-60 %, with an average of 48 % including PBDE-209.

Herring-2019

Within the deadline, 27 laboratories had reported results for tri- to hepta-PBDEs in Herring and 21 laboratories had reported results for PBDE-209. The consensus concentrations varied between 1.1 pg/g fresh weight (PBDE-183) and 301 pg/g fresh weight (PBDE-47). The concentration for PBDE-209 was 11 pg/g fresh weight. The sum of tri- to hepta-PBDEs was 513 pg/g fresh weight. The RSD calculated from the concentrations on fresh weight ranged from 25-111 %, with an average of 43 % for PBDEs including PBDE-209.

Brown meat -2019
Twenty-two laboratories reported results for tri- to hepta-PBDEs in Brown meat, and 17 reported results for PBDE-209. The concentrations varied between 0.76 pg/g fresh weight (PBDE-183) and 50 pg/g (PBDE-47). The concentration for PBDE-209 was 14 pg/g. The sum of tri- to hepta-PBDEs was 102 pg/g fresh weight. The RSDs for the individual congeners were ranging from 18 to 77 % with an average of 35 % 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 6 laboratories reported α-HBCD in the standard solution and 5-11 laboratories reported one or more of the three isomers in the food samples. The consensus concentrations for the sum of individual HBCD isomers were 3.9 pg/g fresh weight for the sample of Veal, 329 pg/g for the Herring and 12 pg/g fresh weight for the Brown meat sample. Since only a few laboratories reported HBCD, these results must be regarded as indicative values.

PFASs

A sample of Perch known to be heavily contaminated with PFOS, was offered to the participants for the determination of PFASs. The participating laboratories were asked to report their results for as many as possible of the following PFASs: PFOS, PFHxS, PFOA, PFNA, PFDA and PFUnDA. Eleven laboratories reported their results by the deadline, but not all participants reported results for all PFASs. The consensus concentration of the sum of individual PFASs was 127485 pg/g fresh weight, with PFOS as the main contributor (125371 ng/g fw, n=10). The concentration of PFUnDA in the sample was 951 pg/g fw, while the concentration of PFDA was705 pg/g fw. The consensus values for PFHxS, PFOA and PFNA are only indicative due to many reported non-detects (147 pg/g fw, 57 pg/g fw and 255 pg/g fw respectively).

Lipid content

The mean and RSDs (in parentheses) for the lipid contents of the food samples were calculated to be 8.2 % (RSD=9.6 %) for the Veal sample, 7.0 % (RSD=16 %) for the Herring sample and 8.2 % (11 %) for the sample of Brown meat.

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 Marie Aune from the Swedish National Food Agency for her valuable help to purchase the Herring sample and Cambridge Isotope Laboratories, Inc. for providing the standard solutions for this interlaboratory study.

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Appendix B:

Study announcement and
instructions for participants

Announcement for
Interlaboratory Comparison on POPs in Food 2019

Introduction

We hereby announce the 20th round of the Interlaboratory Comparison on the Determination of POPs in Food ("The Norwegian POPs in Food-study"). The study is open for academic, regulatory as well as commercial laboratories world-wide. The organizer of this study is Department of Environmental Exposure and Epidemiology at the Norwegian Institute of Public Health, Oslo, Norway. The study is scheduled to take place from January to April 2019.

A draft report will be available by mid-June 2019, and the final report will be available to the participants by November 2019. 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.

New of the year: One matrix for analysis of selected PFASs will also be available!

Participants

We encourage all laboratories 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 analyte solutions 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.

For the matrix intended for the determination of PFASs, the participants are asked to report one or more of the following components: Perfluorooctanesulfonate (PFOS), perfluorohexanesulfonate (PFHxS), perfluorooctanoate (PFOA), perfluorononanoate (PFNA), perfluorodecanoate (PFDA) and perfluoroundecanoate (PFUnDA).

The test materials for the lipophilic POPs 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.

In addition, one sample of PFOS contaminated Perch for the analysis of selected PFASs will be available this year.

Test material
The test materials consist of three unfortified natural food product homogenates:

- Veal (labelled "Veal-2019") ~100 g
- Herring (labelled "Herring-2019") ~100 g
- Brown meat from crab (labelled "Brown meat-2019") ~80 g

- Perch (PFASs only) (labelled Perch-2019)

The samples will be distributed by an international courier service to the participating laboratories.

<u>Please note:</u>
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 2018**
Return of registration form	**January 30th, 2019**
Shipment of test material	**Week 5-6, 2019**
Confirmation of receipt of test material by participant	**Within 7 days after receivement**
Reporting of test results	**April 20th, 2019**

Publication of draft report on web-site	**June 2019**
Final report available to all participants	**November 2019**

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 9 500 NOK, in two food items 11 700 NOK, 13 900 for three food items and for the complete set of all four food items 14 900 NOK.

As the inclusion of the PFASs-matrix is new this year, all the receivers of this invitation are encouraged to spread the words to possibly interested laboratories!

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![NIPH — Norwegian Institute of Public Health]

Interlaboratory Comparison on Dioxins in Food 2019

Instructions for participants

January 2019

1. Introduction

This is the 20th Round of the Interlaboratory Comparison Study on the Determination of POPs in Food organised by the Department of Environmental Exposure and Epidemiology, 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 purpose 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.

New of the year is that we also offer a sample of perch for the determination of PFAS.

Please read these instructions carefully before starting the experimental work.

The participating laboratories will contribute to 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
- indicator 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 the following samples:
- Veal (Veal-2019)
- Herring (Herring-2019)
- Brown meat from crab (Brown meat-2019)

The mentioned analytes can 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.

This year the participants also are given the opportunity to determine

- perfluorooctanesulfonate (PFOS)
- perfluorohexanesulfonate (PFHxS)
- perfluorooctanoate (PFOA)
- perfluorononanoate (PFNA)
- perfluorodecanoate (PFDA)
- perfluoroundecanoate (PFUnDA).

in the following sample:
- Perch (Perch-2019)

The sample of perch is known to be contaminated by PFOS.

2. Participants

A list of participants is attached. 73 laboratories have announced their participation in the study.

3. Design of the study

3.1 Test materials

<u>Samples</u>
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
- approx. 100 g veal
- approx. 100 g herring
- approx. 60 g brown meat from crab
- approx. 25 g perch (PFAS only)

We do not provide any standard solution for the determination of PFAS.

<u>Fortification</u>
The samples are prepared from regular market foods. There is no fortification or spiking of the target analytes in the food samples.

Shipment

The samples are fresh frozen food homogenates. They are distributed by international courier and should reach the receiving laboratory in good condition within a few days.

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 coordinators by e-mail. 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

Veal	Veal-2019
Herring	Herring-2019
Brown meat from crab	Brown meat-2019
Perch	Perch-2019

The above sample coding is marked on the sample bottles.

3.3 Analytical procedure

Storage of the samples

The samples are fresh, frozen homogenates of natural food items. They are shipped frozen and should be stored frozen until they are analysed.

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.

Be aware that sample of perch is likely to be highly contaminated by PFOS.

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.

An estimate of the lipid content in the samples follows below:
- Veal (estimated to be low to medium contaminated): ≈10 %
- Herring (estimated to be medium to high contaminated): 15-20 %
- Brown meat from crab (estimated to be medium contaminated): 10 %

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 **should** include the determined lipid percent for the samples, with the exception of the perch-sample.

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, and the reportform "PFAS-2019" for PFASs.

Laboratories must report one concentration on fresh weight basis for each congener which is detected (S/N ≥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

Four 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

Report form for PFASs

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.

Deadline

The reports must be in our hands no later than April 20th, 2019 to enable us to prepare the draft report to be published by the end of June 2019. 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 20th. 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 the best estimate of the true value as possible. 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 all congeners, and for PCDD/PCDF TEQs and PCB TEQs as well.

6. Final report

The final report will be prepared by the co-ordinators and published in November 2019 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 June.
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, HBCD and PFAS is

- NOK 9500 for one food item
- NOK 11700 for two food items
- NOK 13900 for three food items.
- NOK 14900 for four 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 2018**
Return of registration form	**January 30th, 2019**
Shipment of test material	**Week 5-6, 2019**
Confirmation of receipt of test material by participant	**Within 7 days after receivement**
Reporting of test results	**April 20th, 2019**
Publication of draft report on web-site	**June 2019**
Final report available to all participants	**November 2019**

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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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?

☐ Did you remember to report the lipid percent of the samples?

☐ Are the results of the samples reported on a *fresh weight basis*?

☐ 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	WHO 1998 TEF	WHO 2005 TEF
chlorinated dibenzo-p-dioxiner		
2,3,7,8-TCDD	1	1
1,2,3,7,8-PeCDD	1	1
1,2,3,4,7,8-HxCDD	0.1	0.1
1,2,3,6,7,8-HxCDD	0.1	0.1
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
Chlorinated dibenzofuraner		
2,3,7,8-TCDF	0.1	0.1
1,2,3,7,8-PeCDF	0.05	0.03
2,3,4,7,8-PeCDF	0.5	0.3
1,2,3,4,7,8-HxCDF	0.1	0.1
1,2,3,6,7,8-HxCDF	0.1	0.1
1,2,3,7,8,9-HxCDF	0.1	0.1
2,3,4,6,7,8-HxCDF	0.1	0.1
1,2,3,4,6,7,8-HpCDF	0.01	0.01
1,2,3,4,7,8,9-HpCDF	0.01	0.01
OCDF	0.0001	0.0003
non-orhto substituted PCBs		
PCB 77	0.0001	0.0001
PCB 81	0.0001	0.0003
PCB 126	0.1	0.1
PCB 169	0.01	0.03
mono-ortho substituted PCBs		
PCB 105	0.0001	0.00003
PCB 114	0.0005	0.00003
PCB 118	0.0001	0.00003
PCB 123	0.0001	0.00003
PCB 156	0.0005	0.00003
PCB 157	0.0005	0.00003
PCB 167	0.00001	0.00003
PCB 189	0.0001	0.00003

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., $s_{sam} < 0.3\ \sigma_p$.

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).

The quality of the analytical method used for homogenity testing has a large impact on the results. 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 $\sigma_{an} < 0.5\ \sigma_p$

Consequences for the Interlaboratory Comparison on Dioxins in Food

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

1.

The protocol recommends duplicate analysis of at least 10 distribution units. Due to limited amount of test material in each distribution unit and the requirement for sufficiently low analytical standard deviation, the test analysis has to be restricted to PCB, e.g., 6 indicator PCB or CB-153. It is, however, questionable whether analysis of indicator PCB also reflects the distribution of dioxins and other contaminants in the sample, as the test material is often prepared by mixing specifically contaminated material with background contaminated material in order to achieve a sufficient contamination level. Therefore, the distribution of PCBs in the sample might not be relevant for the distribution of dioxins in the sample. The analytical precision of the method used in the homogeneity test should be less than half of the target standard deviation, i.e., $\sigma_{an} < 0.5\ \sigma_p$. For determination of dioxins, the target standard deviation may be approximated by the requirement for trueness (Commission Regulation (EC) No 1883/2006) of ± 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 10.0 g 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 $RSD^2_{inhomogeneity} = RSD^2_{between} - RSD^2_{within}$[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

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

Appendix E:

Summary results

Consensus of congener concentrations
Consensus of TEQ values
Consensus statistics
Laboratories´ reported TEQs
Laboratories´ Z-scores
Z-score plots

	Veal		Herring		Brown meat	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
2,3,7,8-TCDD	0,0029	0,035	0,080	1,1	0,091	1,1
1,2,3,7,8-PeCDD	0,0070	0,086	0,22	3,2	0,37	4,5
1,2,3,4,7,8-HxCDD	0,0040	0,049	0,034	0,49	0,21	2,5
1,2,3,6,7,8-HxCDD	0,0090	0,11	0,15	2,2	0,46	5,6
1,2,3,7,8,9-HxCDD	0,0038	0,047	0,027	0,38	0,17	2,1
1,2,3,4,6,7,8-HpCDD	0,019	0,23	0,040	0,57	0,52	6,3
1,2,3,4,6,7,8,9-OCDD	0,042	0,52	0,046	0,66	0,52	6,2
2,3,7,8-TCDF	0,0047	0,058	1,5	21	2,4	28
1,2,3,7,8-PeCDF	0,0041	0,051	0,34	4,8	0,36	4,3
2,3,4,7,8-PeCDF	0,020	0,25	1,4	20	1,4	17
1,2,3,4,7,8-HxCDF	0,011	0,14	0,087	1,2	0,34	4,2
1,2,3,6,7,8-HxCDF	0,0080	0,099	0,12	1,7	0,20	2,5
2,3,4,6,7,8-HxCDF	0,0078	0,097	0,12	1,7	0,53	6,4
1,2,3,7,8,9-HxCDF	0,0037	0,046	0,0063	0,090	0,021	0,25
1,2,3,4,6,7,8-HpCDF	0,0083	0,10	0,028	0,39	0,54	6,5
1,2,3,4,7,8,9-HpCDF	0,0032	0,040	0,0051	0,072	0,0087	0,10
1,2,3,4,6,7,8,9-OCDF	0,010	0,12	0,011	0,16	0,034	0,41
PCB 77	0,73	9,0	22	314	26	312
PCB 126	0,55	6,8	9,7	138	8,4	101
PCB 169	0,074	0,92	3,3	48	2,9	35
PCB 81	0,053	0,66	0,55	7,9	1,7	21
PCB 105	11	133	419	5986	278	3353
PCB 114	1,3	16	23	334	11	133
PCB 118	59	732	1426	20371	924	11136
PCB 123	0,80	9,9	16	227	14	165
PCB 156	5,7	70	206	2938	108	1296
PCB 157	1,2	15	50	720	31	379
PCB 167	3,1	38	122	1743	85	1022
PCB 189	0,39	4,8	23	332	13	156

fw. - fresh weight

lw. - lipid weight

	Veal		Herring		Brown meat	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
CB 28	28	346	234	3343	142	1711
CB 52	23	285	516	7371	40	476
CB 101	37	458	1923	27476	238	2865
CB 138	77	951	3262	46593	1787	21530
CB 153	107	1319	5136	73371	3061	36876
CB 180	28	345	1131	16150	570	6867
BDE 28	0,15	1,8	9,0	129	3,8	46
BDE 47	2,7	33	301	4300	50	602
BDE 99	1,3	16	67	960	8	91
BDE 100	0,46	5,6	84	1200	14	173
BDE 153	0,42	5,2	12	169	5,4	65
BDE 154	0,25	3,1	39	559	20	246
BDE 183	0,28	3,4	1,1	16	0,76	9,1
BDE 209	12	152	11	154	14	167
α-HBCD	8,0	99	309	4420	11	137
β-HBCD	3,1	39	5,4	77	3,8	46
γ-HBCD	6,7	82	7,8	111	6,5	78
Tot HBCD	3,9	48	329	4693	12	149
Sum PCB	300	3703	12201	174305	5837	70325
Sum BDE with	5,6	69	513	7333	102	1232
Sum BDE	18	221	524	7487	116	1399

fw. - fresh weight

lw. - lipid weight

Perch-2019: PFAS, consensus values

	Perch pg/g fw.
PFOS	125371
PFHxS*	147
PFOA*	57
PFNA*	255
PFDA	705
PFUnDA	951
Sum PFAS	127485

fw. - fresh weight

lw. - lipid weight

Indicative value due to fue reported results

Consensus of TEQs

TEF$_{2006}$

	Veal		Herring		Brown meat	
	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	0,0029	0,035	0,080	1,1	0,091	1,1
1,2,3,7,8-PeCDD	0,0070	0,086	0,22	3,2	0,37	4,5
1,2,3,4,7,8-HxCDD	0,00040	0,0049	0,0034	0,049	0,021	0,25
1,2,3,6,7,8-HxCDD	0,00090	0,011	0,015	0,22	0,046	0,56
1,2,3,7,8,9-HxCDD	0,00038	0,0047	0,0027	0,038	0,017	0,21
1,2,3,4,6,7,8-HpCDD	0,00019	0,0023	0,00040	0,0057	0,0052	0,063
1,2,3,4,6,7,8,9-OCDD	0,000013	0,00016	0,000014	0,00020	0,00016	0,0019
2,3,7,8-TCDF	0,00047	0,0058	0,15	2,1	0,24	2,8
1,2,3,7,8-PeCDF	0,00012	0,0015	0,010	0,15	0,011	0,13
2,3,4,7,8-PeCDF	0,0061	0,076	0,42	6,1	0,42	5,0
1,2,3,4,7,8-HxCDF	0,0011	0,014	0,0087	0,12	0,034	0,42
1,2,3,6,7,8-HxCDF	0,00080	0,0099	0,012	0,17	0,020	0,25
2,3,4,6,7,8-HxCDF	0,00078	0,0097	0,012	0,17	0,053	0,64
1,2,3,7,8,9-HxCDF	0,00037	0,0046	0,00063	0,0090	0,0021	0,025
1,2,3,4,6,7,8-HpCDF	0,000083	0,0010	0,00028	0,0039	0,0054	0,065
1,2,3,4,7,8,9-HpCDF	0,000032	0,00040	0,000051	0,00072	0,000087	0,0010
1,2,3,4,6,7,8,9-OCDF	0,0000030	0,000037	0,0000033	0,000047	0,000010	0,00012
PCB 77	0,000073	0,00090	0,0022	0,031	0,0026	0,031
PCB 126	0,055	0,68	0,97	14	0,84	10
PCB 169	0,0022	0,028	0,10	1,4	0,086	1,0
PCB 81	0,000016	0,00020	0,00017	0,0024	0,00052	0,0062
PCB 105	0,00032	0,0040	0,013	0,18	0,0083	0,10
PCB 114	0,000038	0,00047	0,00070	0,010	0,00033	0,0040
PCB 118	0,0018	0,022	0,043	0,61	0,028	0,33
PCB 123	0,000024	0,00030	0,00048	0,0068	0,00041	0,0050
PCB 156	0,00017	0,0021	0,0062	0,088	0,0032	0,039
PCB 157	0,000036	0,00044	0,0015	0,022	0,00094	0,011
PCB 167	0,000092	0,0011	0,0037	0,052	0,0025	0,031
PCB 189	0,000012	0,00014	0,00070	0,010	0,00039	0,0047
PCDDs/PCDFs	0,022	0,27	0,94	13	1,3	16
Non-ortho PCBs	0,057	0,71	1,1	15	0,93	11
Mono-ortho PCBs	0,0025	0,031	0,069	0,98	0,044	0,53
Total TEQ	0,082	1,0	2,1	30	2,3	28

fw. - fresh weight

lw. - lipid weight

Consensus of TEQs

TEF$_{1998}$

	Veal		Herring		Brown meat	
	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	0,0029	0,035	0,080	1,1	0,091	1,1
1,2,3,7,8-PeCDD	0,0070	0,086	0,22	3,2	0,37	4,5
1,2,3,4,7,8-HxCDD	0,00040	0,0049	0,0034	0,049	0,021	0,25
1,2,3,6,7,8-HxCDD	0,00090	0,011	0,015	0,22	0,046	0,56
1,2,3,7,8,9-HxCDD	0,00038	0,0047	0,0027	0,038	0,017	0,21
1,2,3,4,6,7,8-HpCDD	0,00019	0,0023	0,00040	0,0057	0,0052	0,063
1,2,3,4,6,7,8,9-OCDD	0,0000042	0,000052	0,0000046	0,000066	0,000052	0,00062
2,3,7,8-TCDF	0,00047	0,0058	0,15	2,1	0,24	2,8
1,2,3,7,8-PeCDF	0,00021	0,0026	0,017	0,24	0,018	0,22
2,3,4,7,8-PeCDF	0,010	0,13	0,71	10	0,70	8,4
1,2,3,4,7,8-HxCDF	0,0011	0,014	0,0087	0,12	0,034	0,42
1,2,3,6,7,8-HxCDF	0,00080	0,0099	0,012	0,17	0,020	0,25
2,3,4,6,7,8-HxCDF	0,00078	0,0097	0,012	0,17	0,053	0,64
1,2,3,7,8,9-HxCDF	0,00037	0,0046	0,00063	0,0090	0,0021	0,025
1,2,3,4,6,7,8-HpCDF	0,000083	0,0010	0,00028	0,0039	0,0054	0,065
1,2,3,4,7,8,9-HpCDF	0,000032	0,00040	0,000051	0,00072	0,000087	0,0010
1,2,3,4,6,7,8,9-OCDF	0,0000010	0,000012	0,0000011	0,000016	0,0000034	0,000041
PCB 77	0,000073	0,00090	0,0022	0,031	0,0026	0,031
PCB 126	0,055	0,68	0,97	14	0,84	10
PCB 169	0,00074	0,0092	0,033	0,48	0,029	0,35
PCB 81	0,0000053	0,000066	0,000055	0,00079	0,00017	0,0021
PCB 105	0,0011	0,013	0,042	0,60	0,028	0,34
PCB 114	0,00064	0,0079	0,012	0,17	0,0055	0,066
PCB 118	0,0059	0,073	0,14	2,0	0,092	1,1
PCB 123	0,000080	0,00099	0,0016	0,023	0,0014	0,017
PCB 156	0,0029	0,035	0,10	1,5	0,054	0,65
PCB 157	0,00060	0,0074	0,025	0,36	0,016	0,19
PCB 167	0,000031	0,00038	0,0012	0,017	0,00085	0,010
PCB 189	0,000039	0,00048	0,0023	0,033	0,0013	0,016
PCDDs/PCDFs	0,026	0,32	1,2	18	1,6	19
Non-ortho PCBs	0,056	0,69	1,0	14	0,87	10
Mono-ortho PCBs	0,011	0,14	0,33	4,7	0,20	2,4
Total TEQ	0,093	1,1	2,6	37	2,7	32

fw. - fresh weight

lw. - lipid weight

Consensus statistics

2019

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	0,13	6,3	61	1
1,2,3,7,8 PeCDD	5,0	5,0	5,0	5,0	0,29	5,9	61	1
1,2,3,4,7,8 HxCDD	5,0	5,0	5,0	5,0	0,35	7,0	61	1
1,2,3,6,7,8 HxCDD	5,0	5,0	4,9	4,9	0,37	7,4	61	1
1,2,3,7,8,9 HxCDD	5,0	5,0	5,0	5,0	0,37	7,4	61	1
1,2,3,4,6,7,8 HpCDD	5,0	5,0	5,0	5,0	0,33	6,7	61	2
1,2,3,4,6,7,8,9 OCDD	10	9,8	9,8	9,8	0,91	9,3	61	1
2,3,7,8 TCDF	2,0	2,0	2,0	2,0	0,13	6,8	61	2
1,2,3,7,8 PeCDF	5,0	4,9	4,9	5,0	0,31	6,3	61	1
2,3,4,7,8 PeCDF	5,0	4,9	4,9	4,8	0,32	6,6	61	2
1,2,3,4,7,8 HxCDF	5,0	5,0	5,0	5,0	0,32	6,4	61	2
1,2,3,6,7,8 HxCDF	5,0	5,0	5,0	5,0	0,30	6,1	61	1
2,3,4,6,7,8 HxCDF	5,0	5,0	5,0	4,9	0,34	6,9	61	1
1,2,3,7,8,9 HxCDF	5,0	5,0	5,0	5,0	0,29	5,8	61	1
1,2,3,4,6,7,8 HpCDF	5,0	4,9	4,9	5,0	0,37	7,4	61	2
1,2,3,4,7,8,9 HpCDF	5,0	5,0	5,0	4,9	0,36	7,4	61	2
1,2,3,4,6,7,8,9 OCDF	10	10	10	9,8	0,77	7,9	61	1
PCB 77	10	10	10	9,9	0,66	6,7	62	2
PCB 126	10	10	10	9,9	0,67	6,7	62	1
PCB 169	10	9,9	9,9	9,8	0,63	6,4	62	1
PCB 81	10	10,0	10	9,9	0,69	6,9	62	1
PCB 105	100	100	100	100	6,3	6,3	60	1
PCB 114	100	100	99	100	7,7	7,6	60	1
PCB 118	100	101	101	101	6,7	6,7	60	1
PCB 123	100	101	101	102	6,2	6,1	60	1
PCB 156	100	100	100	101	5,8	5,8	60	2
PCB 157	100	100	100	100	6,6	6,6	60	1
PCB 167	100	100	100	100	6,7	6,7	60	1
PCB 189	100	100	100	101	5,4	5,4	60	1

Consensus statistics

2019

Analyte solution

	Target value pg/µl	Median, pg/µl all values	Median, pg/µl outliers removed	Mean, pg/µl all values	Mean, pg/µl outliers removed
PCB 28	100	98	98	92	98
PCB 52	100	97	98	92	97
PCB 101	100	100	100	92	99
PCB 138	100	99	100	94	99
PCB 153	100	99	99	93	99
PCB 180	100	100	100	94	99
PBDE 28	25	25	25	25	25
PBDE 47	25	25	25	24	24
PBDE 99	25	25	25	24	24
PBDE 100	25	25	25	25	25
PBDE 153	25	24	24	24	24
PBDE 154	25	24	24	24	24
PBDE 183	25	25	25	24	24
PBDE 209	100	95	95	91	96
α-HBCD *	500	478	478	486	486

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Number of reported values	Number of reported outliers
PCB 28	26	6,6	52	3
PCB 52	26	7,9	52	3
PCB 101	28	7,8	52	4
PCB 138	27	9,3	52	3
PCB 153	26	8,0	52	3
PCB 180	27	9,1	52	3
PBDE 28	7,9	7,9	23	0
PBDE 47	5,1	5,1	23	0
PBDE 99	6,3	6,3	23	0
PBDE 100	8,1	8,1	23	0
PBDE 153	9,7	9,7	23	0
PBDE 154	8,9	8,9	23	0
PBDE 183	10	10	23	0
PBDE 209	27	11	19	1
α-HBCD *	10	10	6	0

NDs: Non-detects

* : Indicative value due to few reported values

Consensus statistics

2019

Veal, 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	0,0029	0,0048	0,0036	0,0025	69	50	10	34
1,2,3,7,8-PeCDD	0,0070	0,0080	0,0075	0,0032	43	50	7	18
1,2,3,4,7,8-HxCDD	0,0040	0,0050	0,0047	0,0025	52	50	11	26
1,2,3,6,7,8-HxCDD	0,0090	0,0099	0,0096	0,0031	32	50	9	16
1,2,3,7,8,9-HxCDD	0,0038	0,0050	0,0041	0,0024	57	50	13	25
1,2,3,4,6,7,8-HpCDD	0,019	0,020	0,019	0,0061	32	50	8	11
1,2,3,4,6,7,8,9-OCDD	0,042	0,046	0,048	0,021	44	50	6	9
2,3,7,8-TCDF	0,0047	0,0073	0,0055	0,0032	57	50	14	22
1,2,3,7,8-PeCDF	0,0041	0,0060	0,0051	0,0033	63	50	9	32
2,3,4,7,8-PeCDF	0,020	0,021	0,020	0,0065	33	50	6	6
1,2,3,4,7,8-HxCDF	0,011	0,011	0,011	0,0043	39	50	10	9
1,2,3,6,7,8-HxCDF	0,0080	0,0090	0,0088	0,0036	41	50	11	12
2,3,4,6,7,8-HxCDF	0,0078	0,0090	0,0083	0,0031	37	50	13	11
1,2,3,7,8,9-HxCDF	0,0037	0,0050	0,0040	0,0025	64	50	14	31
1,2,3,4,6,7,8-HpCDF	0,0083	0,0097	0,0087	0,0038	43	50	11	12
1,2,3,4,7,8,9-HpCDF	0,0032	0,0050	0,0038	0,0028	71	50	15	32
1,2,3,4,6,7,8,9-OCDF	0,010	0,013	0,011	0,0071	65	50	13	28
PCB 77	0,73	0,74	0,73	0,20	27	50	3	3
PCB 126	0,55	0,55	0,54	0,11	21	50	1	2
PCB 169	0,074	0,076	0,076	0,023	30	50	5	6
PCB 81	0,053	0,058	0,054	0,021	39	50	9	9
PCB 105	11	11	11	2,2	20	50	1	0
PCB 114	1,3	1,3	1,3	0,25	20	50	5	7
PCB 118	59	59	60	9,1	15	50	1	0
PCB 123	0,80	0,91	0,87	0,37	42	50	9	8
PCB 156	5,7	5,8	5,8	1,1	19	50	1	3
PCB 157	1,2	1,2	1,2	0,20	17	50	4	4
PCB 167	3,1	3,2	3,1	0,68	22	50	4	5
PCB 189	0,39	0,41	0,42	0,093	22	50	9	12

Consensus statistics

Veal, 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	30	28	28	35	29	29
PCB 52	24	23	23	28	24	24
PCB 101	37	37	37	41	37	37
PCB 138	78	77	77	85	79	79
PCB 153	107	107	107	110	104	104
PCB 180	28	28	28	29	28	27
PBDE 28	0,25	0,14	0,15	0,61	0,15	0,18
PBDE 47	3,1	2,8	2,7	4,1	2,8	2,8
PBDE 99	1,5	1,3	1,3	3,5	1,4	1,4
PBDE 100	0,56	0,46	0,46	1,0	0,47	0,47
PBDE 153	0,57	0,42	0,42	1,4	0,47	0,38
PBDE 154	0,41	0,27	0,25	1,0	0,36	0,32
PBDE 183	0,37	0,28	0,28	1,0	0,28	0,28
PBDE 209	21	12	12	113	15	15
α-HBCD *	10	10	8,0	9,4	9,4	8,0
β-HBCD *	5,7	5,3	3,1	6,5	4,3	3,1
γ-HBCD *	10	10	6,7	8,9	8,9	6,7
Tot HBCD *	5,2	3,9	3,9	13	3,9	3,9

	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	59	31	28	44	4	2
PCB 52	67	31	31	44	3	1
PCB 101	55	23	23	44	2	1
PCB 138	46	23	23	44	1	0
PCB 153	39	18	18	44	1	0
PCB 180	43	23	20	44	1	1
PBDE 28	120	57	47	17	7	5
PBDE 47	81	35	37	17	3	1
PBDE 99	191	51	54	17	4	2
PBDE 100	99	49	49	17	5	2
PBDE 153	128	51	35	17	6	4
PBDE 154	125	63	60	17	5	4
PBDE 183	137	48	48	17	6	4
PBDE 209	233	62	52	14	4	4
α-HBCD *	56	56	99	5	0	3
β-HBCD *	81	58	114	5	1	3
γ-HBCD *	55	55	93	5	0	3
Tot HBCD *	121	49	49	3	1	0

NDs: Non-detects

* : Indicative value due to few reported values

Consensus statistics

2019

Herring, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
2,3,7,8-TCDD	0,080	0,081	0,079	0,019	24	63	1	3
1,2,3,7,8-PeCDD	0,22	0,22	0,22	0,043	19	63	0	1
1,2,3,4,7,8-HxCDD	0,034	0,035	0,034	0,0090	27	63	4	7
1,2,3,6,7,8-HxCDD	0,15	0,15	0,15	0,037	25	63	0	2
1,2,3,7,8,9-HxCDD	0,027	0,028	0,028	0,0083	30	63	5	12
1,2,3,4,6,7,8-HpCDD	0,040	0,041	0,043	0,014	33	63	5	10
1,2,3,4,6,7,8,9-OCDD	0,046	0,048	0,046	0,018	39	63	10	13
2,3,7,8-TCDF	1,5	1,5	1,4	0,26	18	63	1	0
1,2,3,7,8-PeCDF	0,34	0,34	0,34	0,080	23	63	1	0
2,3,4,7,8-PeCDF	1,4	1,4	1,4	0,24	18	63	0	0
1,2,3,4,7,8-HxCDF	0,087	0,088	0,086	0,022	26	63	1	3
1,2,3,6,7,8-HxCDF	0,12	0,12	0,11	0,024	21	63	1	4
2,3,4,6,7,8-HxCDF	0,12	0,12	0,12	0,030	26	63	0	3
1,2,3,7,8,9-HxCDF	0,0063	0,0087	0,0072	0,0039	54	63	18	32
1,2,3,4,6,7,8-HpCDF	0,028	0,030	0,030	0,0094	31	63	8	11
1,2,3,4,7,8,9-HpCDF	0,0051	0,0079	0,0063	0,0035	55	63	18	36
1,2,3,4,6,7,8,9-OCDF	0,011	0,018	0,013	0,0091	67	63	19	28
PCB 77	22	22	22	4,5	20	63	0	0
PCB 126	9,7	9,7	9,7	1,9	20	63	0	0
PCB 169	3,3	3,4	3,3	0,82	25	63	1	2
PCB 81	0,55	0,57	0,54	0,21	39	63	7	5
PCB 105	419	419	423	61	14	63	0	0
PCB 114	23	24	25	6,7	27	63	3	2
PCB 118	1426	1426	1409	269	19	63	0	0
PCB 123	16	18	17	7,1	43	63	11	4
PCB 156	206	206	207	27	13	63	0	0
PCB 157	50	50	51	7,1	14	63	0	0
PCB 167	122	122	120	24	20	63	2	2
PCB 189	23	23	24	3,1	13	63	0	1

Consensus statistics

Herring, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
PCB 28	238	234	234	260	234	234
PCB 52	516	516	516	510	510	510
PCB 101	1923	1923	1923	1886	1886	1886
PCB 138	3262	3262	3262	3330	3330	3330
PCB 153	5137	5136	5136	4896	4756	4756
PCB 180	1131	1131	1131	1080	1080	1080
PBDE 28	9,1	9,0	9,0	9,8	8,6	8,7
PBDE 47	301	301	301	305	305	305
PBDE 99	67	67	67	67	67	67
PBDE 100	84	84	84	83	83	83
PBDE 153	12	12	12	12	12	12
PBDE 154	38	38	39	38	38	38
PBDE 183	1,4	1,1	1,1	2,0	1,3	1,3
PBDE 209	35	8,4	11	66	20	19
α-HBCD *	309	309	309	303	303	303
β-HBCD *	6,0	6,0	5,4	7,6	6,4	5,4
γ-HBCD *	10	10	7,8	13	9,9	7,8
Tot HBCD *	329	329	329	321	321	321

	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	64	33	33	56	2	0
PCB 52	29	29	29	56	0	0
PCB 101	30	30	30	56	0	0
PCB 138	30	30	30	56	0	0
PCB 153	38	33	33	56	1	0
PCB 180	32	32	32	56	0	0
PBDE 28	54	36	36	27	2	1
PBDE 47	28	28	28	27	0	0
PBDE 99	31	31	31	27	0	0
PBDE 100	25	25	25	27	0	0
PBDE 153	24	24	25	27	0	1
PBDE 154	42	42	41	27	0	1
PBDE 183	71	51	49	27	6	9
PBDE 209	124	114	111	21	7	9
α-HBCD *	12	12	12	6	0	0
β-HBCD *	48	33	16	6	1	4
γ-HBCD *	63	28	29	6	1	3
Tot HBCD *	15	15	15	6	0	0

NDs: Non-detects

* : Indicative value due to few reported values

Consensus statistics

2019

Brown meat, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
2,3,7,8-TCDD	0,091	0,091	0,088	0,023	26	56	3	4
1,2,3,7,8-PeCDD	0,37	0,37	0,36	0,10	28	56	1	2
1,2,3,4,7,8-HxCDD	0,21	0,21	0,21	0,042	20	56	1	1
1,2,3,6,7,8-HxCDD	0,46	0,47	0,46	0,095	21	56	1	0
1,2,3,7,8,9-HxCDD	0,17	0,17	0,17	0,050	30	56	1	4
1,2,3,4,6,7,8-HpCDD	0,52	0,52	0,55	0,13	24	56	0	0
1,2,3,4,6,7,8,9-OCDD	0,52	0,52	0,57	0,16	29	56	2	0
2,3,7,8-TCDF	2,4	2,4	2,3	0,45	19	56	1	0
1,2,3,7,8-PeCDF	0,36	0,36	0,35	0,069	20	56	0	1
2,3,4,7,8-PeCDF	1,4	1,4	1,4	0,24	17	56	0	0
1,2,3,4,7,8-HxCDF	0,34	0,35	0,35	0,083	24	56	2	1
1,2,3,6,7,8-HxCDF	0,20	0,20	0,20	0,047	23	56	0	2
2,3,4,6,7,8-HxCDF	0,53	0,53	0,53	0,11	21	56	0	0
1,2,3,7,8,9-HxCDF	0,021	0,024	0,020	0,011	56	56	11	23
1,2,3,4,6,7,8-HpCDF	0,54	0,54	0,55	0,11	19	56	0	0
1,2,3,4,7,8,9-HpCDF	0,0087	0,010	0,0092	0,0045	49	56	16	27
1,2,3,4,6,7,8,9-OCDF	0,034	0,037	0,034	0,011	34	56	10	15
PCB 77	26	26	26	5,1	19	54	0	0
PCB 126	8,4	8,4	8,3	1,8	22	54	0	1
PCB 169	2,9	2,9	2,9	0,60	21	54	0	1
PCB 81	1,7	1,7	1,7	0,54	32	54	1	3
PCB 105	278	278	291	48	17	54	0	0
PCB 114	11	11	12	3,1	27	54	3	2
PCB 118	924	924	946	124	13	54	0	0
PCB 123	14	14	14	4,7	33	54	5	3
PCB 156	108	108	109	14	13	54	0	0
PCB 157	31	32	32	4,3	13	54	2	0
PCB 167	85	85	84	16	20	54	2	2
PCB 189	13	13	13	1,8	14	54	0	2

Consensus statistics

Brown meat, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
PCB 28	153	142	142	182	143	143
PCB 52	43	40	40	70	43	43
PCB 101	242	238	238	258	238	238
PCB 138	1787	1787	1787	1813	1813	1813
PCB 153	3061	3061	3061	2975	2975	2975
PCB 180	570	570	570	575	575	575
PBDE 28	3,8	3,7	3,8	4,3	3,8	3,9
PBDE 47	50	50	50	55	52	52
PBDE 99	7,7	7,6	7,6	9,5	7,5	7,5
PBDE 100	14	14	14	15	15	15
PBDE 153	5,6	5,4	5,4	5,8	5,3	5,3
PBDE 154	20	20	20	21	21	21
PBDE 183	1,6	0,84	0,76	2,8	1,2	1,1
PBDE 209	24	14	14	122	15	15
α-HBCD *	10	10	11	11	11	11
β-HBCD *	6,0	5,5	3,8	6,7	4,7	3,8
γ-HBCD *	10	10	6,5	8,8	8,8	6,5
Tot HBCD *	14	12	12	19	12	12

	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	68	30	30	47	6	1
PCB 52	114	34	34	47	6	2
PCB 101	42	31	31	47	3	1
PCB 138	27	27	27	47	0	0
PCB 153	22	22	22	47	0	0
PCB 180	26	26	26	47	0	0
PBDE 28	44	27	26	22	2	1
PBDE 47	28	18	18	22	1	0
PBDE 99	71	20	20	22	2	0
PBDE 100	29	29	29	22	0	0
PBDE 153	45	23	23	22	1	0
PBDE 154	31	31	32	22	0	1
PBDE 183	112	71	77	22	6	8
PBDE 209	159	54	54	17	8	4
α-HBCD *	37	37	42	5	0	3
β-HBCD *	74	46	86	5	1	3
γ-HBCD *	61	61	118	5	0	3
Tot HBCD *	62	15	15	3	1	0

NDs: Non-detects

* : Indicative value due to few reported values

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

TEF$_{2006}$	Median pg/g	Mean pg/g	Standard deviation, pg/g	Relative standard deviation, %	Min pg/g	Max pg/g	Reporting laboratories
Brown meat, fresh weight							
PCDD/PCDF TEQ	1,3	1,7	0,42	25	0,14	3,8	57
Non-ortho PCB TEQ	0,93	0,92	0,20	21	0,099	1,4	54
Mono-ortho PCB TEQ	0,045	0,045	0,0056	12	0,037	0,063	54
Total TEQ	2,3	2,3	0,54	23	0,29	4,7	57
Sum indicator PCB	5974	5874	1320	22	5,9	8536	47
Sum PBDE without PBDE 209	103	112	30	27	63	199	22
Herring, fresh weight							
PCDD/PCDF TEQ	0,96	1,2	0,19	15	0,13	1,7	64
Non-ortho PCB TEQ	1,1	1,1	0,21	19	0,11	1,5	63
Mono-ortho PCB TEQ	0,068	0,069	0,011	16	0,030	0,094	63
Total TEQ	2,1	2,1	0,34	16	0,32	2,8	64
Sum indicator PCB	12357	11962	3056	26	12	19715	56
Sum PBDE without PBDE 209	521	517	136	26	20	776	27
Veal, fresh weight							
PCDD/PCDF TEQ	0,025	0,053	0,077	146	0,0096	0,48	51
Non-ortho PCB TEQ	0,058	0,071	0,083	117	0,021	0,63	50
Mono-ortho PCB TEQ	0,0025	0,0027	0,0012	44	0,0019	0,010	50
Total TEQ	0,086	0,12	0,14	115	0,017	0,90	52
Sum indicator PCB	309	328	146	44	107	1195	44
Sum PBDE without PBDE 209	8,6	13	12	98	2,2	54	17

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

TEF$_{1998}$	Median pg/g	Mean pg/g	Standard deviation, pg/g	Relative standard deviation, %	Min pg/g	Max pg/g	Reporting laboratories
Brown meat, fresh weight							
PCDD/PCDF TEQ	1,6	1,7	0,43	26	0,17	4,1	57
Non-ortho PCB TEQ	0,87	0,86	0,19	22	0,093	1,3	54
Mono-ortho PCB TEQ	0,20	0,21	0,025	12	0,17	0,29	54
Total TEQ	2,7	2,7	0,57	21	0,47	5,1	57
Sum indicator PCB	5974	5874	1320	22	5,9	8536	47
Sum PBDE without PBDE 209	103	112	30	27	63	199	22
Herring, fresh weight							
PCDD/PCDF TEQ	1,2	1,2	0,24	20	0,16	1,9	64
Non-ortho PCB TEQ	1,0	1,0	0,20	20	0,10	1,5	63
Mono-ortho PCB TEQ	0,33	0,33	0,048	14	0,20	0,46	63
Total TEQ	2,6	2,5	0,39	15	0,63	3,3	64
Sum indicator PCB	12357	11962	3056	26	12	19715	56
Sum PBDE without PBDE 209	521	517	136	26	20	776	27
Veal, fresh weight							
PCDD/PCDF TEQ	0,029	0,053	0,080	152	0,010	0,50	51
Non-ortho PCB TEQ	0,056	0,065	0,064	98	0,021	0,50	50
Mono-ortho PCB TEQ	0,011	0,013	0,0055	44	0,0089	0,044	50
Total TEQ	0,097	0,13	0,12	98	0,020	0,80	52
Sum indicator PCB	309	328	146	44	107	1195	44
Sum PBDE without PBDE 209	8,6	13	12	98	2,2	54	17

Laboratories' Z-scores: Analyte solution

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4							
5	0,050	0,075	-0,20	0,13			
6							
7	-0,021	0,024	-0,45	0,53	-0,48		
8							
9							
10	-0,037	-0,066	0,24	0,023	-0,061		
11	0,24	0,27	0,012	0,51	0,77	0,61	-0,022
12	0,0037	0,0047	-0,0060	-0,024	0,056		
13							
14							
15	0,032	0,018	0,16	0,026	0,060		
16							
17	0,094	0,092	0,10	0,74	0,33		
18							
19							
20	0,056	0,052	0,088	-0,019			
21							
22							
23	0,26	0,27	0,078	-0,10	0,0068	0,10	0,14
24	0,027	0,0020	0,27	-0,44	0,075		
25	-0,24	-0,29	0,26	-0,11	-0,73	-0,0098	0,081
26							
27							
28	-0,14	-0,19	0,40	0,58	-0,59		
29							
30							
31	0,018	0,024	-0,038	0,13	0,36	0,22	0,26
32	0,47	0,54	-0,21	0,50	0,64		
33	-0,078	-0,075	-0,10	-0,046			
34	0,084	0,10	-0,068	-0,021	0,10		
35							
36	-0,28	-0,21	-0,90	-0,79		0,11	0,11
37	-0,053	-0,035	-0,24	-0,0091	0,36	0,020	0,033
38	-0,21	-0,22	-0,14	-0,014	-0,23		
39							
40	-0,40	-0,43	-0,073	-0,050	-0,90	-1,8	0,013
41							
42	-0,27	-0,32	0,22	-0,70	-0,86	-2,2	-0,71
43							
44	-0,25	-0,24	-0,37	-0,090	-0,060		
45	0,016	0,015	0,027	0,0054	0,026		
46							
47							
48	-0,10	-0,11	-0,000077	0,00000000000000072	0,16		
49	-0,24	-0,20	-0,59	-0,028	-0,40	-2,3	-0,87
50							
51							
52							
53							
54	-0,0093	-0,093	0,79	0,22	0,20	-1,9	-0,20
55							
56	0,13	0,14	0,085				
57	-0,10	-0,10	-0,11	-0,34	-0,23	-0,38	-0,34
58		0,12	-0,14		0,28		
59							
60							
61	0,098	0,099	0,091	-0,33	0,32		
62							
63	-0,052	-0,029	-0,28	-0,13	-0,00021	-1,7	0,047
64	0,19	0,16	0,50	0,10	0,059		
65	0,40	0,39	0,49	0,49	-0,38	0,057	0,086
66							
67							
68							
69							
70	-5,0	-5,0	-5,0	-5,0	-5,0		

Laboratories' Z-scores: Analyte solution (continued)

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71	0,021	0,025	-0,0090	-0,0085	0,064		
72							
73	0,45	0,50	0,010	0,039			
74							
75	0,077	0,062	0,21	0,050	0,088		
76	-0,12	-0,14	0,15	0,11	0,19		
77			0,016	0,18	-0,078	0,105	0,021
78							
79							
80	0,26	0,27	0,13	0,20	-0,12		
81					-0,41	-0,86	-0,89
82							
83							
84	-0,16	-0,13	-0,46	-0,052	0,31		
85							
86							
87	-0,30	-0,32	-0,12	-0,25	-0,33		
88	0,023	0,011	0,14	0,051			
89	-0,090	-0,15	0,46	0,49			
90	-0,50	-0,55	-0,036	-0,18	-5,0	0,12	0,11
91	-0,020	-0,022	0,00096	-0,017			
92	-0,072	-0,018	-0,59	0,084			
93							
94	-0,015	-0,017	-0,00054	-0,010	-0,16	0,126	0,0040
95	0,24	0,33	-0,57	-0,18	-0,091	-0,17	-0,16
96							
97							
98							
99							
100	-0,042	-0,052	0,050	0,18	0,17	-0,061	-0,092
101							
102	0,051	0,052	0,050	-0,24	-0,013	-0,02	0,076
103	0,47	0,55	-0,26	-0,094	-5,0		
104							
105					0,49		
106	-0,26	-0,24	-0,37	0,034	-0,18		
107							
108							
109	-0,15	-0,17	0,018	-0,032	-0,092		
110	-0,49	-0,44	-0,95	-0,062	-0,055		
111							
112							
113	-0,086	-0,085	-0,10	-0,085	0,12	0,048	0,22
114	0,33	0,36	-0,014	0,22	0,47		
115	-0,077	-0,078	-0,074	0,089	0,042	0,079	0,062
116	-0,21	-0,24	0,029	0,13		-0,20	0,068
117							
118	0,13	0,17	-0,28	0,17	-0,71		
119	0,13	0,17	-0,21	-0,10			
120	-0,20	-0,20	-0,18	-0,025	-0,14		

Laboratories' Z-scores: Veal-2019, fresh weight

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4	14	35	6,3	3,9	0,85		
5	0,11	-1,7	0,77	0,17	0,85		
6							
7	0,68	-0,71	1,2	0,38	1,1		
8							
9							
10	-0,22	-0,85	0,018	-0,23	0,12		
11	0,39	-0,24	0,63	0,51	1,3	49	11
12							
13							
14							
15	0,54	1,1	0,36	0,26	1,2		
16							
17	-0,49	-2,8	0,33	0,47	0,55		
18							
19							
20	0,21	0,18	0,22	0,18			
21							
22							
23	3,1	11	0,41	0,51	0,25	0,26	2,5
24	0,12	0,47	-0,012	0,034	0,29		
25							
26							
27	4,2	5,4	3,9	-0,32	-0,69		
28	29	107	1,1	-0,30	-1,1		
29							
30							
31	-0,38	-0,67	-0,27	-0,61	-0,20	14	2,7
32	-0,55	-0,58	-0,57	0,0027	0,13		
33	0,41	-0,44	0,73	0,68			
34	-0,70	-1,1	-0,56	-0,69	-0,066		
35							
36	-0,36	0,58	-0,71	-0,59		4,1	0,41
37	-0,90	-1,4	-0,70	-1,0	-0,26	-1,0	-3,2
38							
39							
40	-1,4	2,0	-2,7	-0,46	-0,69	-1,4	5,9
41							
42							
43	0,79	6,4	-1,3	-0,11	-0,13	0,97	12
44	0,56	-0,82	1,1	-0,082	-0,13		
45	0,89	2,5	0,36	-0,74	-0,85		
46							
47							
48							
49	-0,0025	-0,0043	0,0049	-0,16	-0,77	-3,0	1,3
50							
51							
52							
53							
54	0,28	1,1	-0,018	0,10	-0,10	-3,7	-0,83
55							
56							
57	-0,30	-0,95	-0,063	-0,25	0,28	-1,9	1,0
58	8,9	32	0,57	3,0	1,1		
59							
60							
61	0,28	6,0	-1,9	0,0051	2,7		
62							
63	0,47	1,0	0,28	0,26	0,25	55	18
64	5,6	19	0,89	1,0	-0,12		
65	-0,25	-1,1	0,067	-0,35	-1,1	4,0	-0,69
66							
67							
68							
69							
70	50	56	50	1,1	-0,67		

Laboratories' Z-scores: Veal-2019, fresh weight (continued)

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72							
73	2,6	5,5	1,6	2,4			
74							
75	0,45	0,95	0,27	0,22	1,3		
76		-1,1					
77							
78							
79							
80	2,2	8,6	-0,11	0,43	0,25		
81							
82							
83							
84							
85							
86							
87	0,92	2,2	0,46	0,052	0,13		
88	0,46	3,7	-0,71	-0,95			
89	-0,91	-1,1	-0,83	-1,1			
90							
91							
92							
93							
94							
95	0,042	2,1	-0,71	-0,13	0,30	-0,26	-0,66
96							
97							
98							
99							
100	-0,053	2,5	-0,99	-0,55	-0,81		
101							
102							
103	1,5	4,8	0,29	0,025	-0,21		
104							
105	-3,8	-2,7			-3,2		
106	-0,93	-1,0	-0,92	-0,82	-1,1		
107							
108	0,66	3,5	-0,38	-0,31	-0,014	14	40
109	0,81	3,0	0,0093	0,47	0,22		
110							
111							
112							
113	-0,66	-0,73	-0,72	1,3	1,4	3,1	-0,81
114	-1,5	0,87	-3,1	16	15		
115	-0,47	-1,6	-0,079	0,14	0,47	273	4,7
116	1,3	-0,03	1,9	-0,21		0,47	2,2
117	-2,2		-1,2	-1,1	-0,43		
118	-0,42	-2,0	0,14	0,68	1,3		
119							
120	3,1	4,0	2,8	2,5	1,4		

Laboratories' Z-scores: Veal-2019, lipid weight

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4	12	31	5,2	3,0	0,30		
5	-0,13	-1,8	0,50	-0,070	0,57		
6							
7	-0,11	-1,3	0,36	-0,36	0,25		
8							
9							
10	-0,70	-1,3	-0,48	-0,71	-0,39		
11	-1,1	-1,6	-0,97	-1,1	-0,46	34	6,2
12							
13							
14							
15	0,61	1,1	0,42	0,32	1,3		
16							
17	-0,66	-2,9	0,13	0,27	0,35		
18							
19							
20	-0,24	-0,25	-0,23	-0,26			
21							
22							
23	2,8	10	0,18	0,28	0,025	0,037	2,2
24	1,3	1,7	1,1	1,2	1,5		
25							
26							
27	4,5	5,8	4,2	-0,16	-0,54		
28	28	103	0,92	-0,48	-1,2		
29							
30							
31	-0,28	-0,57	-0,16	-0,51	-0,36	14	3,0
32	-0,40	-0,43	-0,42	0,18	0,31		
33	0,22	-0,61	0,52	0,47			
34	0,36	-0,097	0,53	0,38	1,1		
35							
36	-0,29	0,66	-0,64	-0,52		4,3	0,50
37	-0,60	-1,2	-0,39	-0,74	0,089	-0,71	-3,1
38							
39							
40	-1,4	2,0	-2,7	-0,46	-0,69	-1,4	5,9
41							
42							
43	0,51	5,8	-1,5	-0,34	-0,36	0,69	12
44	-0,28	-1,5	0,18	-0,82	-0,86		
45	0,37	1,8	-0,12	-1,1	-1,2		
46							
47							
48							
49	0,36	0,36	0,37	0,19	-0,47	-2,8	1,7
50							
51							
52							
53							
54	0,30	1,1	0,00089	0,12	-0,083	-3,7	-0,82
55							
56							
57	-0,37	-1,0	-0,13	-0,31	0,20	-1,9	0,92
58	12	39	1,7	4,6	2,4		
59							
60							
61	-0,48	4,5	-2,3	-0,71	1,6		
62							
63	0,21	0,73	0,031	0,016	0,0074	52	17
64	5,0	17	0,57	0,64	-0,39		
65	0,20	-0,69	0,55	0,09	-0,73	4,9	-0,29
66							
67							
68							
69							
70	51	56	51	1,2	-0,62		

Laboratories' Z-scores: Veal-2019, lipid weight (continued)

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72							
73	2,9	5,8	1,8	2,7			
74							
75	0,40	0,90	0,22	0,17	1,3		
76		-1,7					
77							
78							
79							
80	2,2	8,6	-0,105	0,43	0,25		
81							
82							
83							
84							
85							
86							
87	0,77	2,0	0,33	-0,070	0,0019		
88	1,2	4,9	-0,13	-0,40			
89	-0,64	-0,82	-0,56	-0,83			
90							
91							
92							
93							
94							
95	-0,61	1,15	-1,3	-0,76	-0,38	-0,87	-1,2
96							
97							
98							
99							
100	-0,33	2,1	-1,2	-0,80	-1,0		
101							
102							
103	1,6	5,0	0,36	0,087	-0,15		
104							
105	-3,4	-2,1			-2,8		
106	-0,27	-0,32	-0,26	-0,15	-0,48		
107							
108	0,66	3,5	-0,38	-0,31	-0,014	14	40
109	0,88	3,1	0,072	0,54	-0,33		
110							
111							
112							
113	-1,1	-1,2	-1,2	0,63	0,76	2,3	-1,2
114	3,9	9,9	-0,29	47	11		
115	-0,1	-1,3	0,29	0,52	-0,98	199	2,1
116	0,84	-0,39	1,4	-0,56		0,071	1,7
117	-1,9		-0,84	-0,71	0,025		
118	-0,42	-2,0	0,14	0,68	1,3		
119							
120	2,9	3,7	2,6	2,2	1,1		

Laboratories' Z-scores: Herring-2019, fresh weight

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4	1,5	1,2	1,7	1,7	-1,4		
5	1,3	1,1	1,5	1,3	-1,6		
6							
7	0,59	0,37	0,76	0,94	-0,71		
8							
9							
10							
11	-0,020	0,010	-0,030	-0,26	-5,0	0,46	-0,91
12	0,49	0,75	0,22	1,0	1,9		
13							
14							
15	0,043	0,15	-0,039	-0,11	0,67		
16							
17	0,34	0,11	0,54	0,46	1,1		
18							
19	-0,61	-0,53	-0,69	-0,48			
20	0,16	0,0047	0,31	0,054			
21							
22							
23	0,25	0,11	0,38	0,19			
24	0,42	0,14	0,68	0,29	0,65		
25	0,58	-1,0	2,1	-0,59	-1,3	0,34	0,40
26							
27	-0,070	0,11	-0,21	-0,23	-0,51		
28	0,27	0,23	0,34	-0,36	-0,47		
29							
30	0,41	-0,18	0,91	0,68	0,83	2,2	0,98
31	-0,28	-0,13	-0,42	-0,19	-0,15	0,68	0,17
32	-0,12	0,16	-0,35	-0,24	-0,55		
33	0,68	0,10	1,1	1,3			
34	-0,18	-0,24	-0,13	-0,25	-0,021		
35							
36	-0,16	0,42	-0,66	-0,39		0,19	0,042
37	-0,59	-0,77	-0,42	-0,66	0,042	-0,84	-0,81
38	0,71	0,59	0,81	0,95			
39							
40	1,4	0,60	2,1	1,8	1,2	1,6	1,8
41							
42	0,52	0,37	0,68	0,10	-2,4	-1,5	-1,4
43	-0,58	-0,32	-0,79	-0,80	-0,13	-0,031	0,063
44	0,52	0,92	0,21	-0,11			
45	-0,016	0,18	-0,14	-0,85	-0,94		
46							
47							
48	-0,073	0,051	-0,20	0,25	0,36		
49	-0,30	0,26	-0,80	-0,34	-0,63	-0,73	-0,64
50							
51							
52							
53							
54	0,066	0,17	-0,056	0,55	0,88	0,17	0,27
55							
56							
57	0,68	0,22	1,2	-1,1	0,90	0,26	0,35
58	0,40	0,37	0,40	0,70	1,1		
59							
60							
61	-1,1	-0,35	-1,8	0,62	-1,2		
62							
63	0,13	0,12	0,14	0,047	-0,17	0,8	-0,13
64	0,019	-0,75	0,66	0,50	1,3		
65	0,35	0,13	0,55	0,16	-0,33	1,2	0,042
66							
67							
68							
69							
70							

Laboratories' Z-scores: Herring-2019, fresh weight (continued)

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71	0,31	0,68	-0,0018	0,13	-1,4	-4,9	-4,9
72							
73	0,52	0,21	0,74	1,3			
74							
75	0,086	0,10	0,080	-0,054	0,63		
76							
77							
78	-1,1	-0,93	-1,3	-0,14	-0,53	-0,16	-0,059
79							
80	-0,24	0,34	-0,79	0,19	-0,070		
81					-0,95	0,25	-0,81
82							
83							
84	-0,066	0,16	-0,26	-0,12	0,80		
85							
86							
87	1,6	3,8	-0,15	-0,18	-0,13		
88	-0,051	0,12	-0,19	-0,25			
89	0,15	0,060	0,34	-1,6			
90	-0,053	-0,58	0,37	0,50	-5,0	0,68	-0,21
91							
92	0,62	0,97	0,32	0,66			
93							
94							
95	-0,21	-0,34	-0,046	-1,0	-0,66	-0,22	-0,23
96							
97							
98							
99							
100	-1,6	-1,6	-1,5	-0,78	-0,037	-0,86	-0,82
101							
102	-0,12	0,060	-0,26	-0,36	0,38	0,28	-0,15
103	0,051	0,70	-0,34	-2,8	-0,018		
104							
105	-0,42	-3,5			0,46		
106	-0,65	-0,42	-0,86	-0,61	-0,47		
107							
108	-0,54	-0,85	-0,30	-0,19	0,68	3,0	3,2
109	-0,54	-0,38	-0,71	0,036	-0,24		
110	-0,14	-0,43	0,13	-0,28	-3,8		
111							
112							
113	0,43	0,48	0,34	1,1	0,18	-0,69	-0,90
114	-4,2	-4,3	-4,5	1,2	24		
115	0,025	-0,42	0,39	0,32	0,25	3,4	0,46
116	0,093	-0,27	0,42	0,049		1,3	1,3
117	-0,64	-0,50	-0,76	-0,71	-0,11		
118	0,52	0,22	0,82	-0,025	-1,6		
119	-1,4	-1,1	-1,7	-1,6			
120	0,13	-0,042	0,24	0,72	0,66		

Laboratories' Z-scores: Herring-2019, lipid weight

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4	1,3	1,0	1,5	1,5	-1,4		
5	0,87	0,66	1,1	0,91	-1,6		
6							
7	-0,34	-0,53	-0,20	-0,047	-0,71		
8							
9							
10							
11	-1,2	-1,2	-1,2	-1,4	-5,0	0,46	-0,91
12	0,75	1,0	0,47	1,3	1,9		
13							
14							
15	0,043	0,15	-0,039	-0,11	0,67		
16							
17	-0,072	-0,29	0,11	0,036	1,1		
18							
19							
20							
21							
22							
23							
24	1,2	0,87	1,5	1,0	0,65		
25	0,83	-0,84	2,4	-0,40	-1,3	0,34	0,40
26							
27	-0,31	-0,14	-0,45	-0,46	-0,51		
28	0,092	0,053	0,16	-0,51	-0,47		
29							
30	1,0	0,39	1,6	1,3	0,83	2,2	0,98
31	-0,20	-0,038	-0,34	-0,10	-0,15	0,68	0,17
32	-0,13	0,15	-0,37	-0,25	-0,55		
33	-0,12	-0,61	0,28	0,41			
34	-0,11	-0,17	-0,062	-0,18	-0,021		
35							
36	0,12	0,74	-0,41	-0,12		0,19	0,042
37	-0,61	-0,79	-0,45	-0,69	0,042	-0,84	-0,81
38							
39							
40	0,77	0,034	1,4	1,1	1,2	1,6	1,8
41							
42	-2,2	-2,3	-2,2	-2,4	-2,4	-1,5	-1,4
43	-0,16	0,12	-0,40	-0,40	-0,13	-0,031	0,063
44							
45	-0,19	0,0045	-0,31	-1,0	-0,94		
46							
47							
48	-0,21	-0,089	-0,34	0,11	0,36		
49	-0,26	0,31	-0,76	-0,29	-0,63	-0,73	-0,64
50							
51							
52							
53							
54	-0,22	-0,12	-0,34	0,23	0,56	-0,12	-0,014
55							
56							
57	0,86	0,38	1,4	-0,99	0,90	0,26	0,35
58	1,3	1,3	1,3	1,7	1,1		
59							
60							
61	-1,5	-0,80	-2,1	0,072	-1,2		
62							
63	-0,15	-0,16	-0,14	-0,23	-0,17	0,81	-0,13
64	0,39	-0,44	1,1	0,90	1,3		
65	0,35	0,13	0,55	0,16	-0,33	1,2	0,042
66							
67							
68							
69							
70							

Laboratories' Z-scores: Herring-2019, lipid weight (continued)

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71	-1,3	-1,0	-1,5	-1,4	-1,4	-4,9	-4,9
72							
73	0,72	0,39	0,95	1,5			
74							
75	0,036	0,053	0,030	-0,10	0,63		
76							
77							
78	-1,7	-1,6	-1,8	-0,90	-0,53	-0,16	-0,059
79							
80	-0,10	0,50	-0,66	0,34	-0,070		
81					-0,95	0,25	-0,81
82							
83							
84	-0,16	0,056	-0,35	-0,21	0,80		
85							
86							
87	1,3	3,3	-0,41	-0,44	-0,13		
88	1,6	1,8	1,4	1,3			
89	-0,063	-0,15	0,12	-1,7			
90	0,37	-0,20	0,83	0,97	-5,0	0,68	-0,21
91							
92	0,26	0,58	-0,031	0,29			
93							
94							
95	-0,21	-0,34	-0,046	-1,0	-0,66	-0,22	-0,23
96							
97							
98							
99							
100	-1,4	-1,5	-1,4	-0,65	-0,037	-0,86	-0,82
101							
102	0,20	0,39	0,047	-0,059	0,38	0,28	-0,15
103	0,12	0,79	-0,27	-2,8	-0,018		
104							
105	1,0	-3,0			0,46		
106	-0,65	-0,41	-0,86	-0,60	-0,47		
107							
108	-0,20	-0,53	0,062	0,18	0,68	3,0	3,2
109	-0,82	-0,67	-0,98	-0,28	-0,24		
110	-3,8	-3,9	-3,8	-3,9	-3,8		
111							
112							
113	-0,33	-0,28	-0,40	0,23	0,18	-0,69	-0,90
114	-1,2	-1,6	-2,4	26	24		
115	-0,053	-0,5	0,31	0,24	0,25	3,4	0,5
116	1,3	0,84	1,7	1,2		1,3	1,3
117	-0,60	-0,46	-0,71	-0,66	-0,11		
118	0,018	-0,26	0,29	-0,48	-1,6		
119	0,21	0,66	-0,16	-0,13			
120	0,46	0,28	0,58	1,1	0,66		

Laboratories' Z-scores: Brown meat-2019, fresh weight

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4	-0,42	-0,90	0,20	0,94	0,99		
5	1,8	1,5	2,3	1,7	0,99		
6							
7	-0,12	-0,44	0,31	0,45	-1,6		
8							
9							
10	0,34	0,22	0,51	0,11	0,78		
11	0,049	0,062	0,028	0,12	0,23	10	0,55
12							
13							
14							
15	0,091	-0,013	0,24	0,085	0,64		
16							
17	0,19	0,027	0,42	0,38	1,6		
18							
19	-0,46	-0,41	-0,52	-0,56	-0,48	-0,64	-0,051
20	-0,90	-1,2	-0,50	-0,31			
21							
22							
23	1,3	1,8	0,74	0,14	0,38	4,6	4,7
24	0,088	0,065	0,11	0,27	-0,19		
25	-0,015	-0,17	0,23	-0,32	-1,3	-0,11	0,40
26							
27	0,038	0,31	-0,35	-0,16	-0,47		
28	-0,38	-0,77	0,16	-0,30	-0,32		
29							
30							
31	-0,29	-0,35	-0,22	-0,096	-0,17	2,3	-0,21
32	-0,51	0,19	-1,5	0,054	-0,16		
33	1,4	0,95	2,1	2,1			
34	-0,22	0,013	-0,55	-0,44	-0,11		
35							
36	0,11	0,45	-0,35	-0,36		-0,30	-0,16
37							
38	0,77	0,86	0,64	0,84	0,11		
39							
40	-0,14	-0,12	-0,23	1,4	2,3	0,41	1,14
41							
42							
43	-0,42	-0,29	-0,61	-0,27	0,72	2,2	2,0
44							
45	0,21	0,28	0,16	-0,82	-0,81		
46							
47							
48							
49	-0,093	0,26	-0,60	-0,25	-0,67	-1,3	-0,77
50							
51							
52							
53							
54	0,51	0,97	-0,16	0,56	0,15	-1,2	-0,66
55							
56							
57	0,46	0,80	0,027	-0,62	0,70	-0,64	-0,33
58	1,5	1,2	2,0	0,58	0,19		
59							
60							
61	-1,4	-1,1	-1,8	0,21	1,6		
62							
63	0,36	0,39	0,35	0,012	0,26	11	1,1
64							
65	0,30	0,39	0,16	0,36	0,67	-0,069	-0,083
66							
67							
68							
69							
70	-0,93	0,27	-2,7	0,0097	-0,020		

Laboratories' Z-scores: Brown meat-2019, fresh weight (continued)

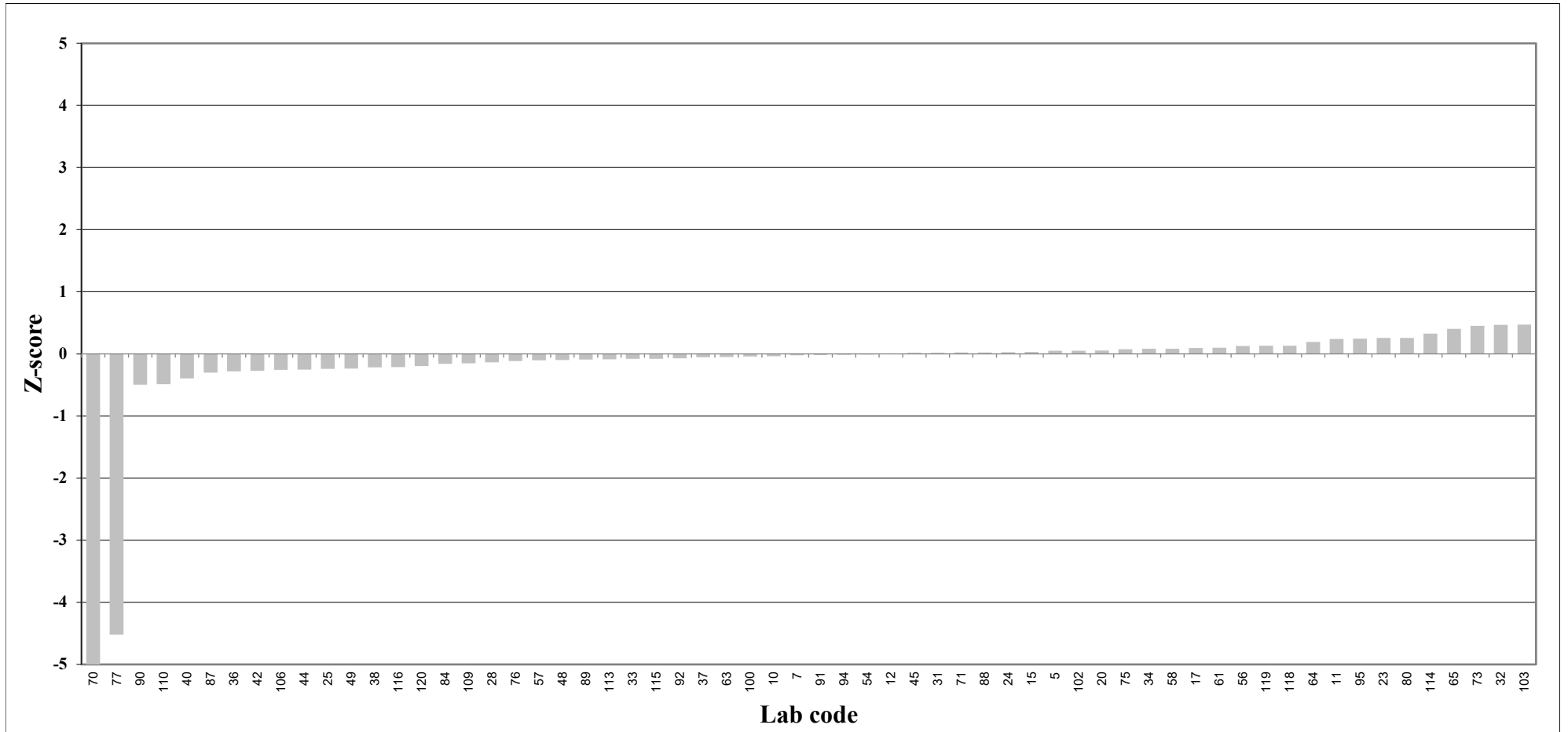| LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72							
73		-0,052					
74							
75	0,087	-0,045	0,28	0,036	0,54		
76		-0,24					
77	0,64	0,22	1,2	1,0	0,84	9,1	1,3
78							
79							
80	0,17	0,66	-0,54	0,35	-0,29		
81					-1,3	-2,3	-1,9
82							
83							
84							
85							
86							
87	5,2	9,2	-0,12	-0,33	0,10		
88	-0,21	-0,37	0,018	0,00034			
89	-0,11	0,044	-0,30	-0,54			
90	-0,16	-0,26	-0,027	0,080	-5,0	6,0	-0,88
91	0,072	-0,033	0,22	0,20			
92	0,060	-0,022	0,15	0,74			
93							
94	-0,35	-0,31	-0,41	-0,31	-0,40	2,9	-0,13
95	0,29	0,18	0,49	-0,74	-0,22	-0,11	-0,092
96							
97							
98							
99							
100	-0,46	-0,50	-0,43	-0,032	1,2		
101							
102	0,37	0,47	0,24	0,17	0,24	34	0,29
103	-0,17	-0,17	-0,18	-0,073	-0,29		
104							
105	1,1	4,4			-2,2		
106	-0,40	-0,30	-0,55	-0,62	-0,62		
107							
108	-0,32	-0,57	0,020	-0,025	0,32	3,5	3,5
109	-0,59	-0,73	-0,43	0,14	0,039		
110							
111							
112							
113	0,91	-0,024	2,2	2,1	3,6	5,8	0,58
114	-4,4	-4,5	-4,5	0,44	0,53		
115							
116	0,35	0,13	0,66	0,67		0,054	0,066
117	-0,34	-0,34	-0,35	-0,21	0,53		
118							
119	0,14	0,35	-0,15	-0,13			
120	-0,24	-0,35	-0,10	0,41	-0,13		

Laboratories' Z-scores: Brown meat-2019, lipid weight

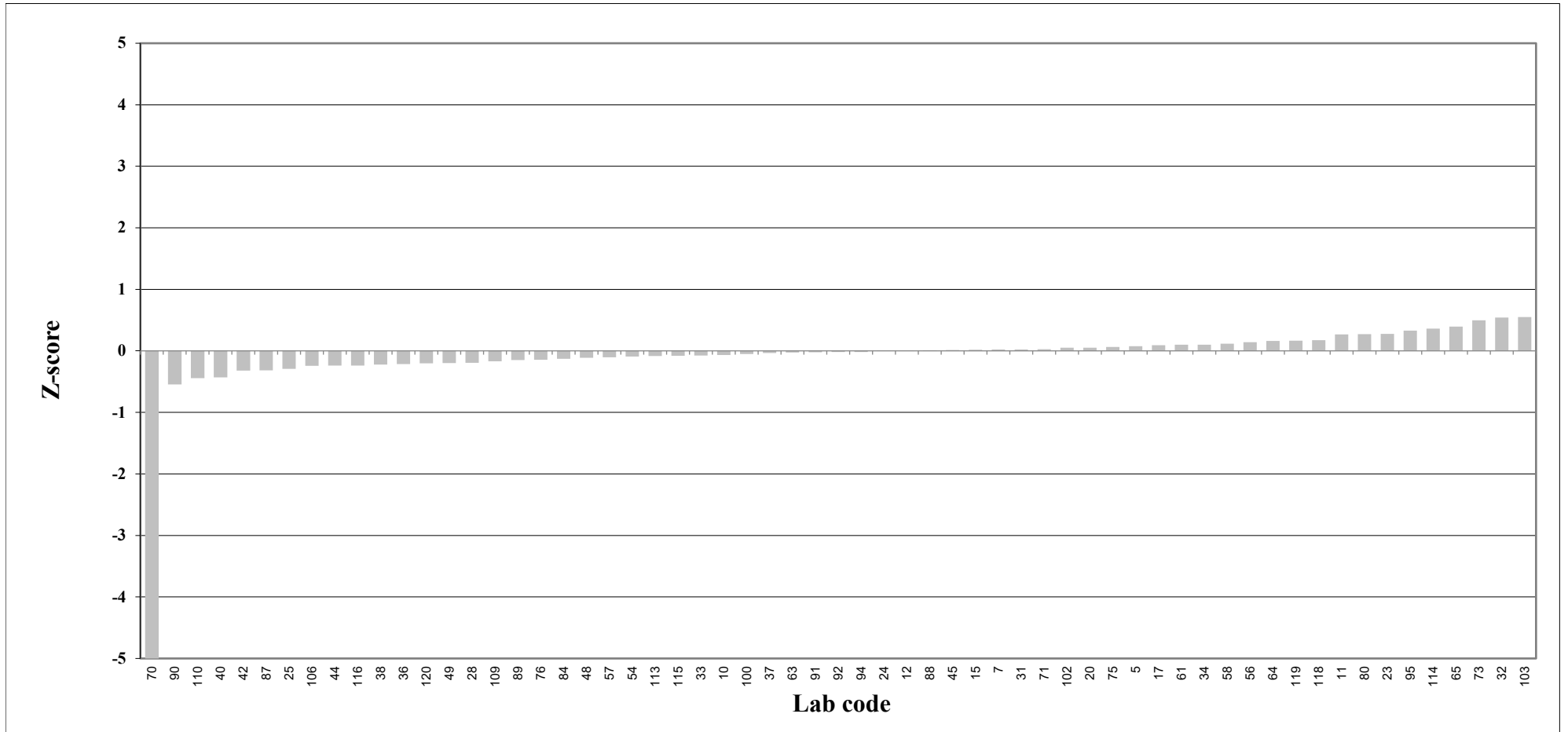| LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4	0,19	-0,36	0,90	1,7	1,8		
5	1,5	1,2	1,9	1,3	0,65		
6							
7	-0,66	-0,95	-0,27	-0,16	-2,0		
8							
9							
10	-0,19	-0,29	-0,028	-0,39	0,21		
11	-0,30	-0,28	-0,32	-0,23	-0,12	9,0	0,17
12							
13							
14							
15	1,6	1,5	1,8	1,6	2,3		
16							
17	-0,052	-0,21	0,17	0,13	1,3		
18							
19							
20	-1,3	-1,5	-0,88	-0,71			
21							
22							
23	1,1	1,5	0,56	-0,015	0,22	4,3	4,4
24	0,30	0,27	0,32	0,49	0,0076		
25	0,37	0,20	0,64	0,049	-0,97	0,27	0,82
26							
27	-0,12	0,15	-0,50	-0,32	-0,61		
28	-0,88	-1,2	-0,39	-0,81	-0,82		
29							
30							
31	0,011	-0,051	0,091	0,22	0,14	2,8	0,10
32	-0,47	0,23	-1,5	0,097	-0,11		
33	-0,0049	-0,38	0,51	0,52			
34	0,36	0,62	-0,013	0,12	0,48		
35							
36	0,23	0,57	-0,24	-0,25		-0,19	-0,045
37							
38							
39							
40	-0,36	-0,35	-0,45	1,1	2,0	0,16	0,85
41							
42							
43	-0,42	-0,29	-0,61	-0,27	0,72	2,2	2,0
44							
45	0,41	0,48	0,35	-0,67	-0,65		
46							
47							
48							
49	0,36	0,75	-0,19	0,19	-0,27	-0,93	-0,38
50							
51							
52							
53							
54	0,68	1,2	-0,0065	0,74	0,31	-1,1	-0,54
55							
56							
57	1,2	1,6	0,75	0,0059	1,5	-0,014	0,34
58	3,1	2,7	3,7	1,9	1,4		
59							
60							
61	-1,8	-1,6	-2,2	-0,42	0,84		
62							
63	0,0015	0,024	-0,015	-0,33	-0,097	9,7	0,71
64							
65	0,30	0,39	0,16	0,36	0,67	-0,069	-0,083
66							
67							
68							
69							
70	-0,67	0,61	-2,5	0,33	0,30		

Laboratories' Z-scores: Brown meat-2019, lipid weight (continued)

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72							
73	-1,6	0,93					
74							
75	1,5	1,3	1,7	1,4	2,0		
76		-0,89					
77	2,3	1,8	3,1	2,8	2,6	13	3,2
78							
79							
80	0,50	1,0	-0,25	0,70	0,011		
81					-1,5	-2,4	-2,1
82							
83							
84							
85							
86							
87	4,6	8,2	-0,45	-0,64	-0,24		
88	2,4	2,1	2,7	2,7			
89	-0,11	0,044	-0,30	-0,54			
90	0,99	0,87	1,2	1,3	-5,0	8,6	0,106
91	0,0237	-0,080	0,17	0,15			
92	0,0054	-0,076	0,090	0,68			
93							
94	-0,89	-0,86	-0,95	-0,86	-0,94	1,9	-0,70
95	0,22	0,12	0,43	-0,79	-0,27	-0,17	-0,15
96							
97							
98							
99							
100	-0,75	-0,78	-0,72	-0,34	0,81		
101							
102	0,50	0,60	0,36	0,30	0,36	35	0,41
103	0,34	0,34	0,34	0,45	0,22		
104							
105	0,61	3,7			-2,4		
106	0,026	0,14	-0,13	-0,21	-0,21		
107							
108	-0,21	-0,46	0,14	0,098	0,45	3,7	3,7
109	-0,96	-1,1	-0,81	-0,29	-0,38		
110							
111							
112							
113	-0,011	-0,80	1,1	1,0	2,2	4,2	-0,29
114	-2,1	-2,6	-2,5	20	21		
115							
116	-1,2	-1,4	-1,0	-1,0		-1,4	-1,4
117	0,14	0,15	0,14	0,29	1,1		
118							
119	0,31	0,53	0,015	0,038			
120	-0,50	-0,61	-0,38	0,11	-0,40		

Z-score analyte solution; total TEQ

Y-axis: Z-score

X-axis: Lab code

Lab codes (left to right): 70, 77, 90, 110, 40, 87, 36, 42, 106, 44, 25, 49, 38, 116, 120, 84, 109, 28, 76, 57, 48, 89, 113, 33, 115, 92, 37, 63, 100, 10, 7, 91, 94, 54, 12, 45, 31, 71, 88, 24, 15, 5, 102, 20, 75, 34, 58, 17, 61, 56, 119, 118, 64, 11, 95, 23, 80, 114, 65, 73, 32, 103
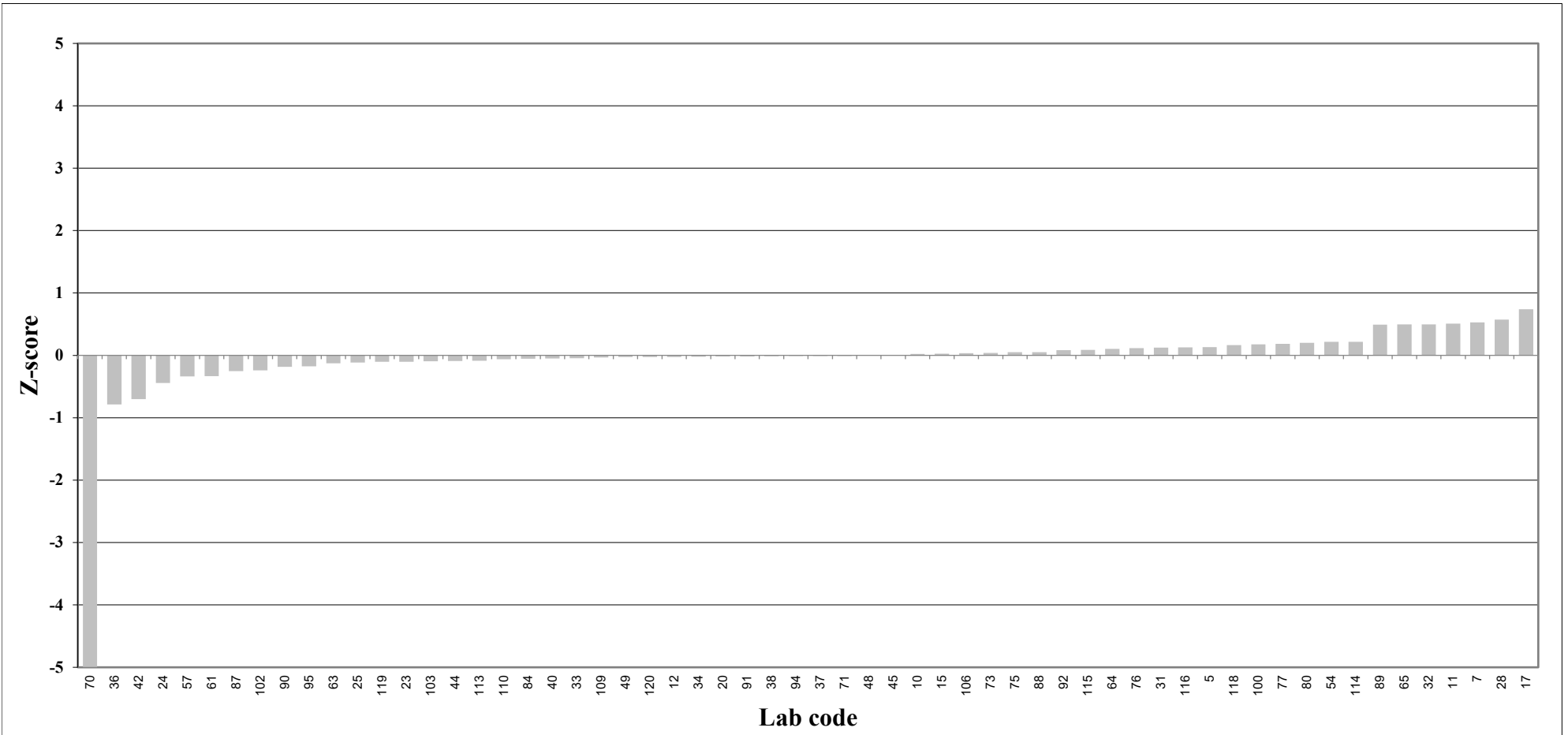
Z-score analyte solution; PCDD/PCDF TEQ

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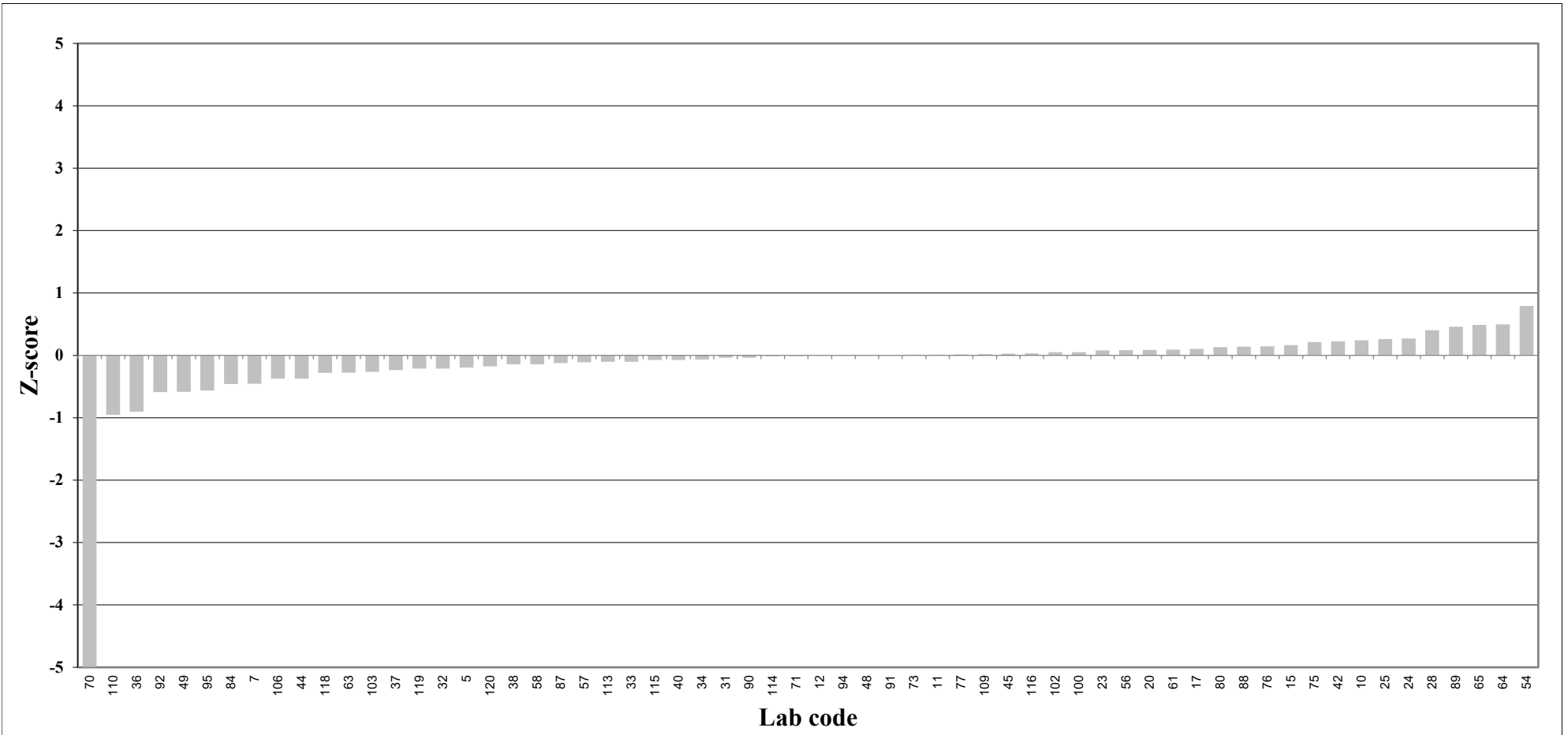
Z-score analyte solution; mono-ortho PCB TEQ

Bar chart titled "Z-score analyte solution; mono-ortho PCB TEQ" with Z-score on the y-axis (ranging from -5 to 5) and Lab code on the x-axis. Lab codes from left to right: 70, 36, 42, 24, 57, 61, 87, 102, 90, 95, 63, 25, 119, 23, 103, 44, 113, 110, 84, 40, 33, 109, 49, 120, 12, 34, 20, 91, 38, 94, 37, 71, 48, 45, 10, 15, 106, 73, 75, 88, 92, 115, 64, 76, 31, 116, 5, 118, 100, 77, 80, 54, 114, 89, 65, 32, 11, 7, 28, 17.

Z-score analyte solution; sum indicator PCB
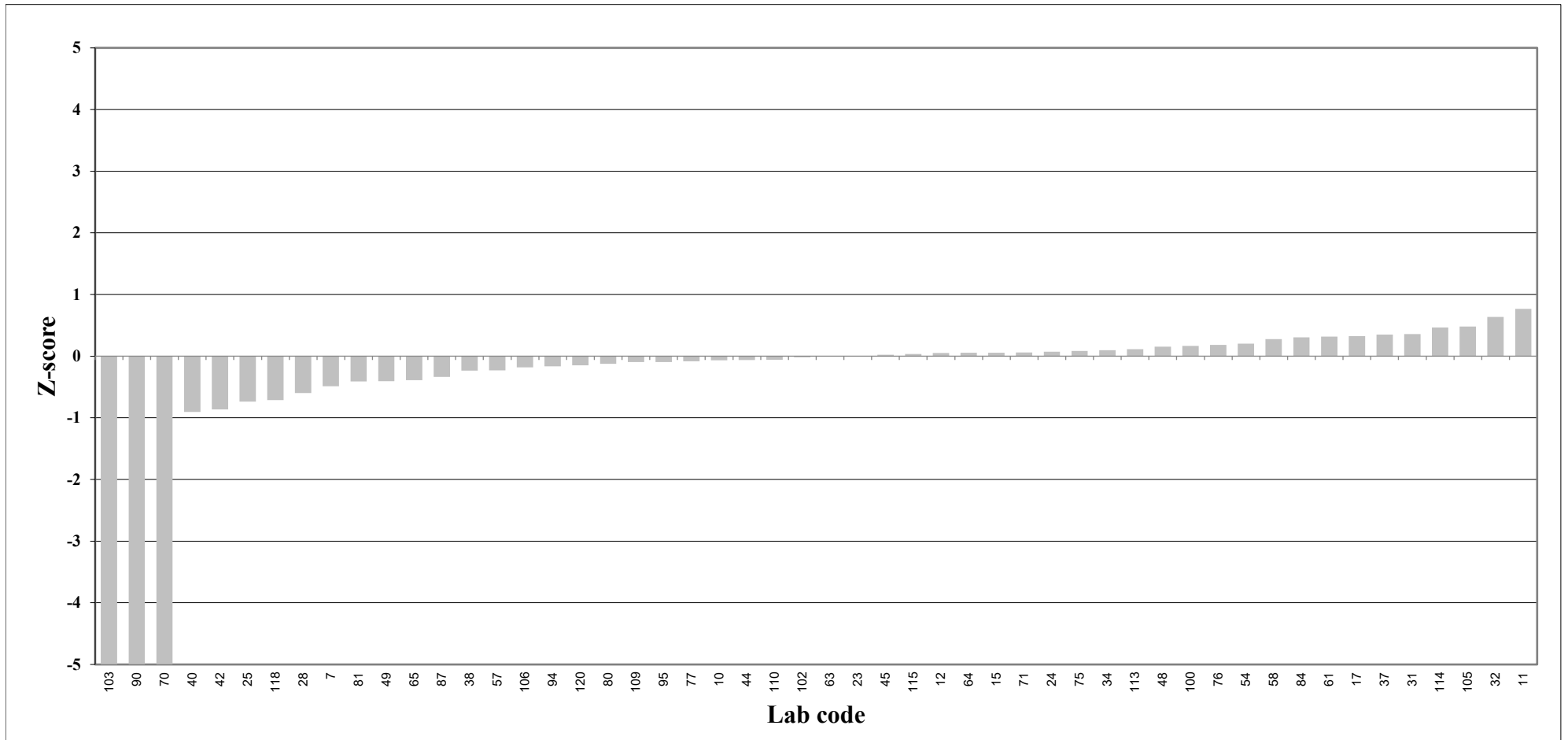
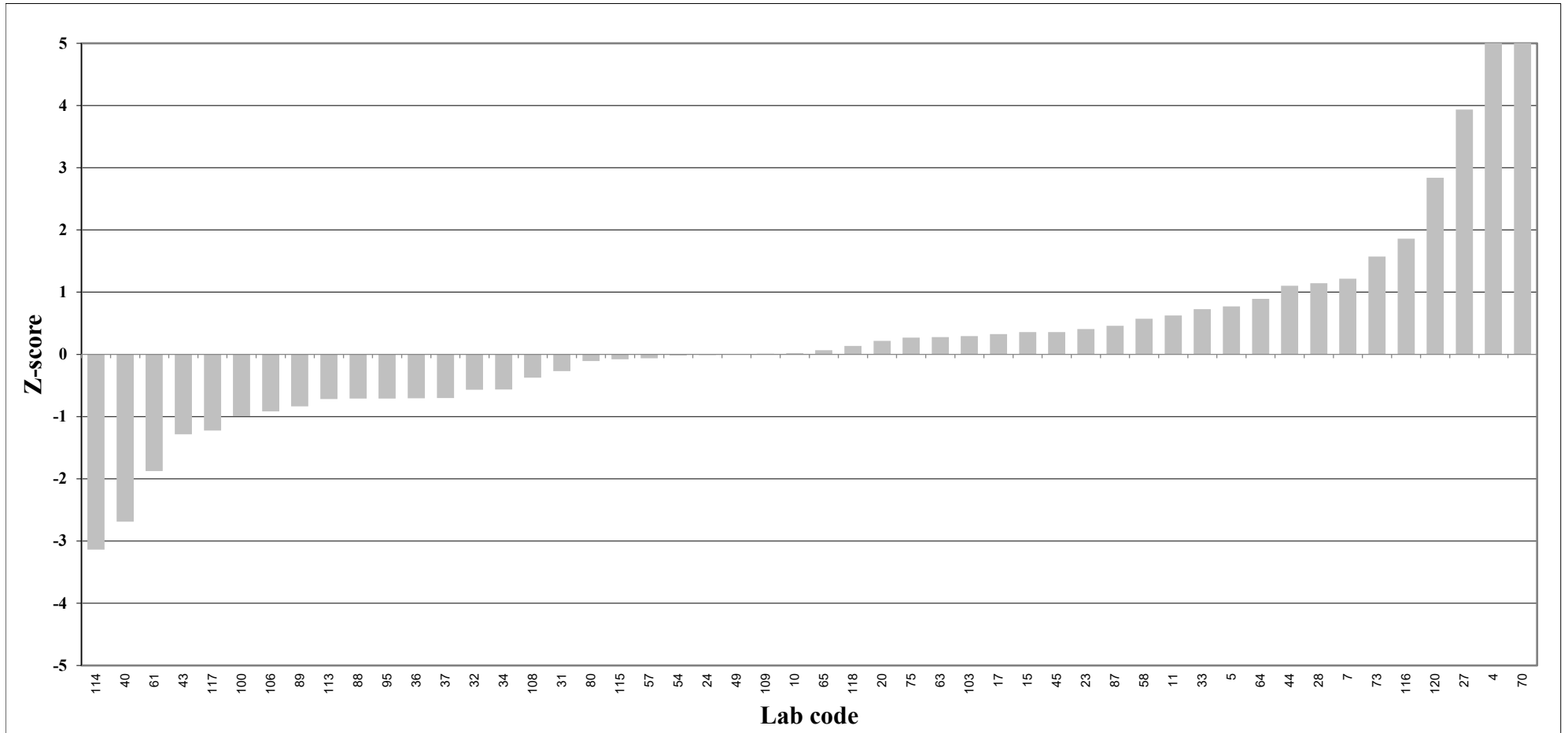**Z-score analyte solution; sum PBDE without PBDE-209**
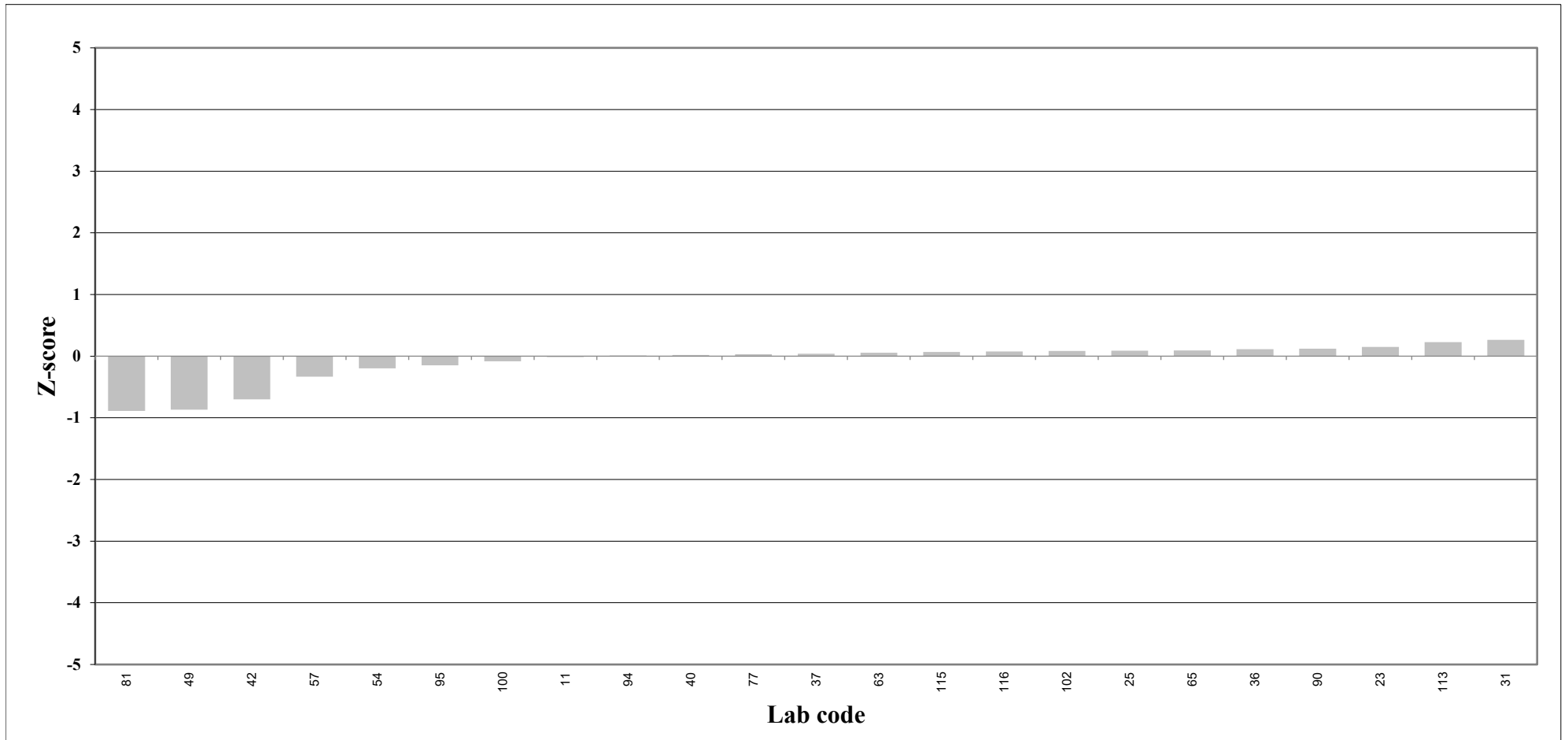
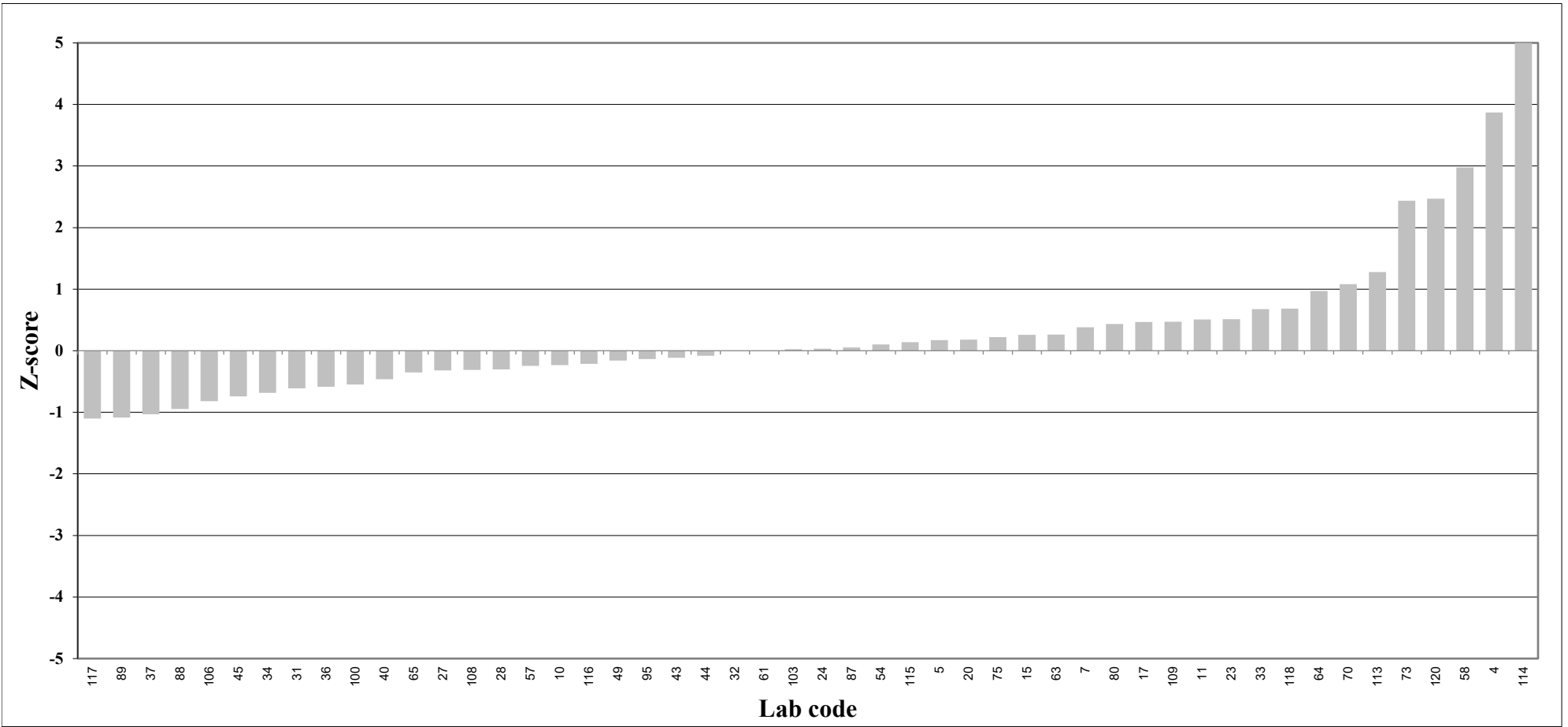**Z-score Veal, fresh weight; total TEQ**
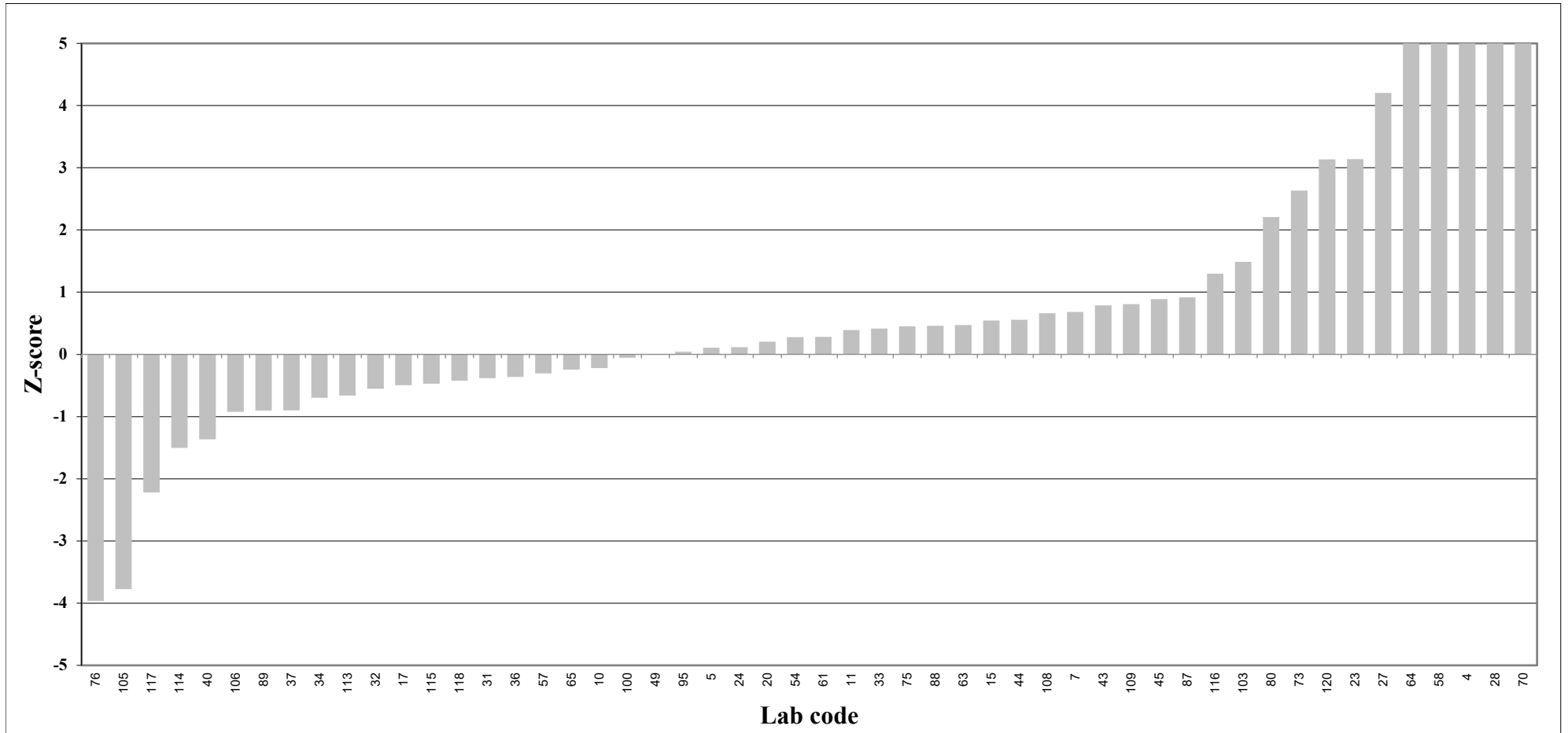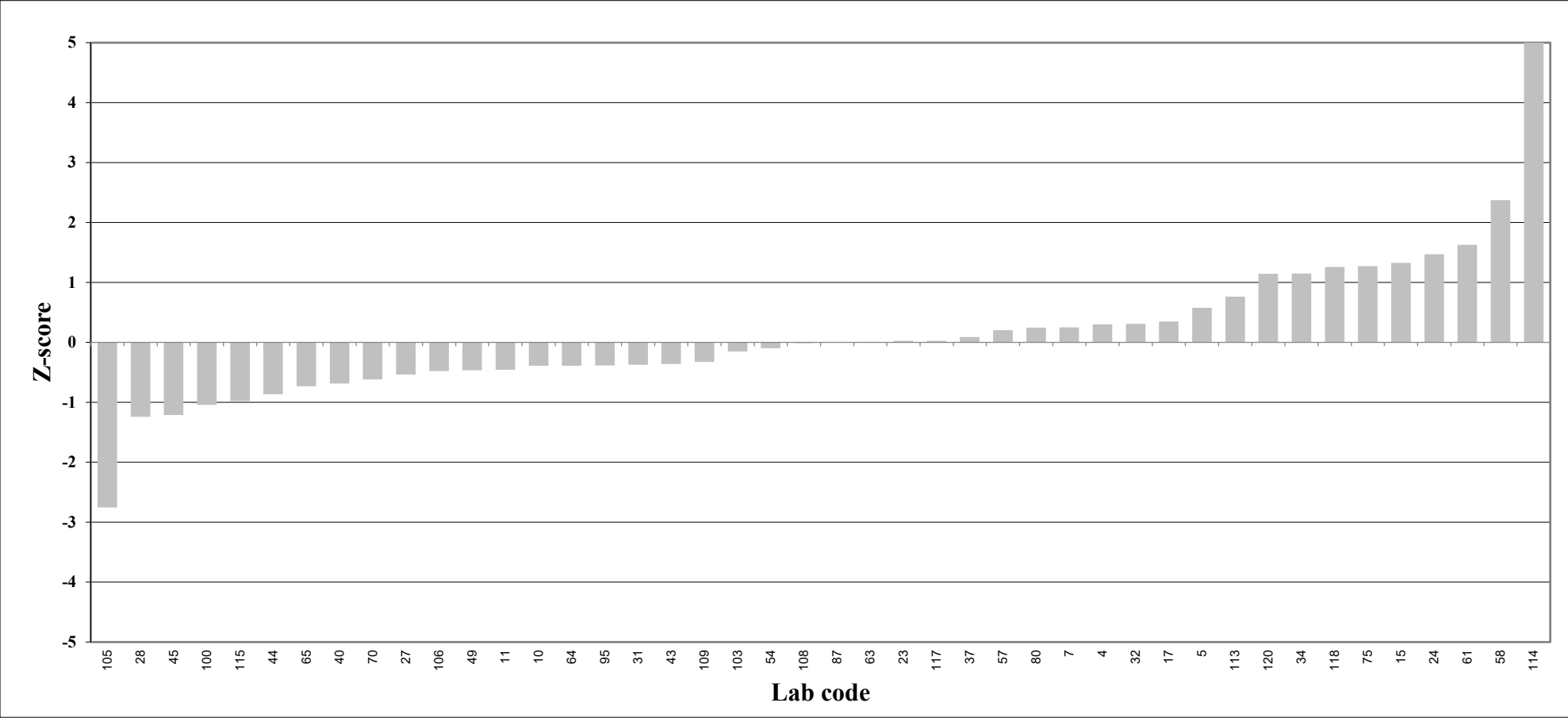
Z-score Veal, fresh weight; PCDD/PCDF TEQ
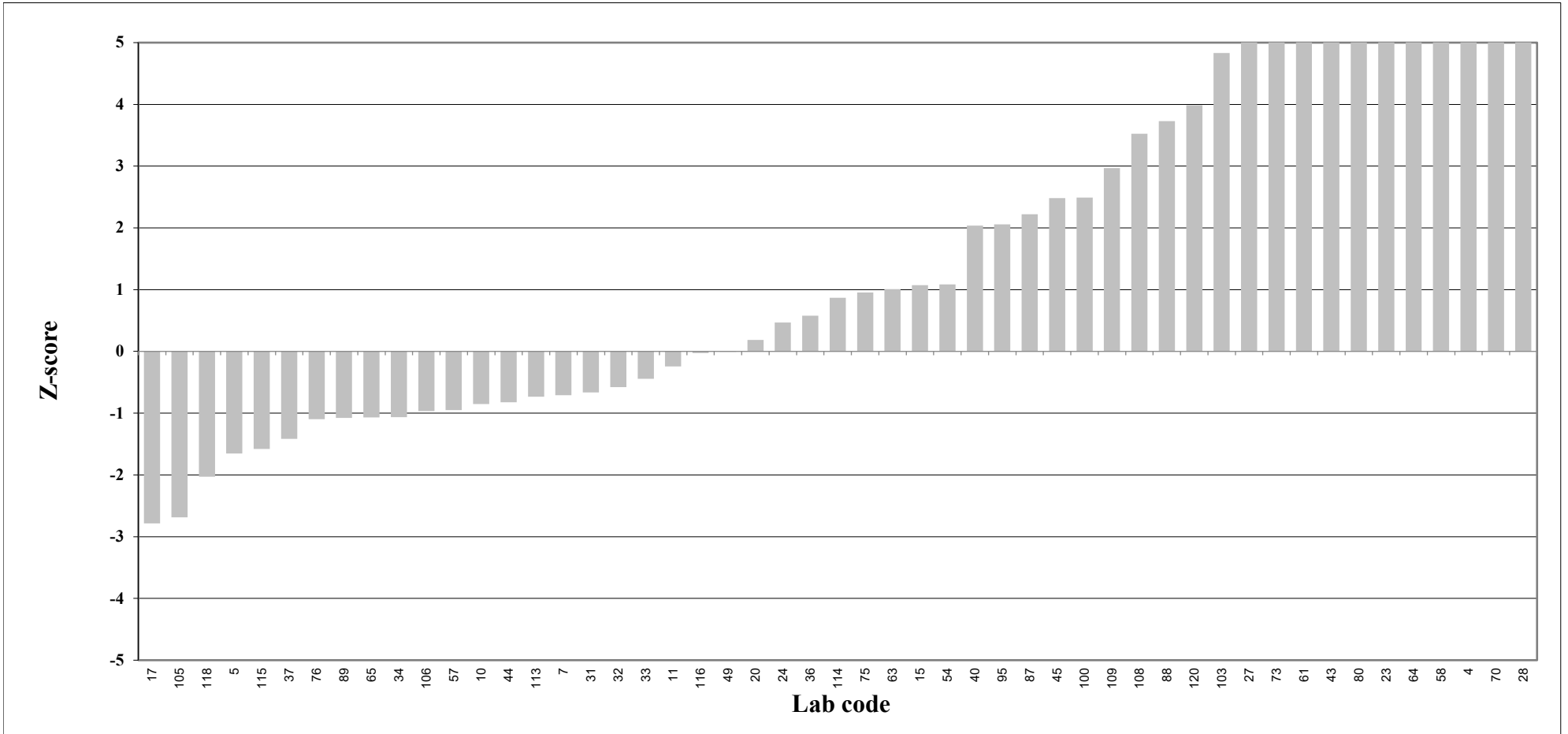
Z-score Veal, fresh weight; non-ortho PCB TEQ

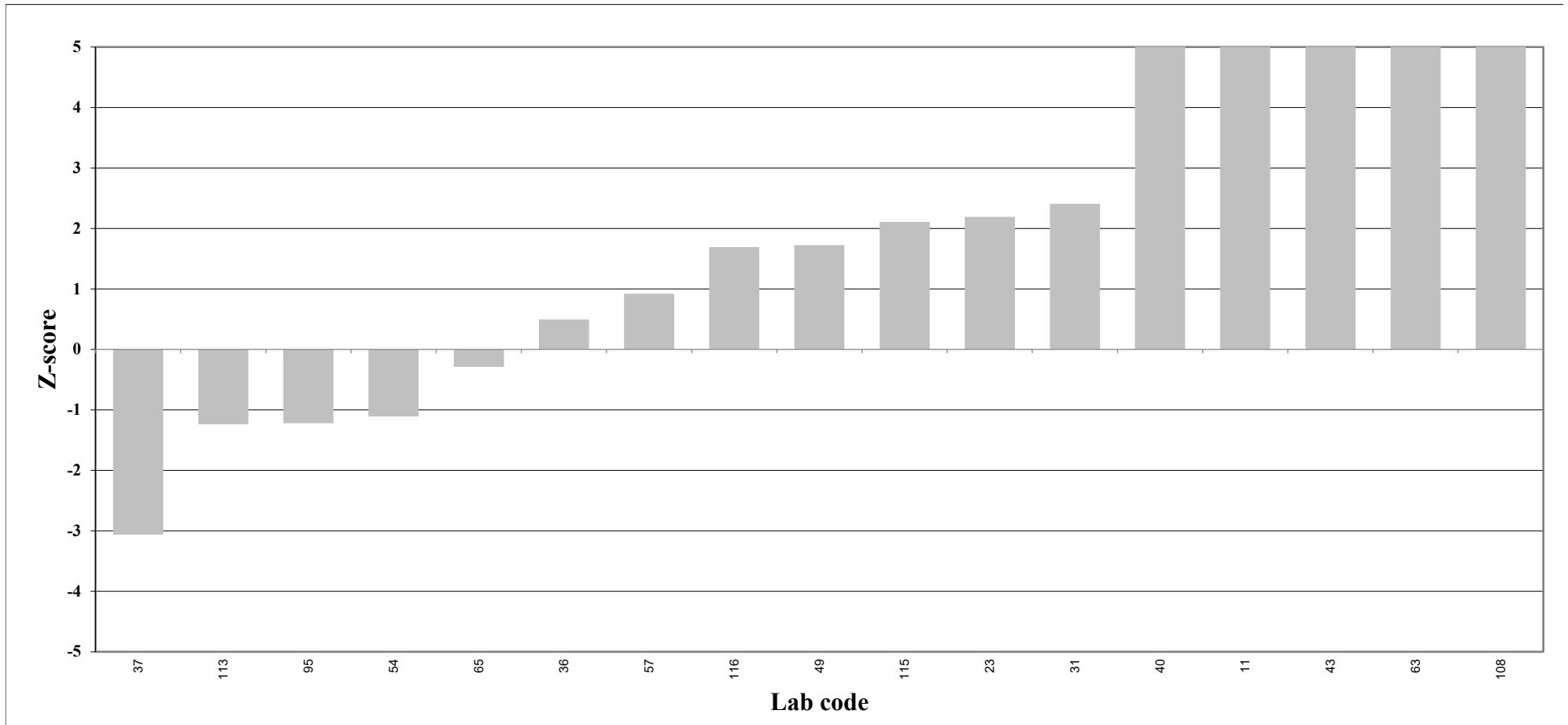# Z-score Veal, fresh weight; mono-ortho PCB TEQ

Z-score Veal, fresh weight; sum indicator PCB

Z-score (y-axis) vs Lab code (x-axis): 105, 28, 45, 100, 115, 44, 65, 40, 70, 27, 106, 49, 11, 10, 64, 95, 31, 43, 109, 103, 54, 108, 87, 63, 23, 117, 37, 57, 80, 7, 4, 32, 17, 5, 113, 120, 34, 118, 75, 15, 24, 61, 58, 114

Z-score Veal, fresh weight; sum PBDE without PBDE-209

Z-score Veal, lipid weight; total TEQ

Chart showing Z-score values by Lab code. Y-axis labeled "Z-score" ranging from -5 to 5. X-axis labeled "Lab code" with values: 76, 105, 117, 40, 11, 113, 10, 17, 89, 95, 37, 61, 118, 32, 57, 100, 36, 44, 31, 106, 20, 115, 5, 7, 65, 63, 33, 54, 34, 49, 45, 75, 43, 15, 108, 87, 116, 109, 88, 24, 103, 80, 23, 120, 73, 114, 27, 64, 58, 4, 28, 70.
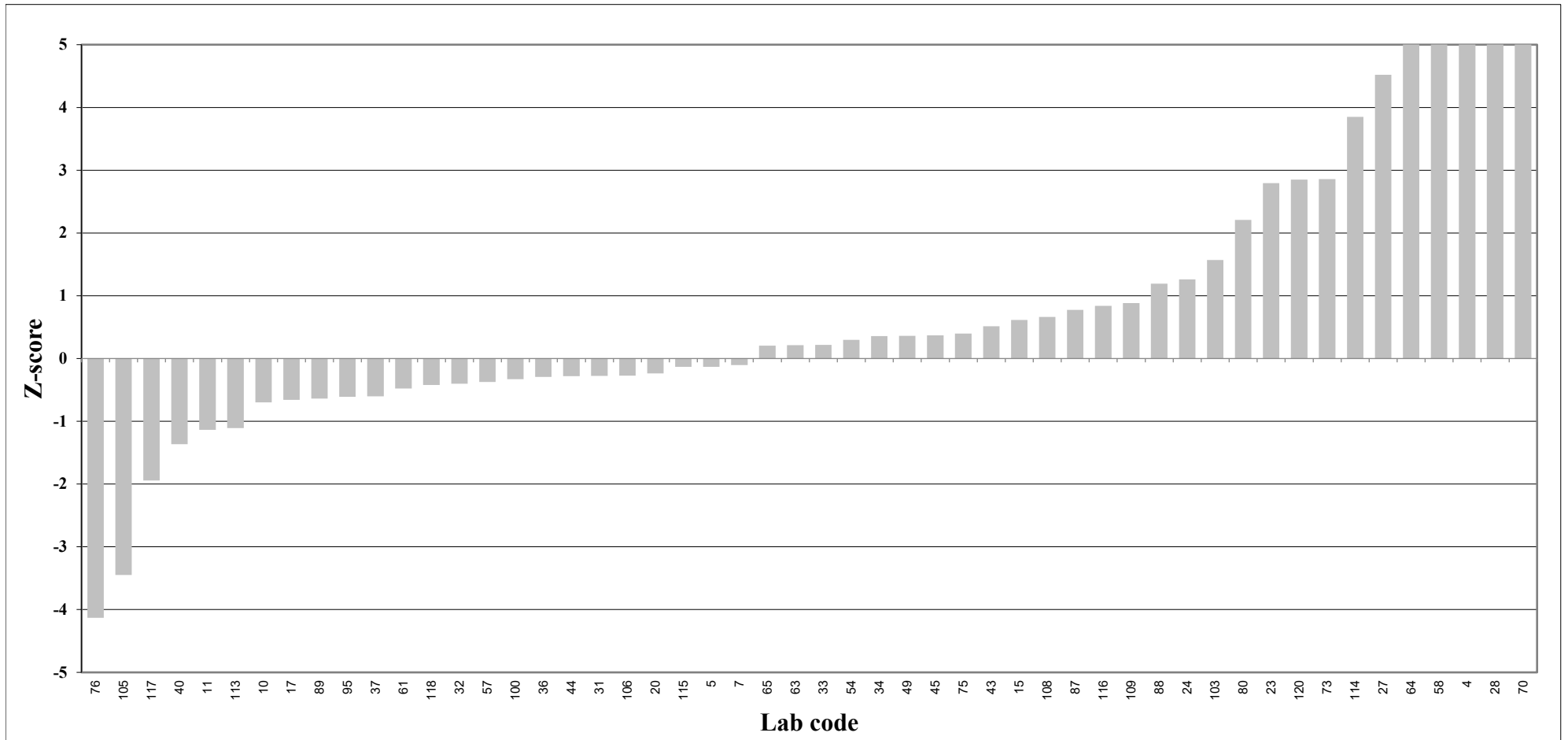
Z-score Veal, lipid weight; PCDD/PCDF TEQ
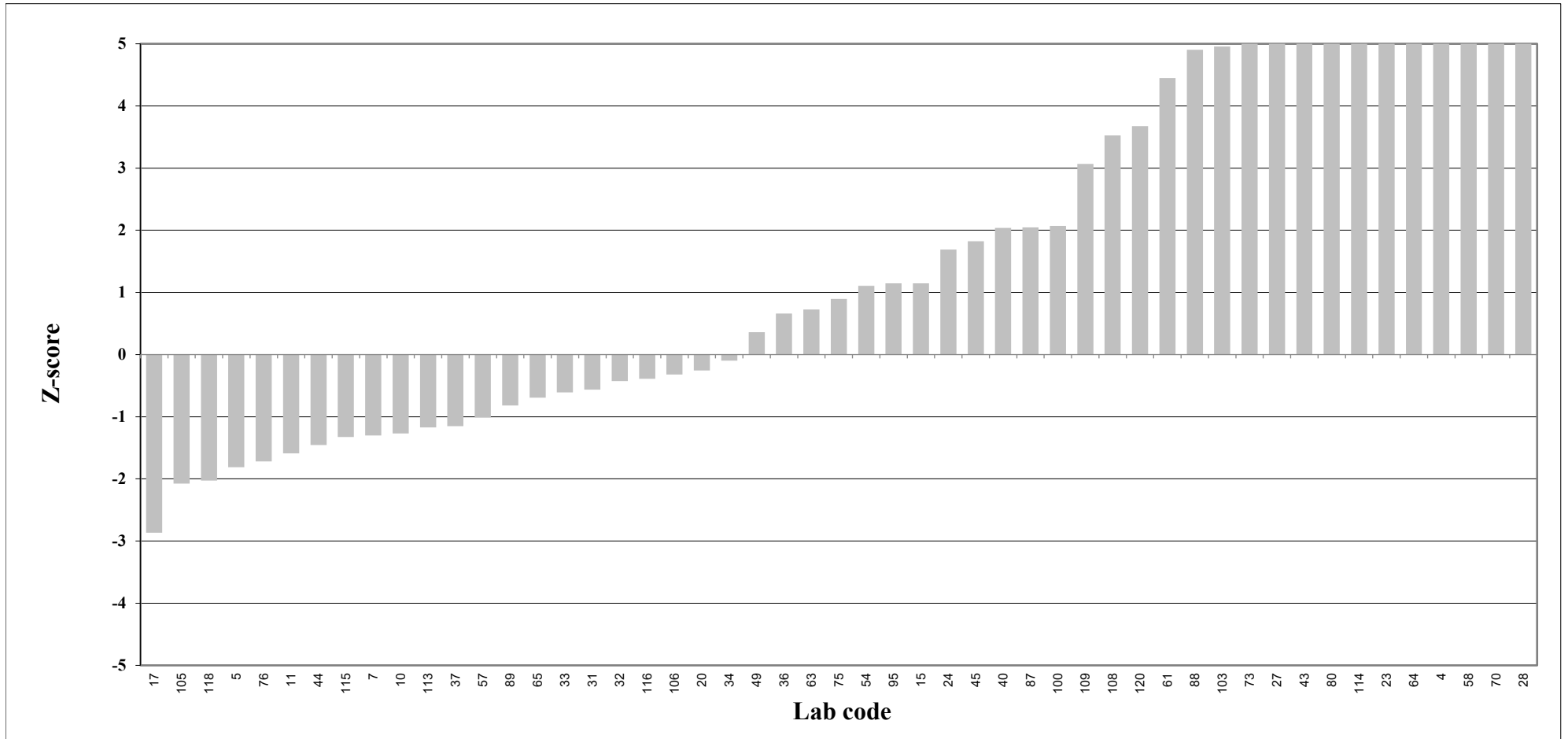
Z-score Veal, lipid weight; non-ortho PCB TEQ

Z-score Veal, lipid weight; mono-ortho PCB TEQ

Z-score Veal, lipid weight; sum indicator PCB

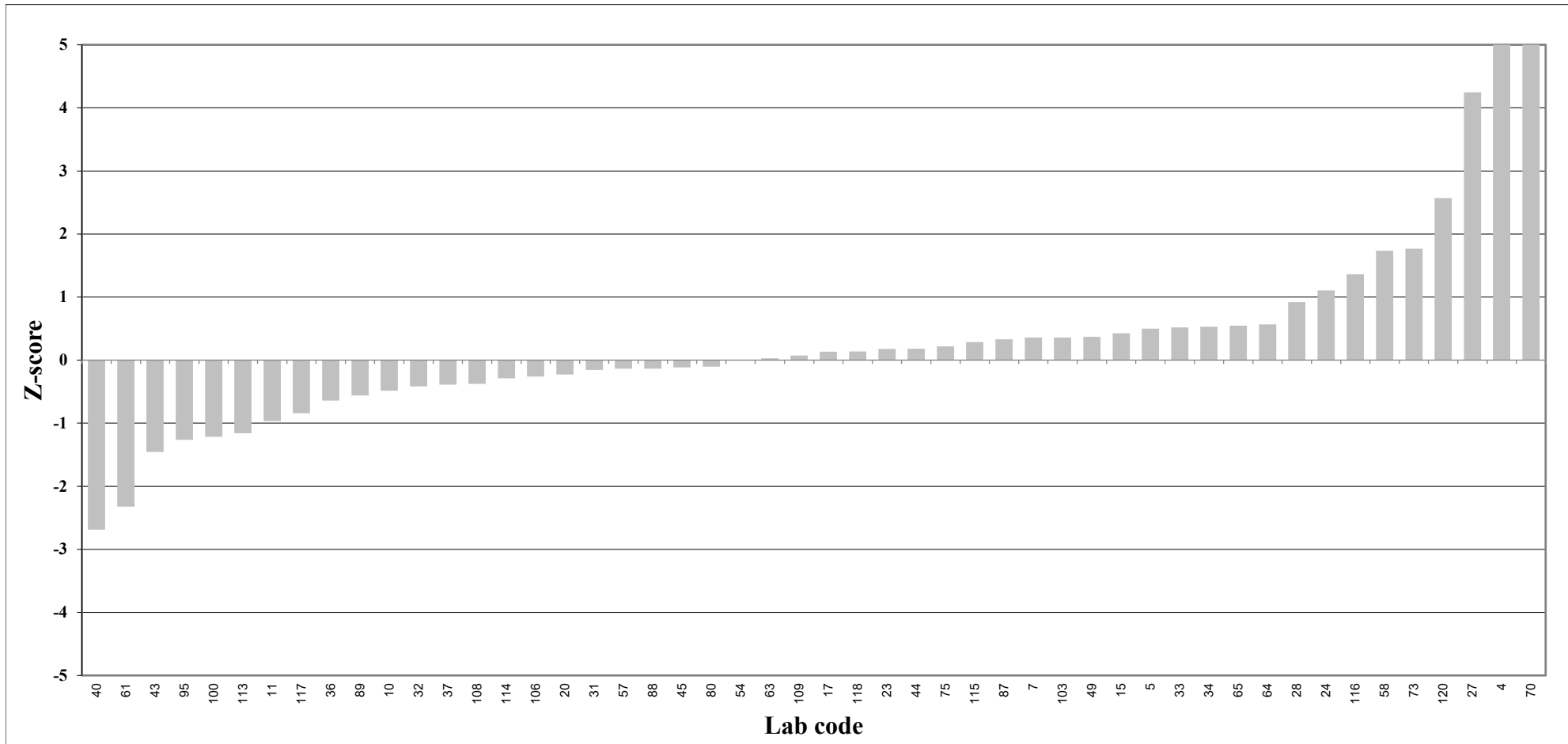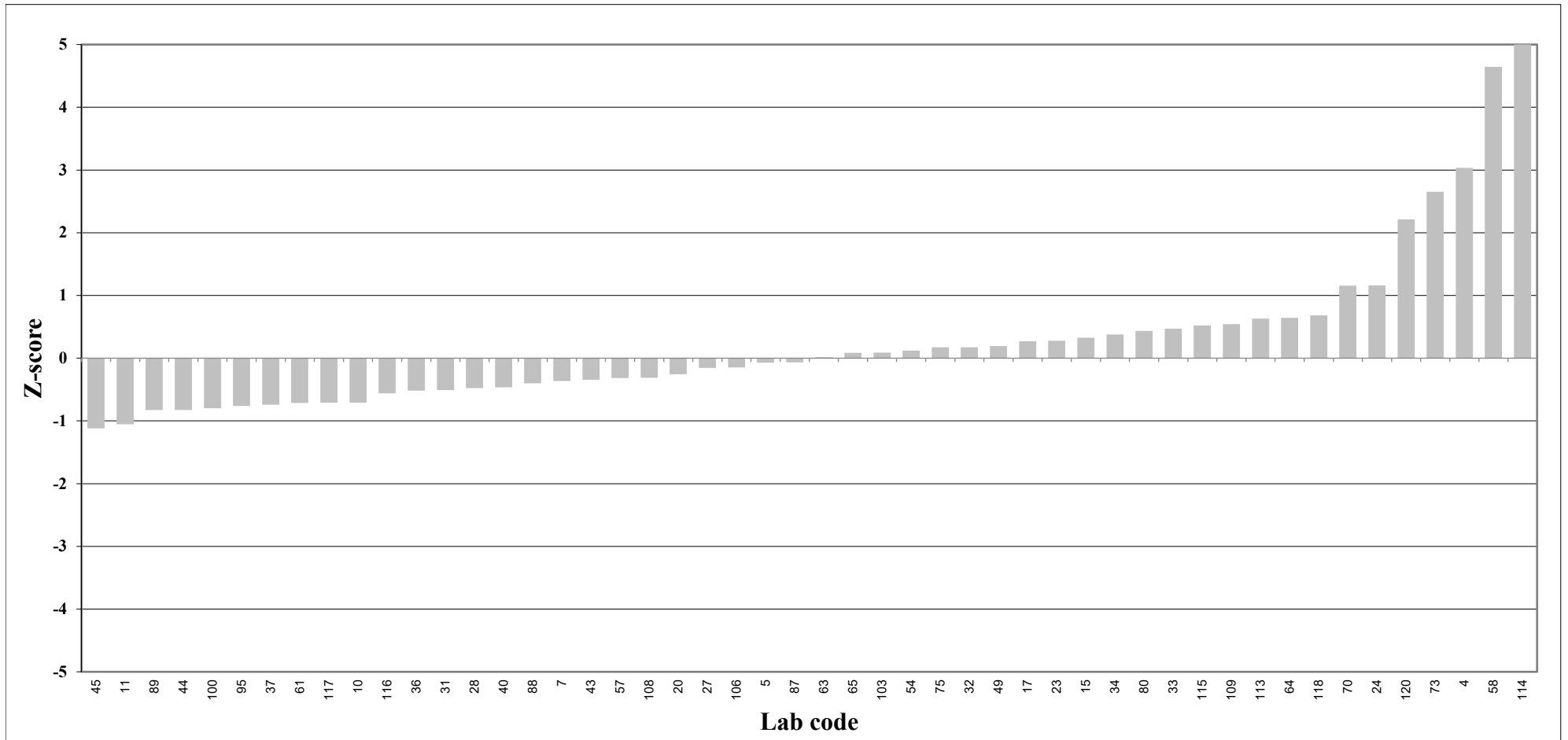# Z-score Veal, lipid weight; sum PBDE without PBDE-209

Z-score bar chart. X-axis: Lab code. Y-axis: Z-score.

Lab code	Z-score (approx.)
37	-3.0
113	-1.2
95	-1.2
54	-1.1
65	-0.3
36	0.5
57	0.9
116	1.7
49	1.7
115	2.1
23	2.2
31	2.4
40	5.0
11	5.0
43	5.0
63	5.0
108	5.0

Z-score Herring, fresh weight; total TEQ

Z-score (y-axis, range −5 to 5)

Lab code (x-axis): 114, 100, 119, 78, 61, 106, 117, 19, 37, 43, 108, 109, 105, 49, 31, 80, 95, 34, 36, 110, 102, 32, 48, 27, 84, 90, 88, 11, 45, 64, 115, 15, 103, 54, 75, 116, 63, 120, 89, 20, 23, 28, 71, 17, 65, 58, 30, 24, 113, 12, 118, 42, 73, 44, 25, 7, 92, 33, 57, 38, 5, 40, 4, 87

Z-score Herring, fresh weight; PCDD/PCDF TEQ

Z-score Herring, fresh weight; non-ortho PCB TEQ

Z-score Herring, fresh weight; mono-ortho PCB TEQ
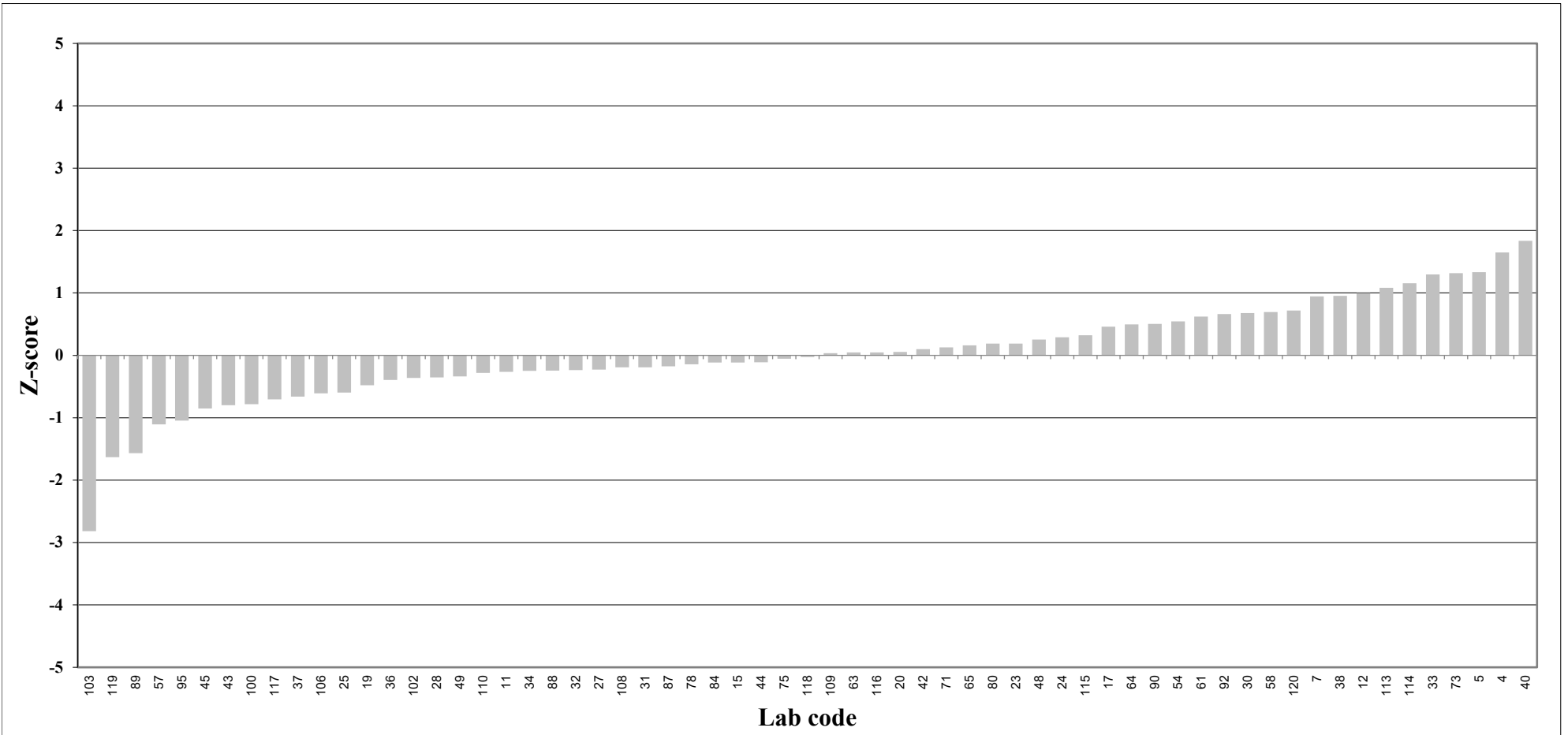
Z-score Herring, fresh weight; sum indicator PCB
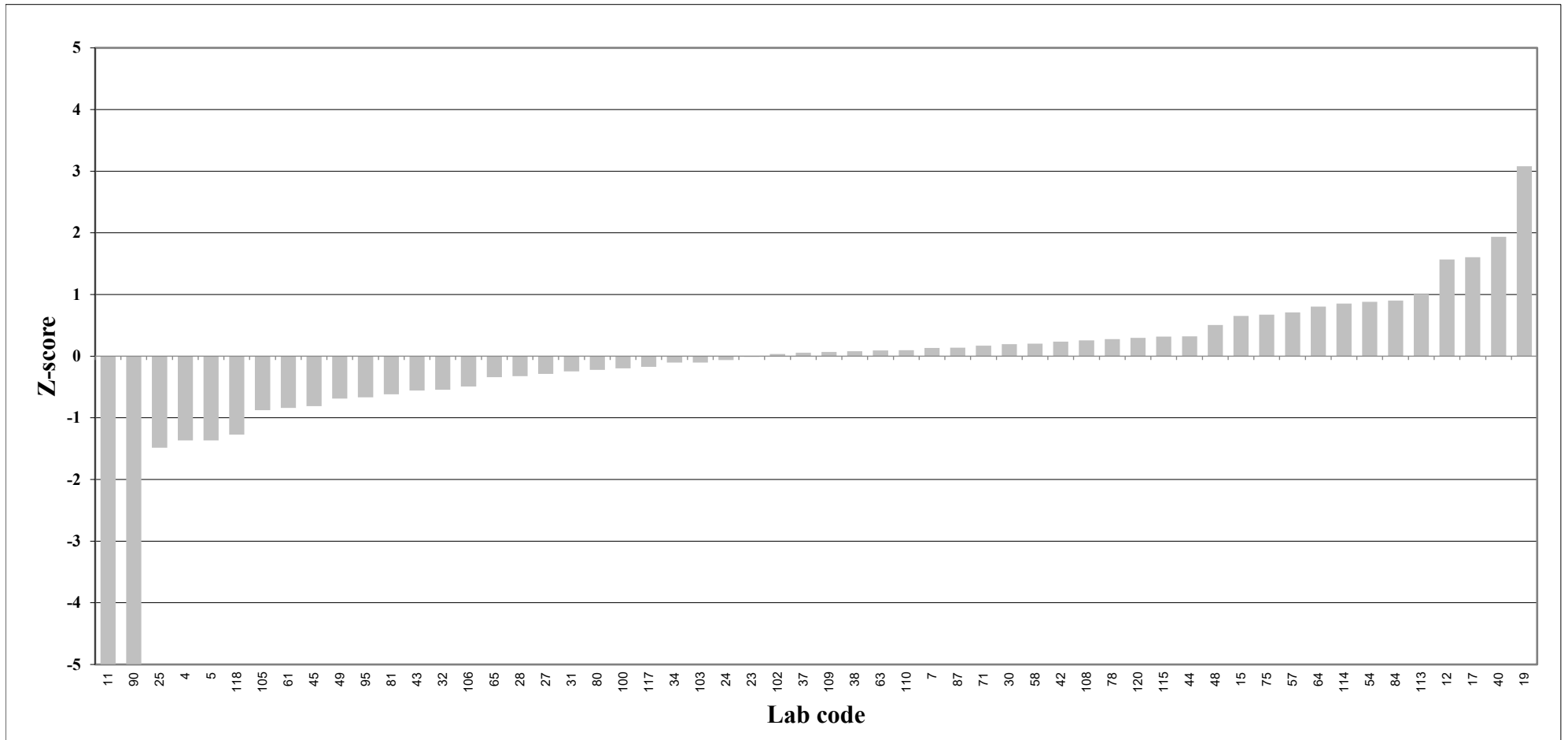
Z-score Herring, fresh weight; sum PBDE without BDE-209
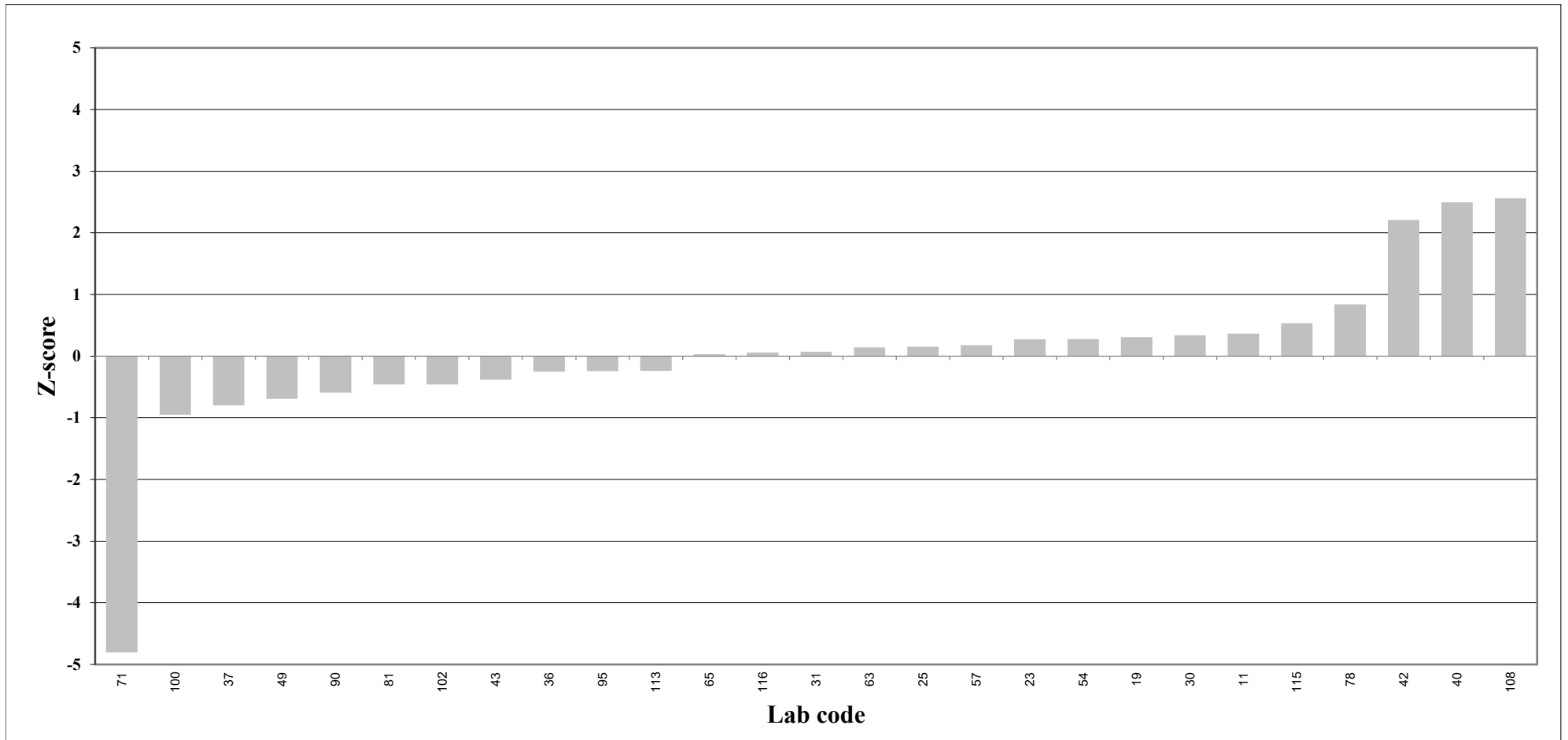
Z-score Herring, lipid weight; total TEQ
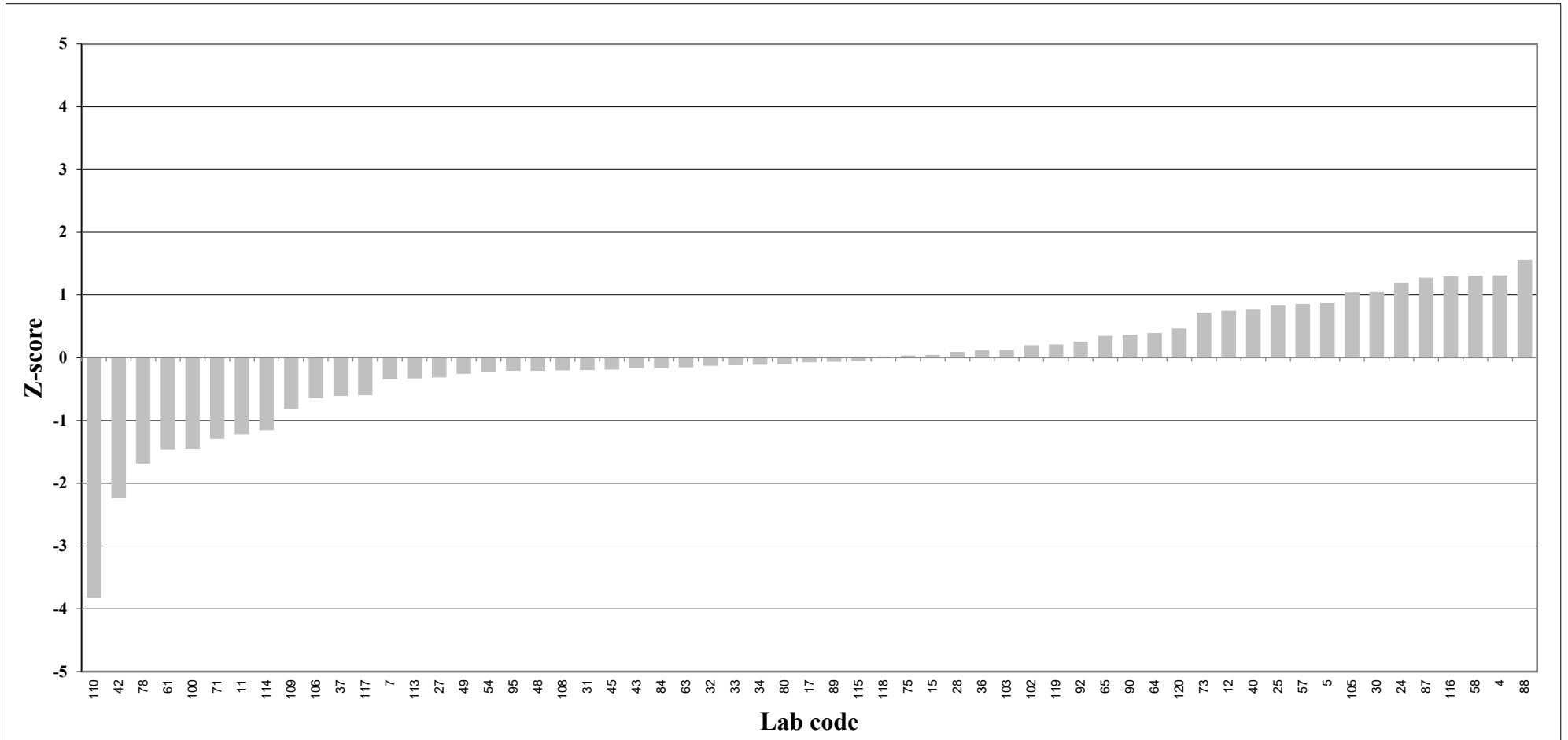
Z-score Herring, lipid weight; PCDD/PCDF TEQ
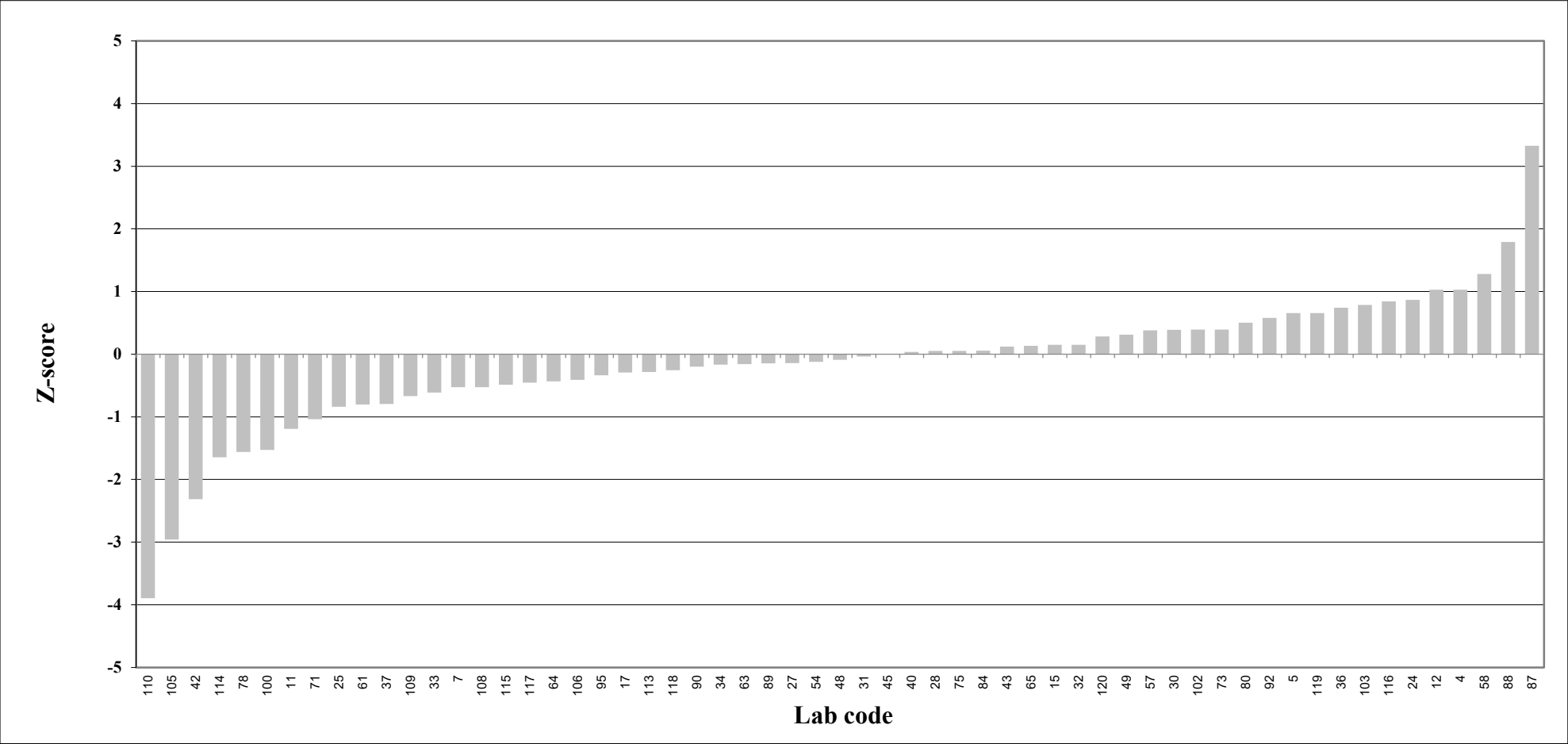
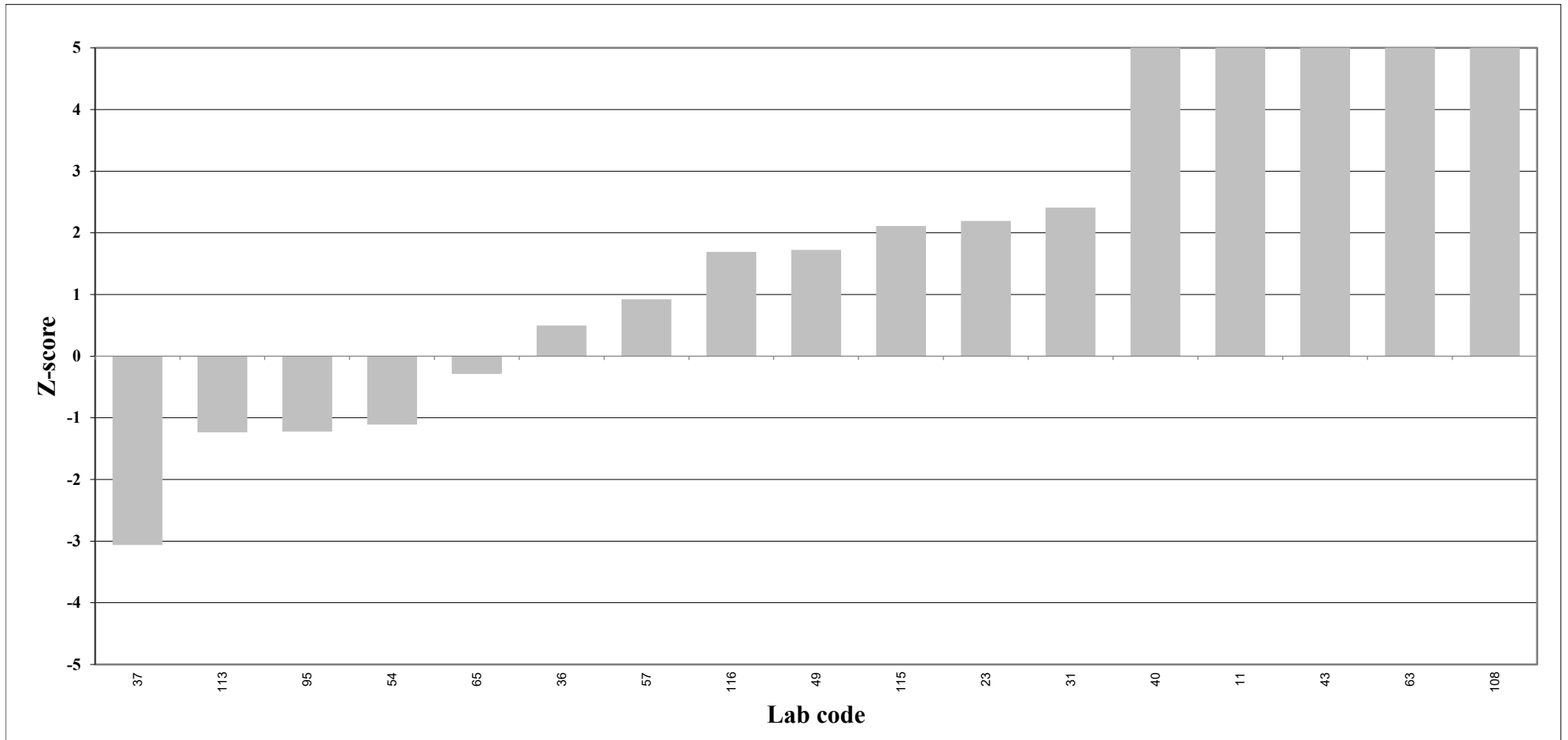**Z-score Herring, lipid weight; non-ortho PCB TEQ**
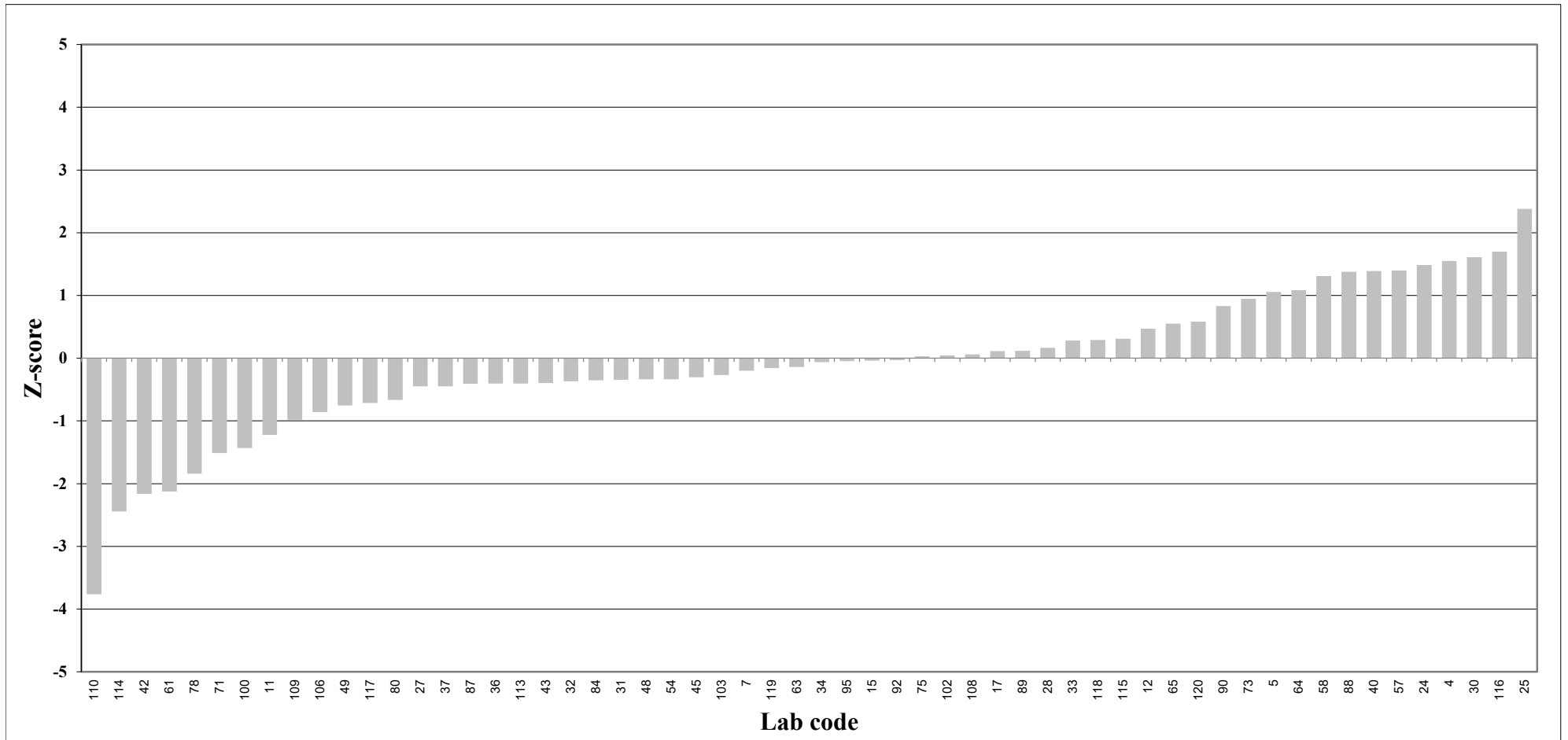
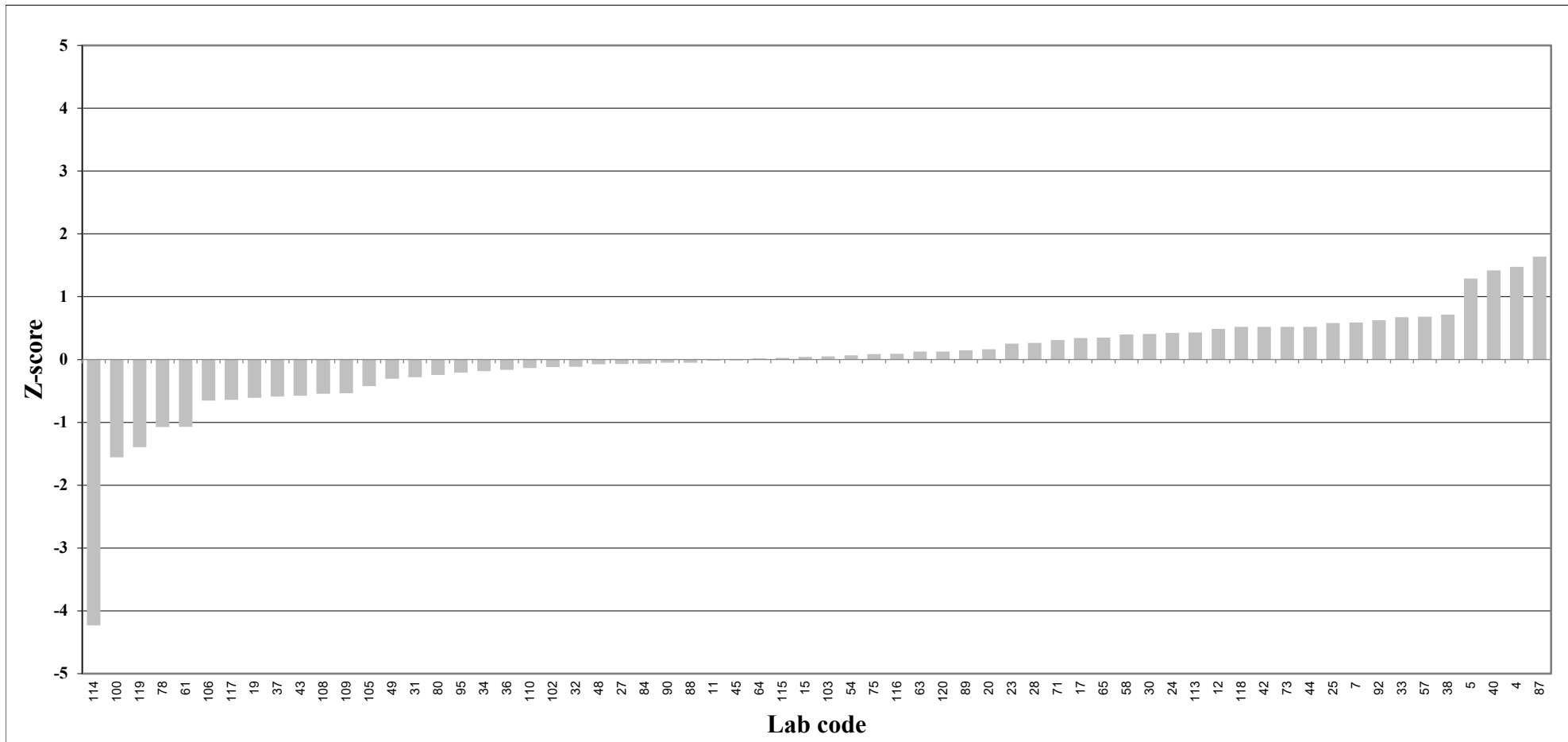# Z-score Herring, lipid weight; mono-ortho PCB TEQ

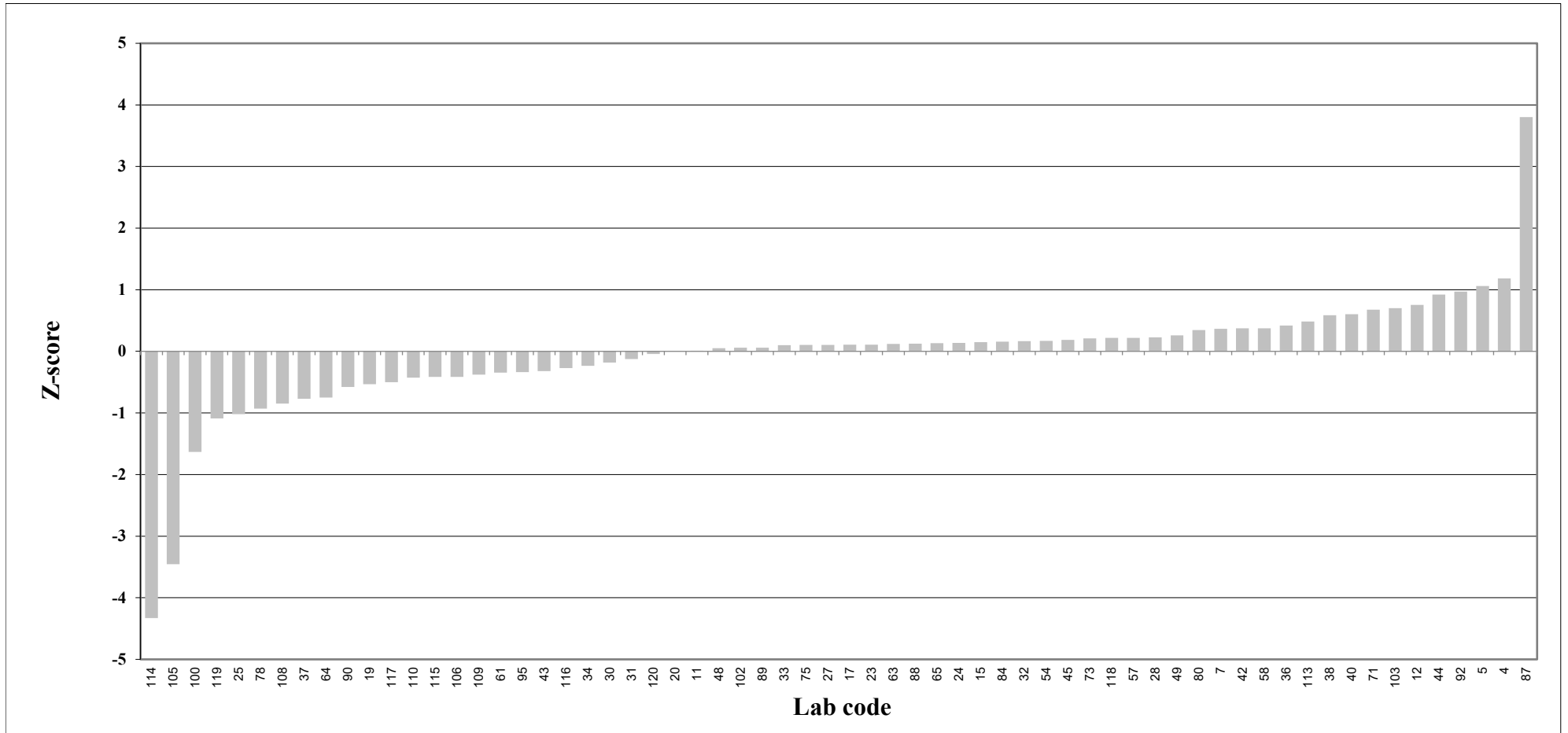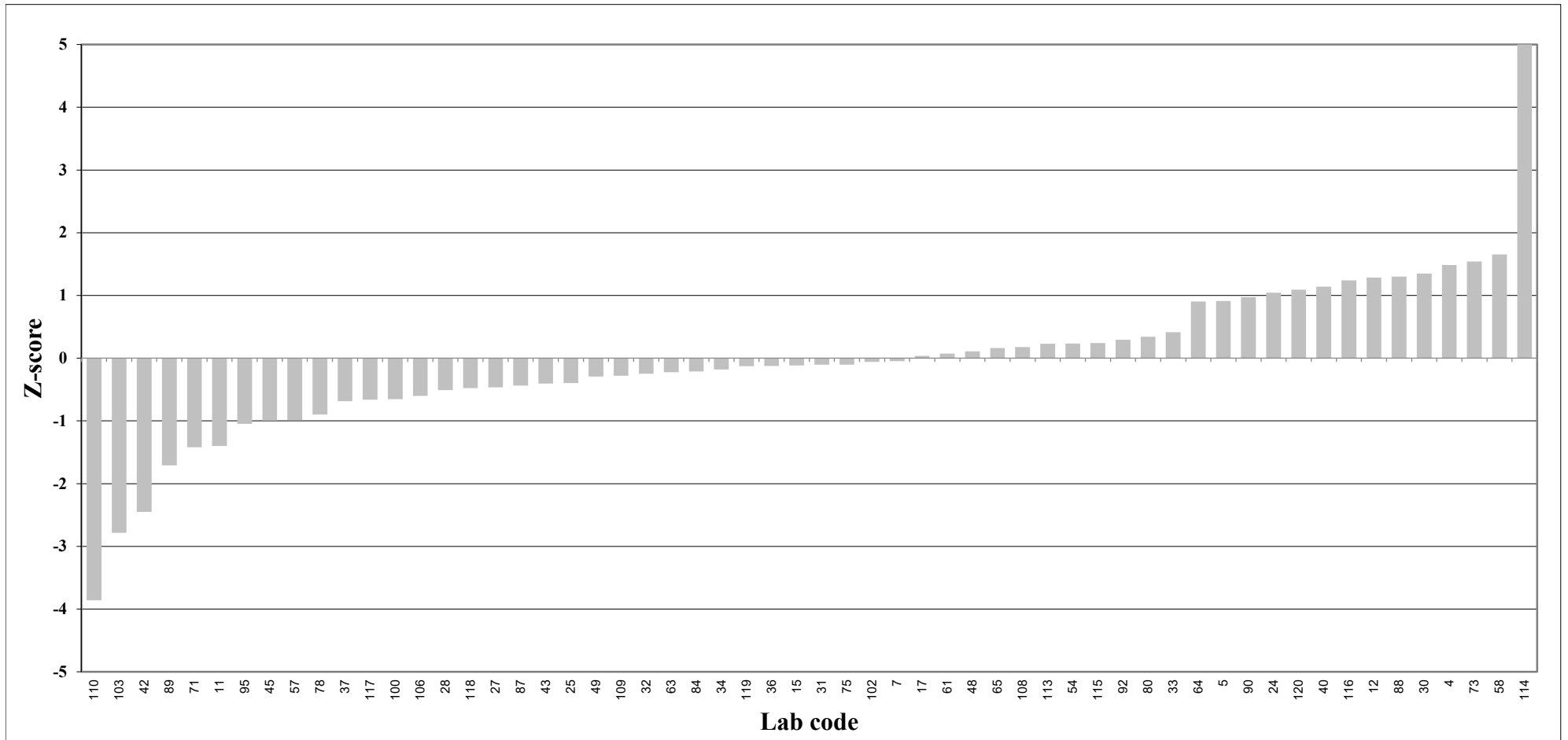Z-score Herring, lipid weight; sum indicator PCB
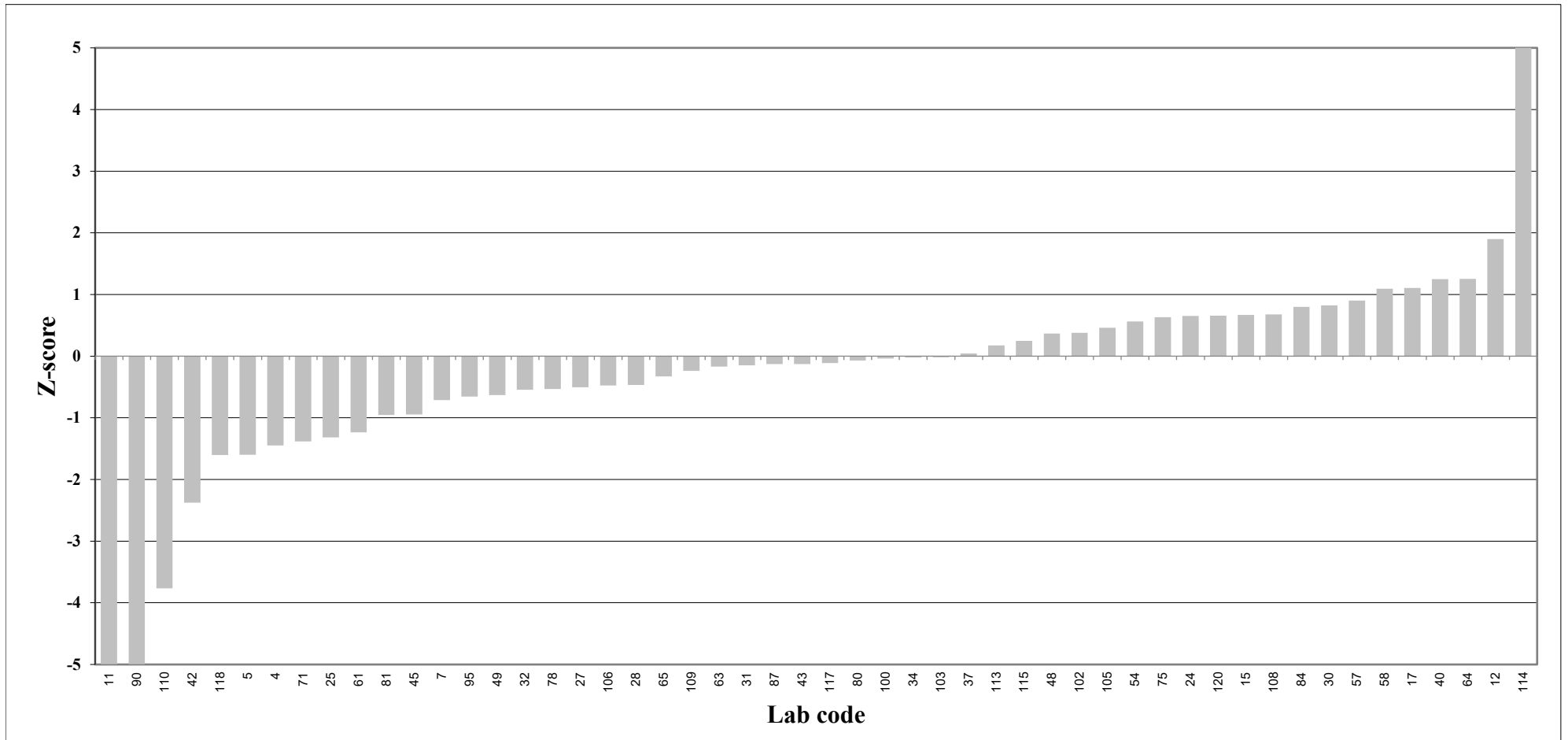
Z-score Herring, lipid weight; sum PBDE without BDE-209
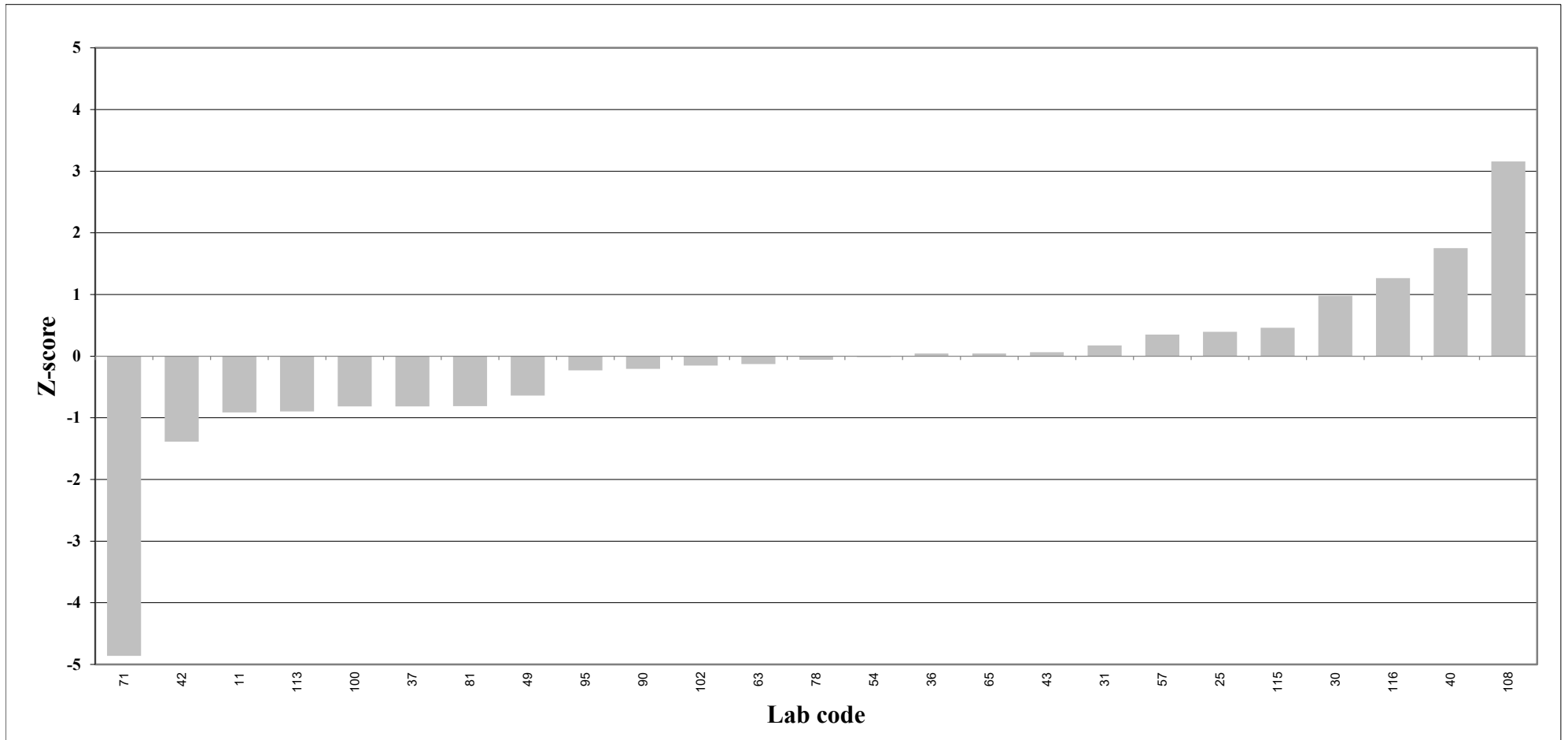
Z-score Brown meat, fresh weight; total TEQ

Lab code

Z-score Brown meat, fresh weight; PCDD/PCDF TEQ

Lab code

Z-score Brown meat, fresh weight; non-ortho PCB TEQ
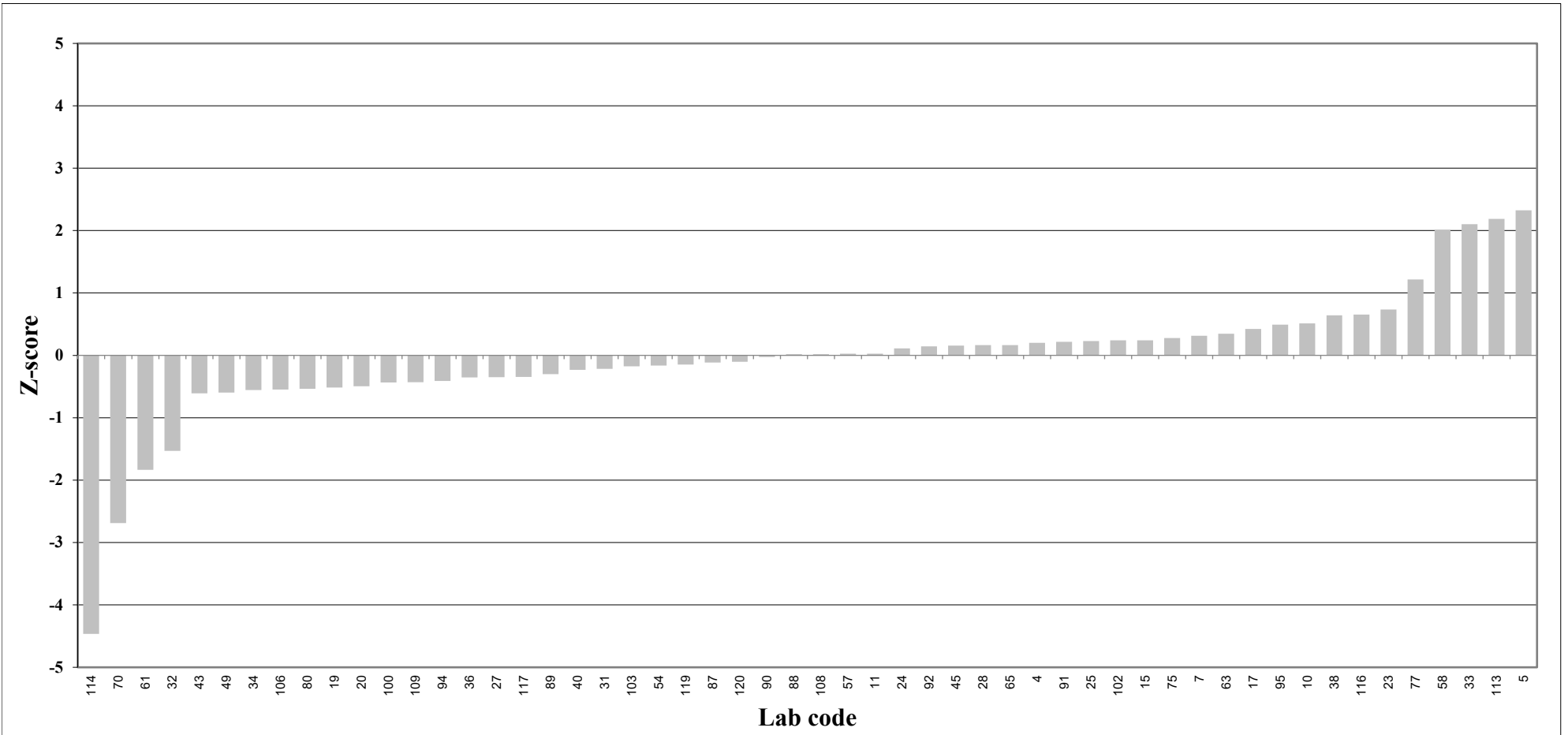
Z-score Brown meat; mono-ortho PCB TEQ
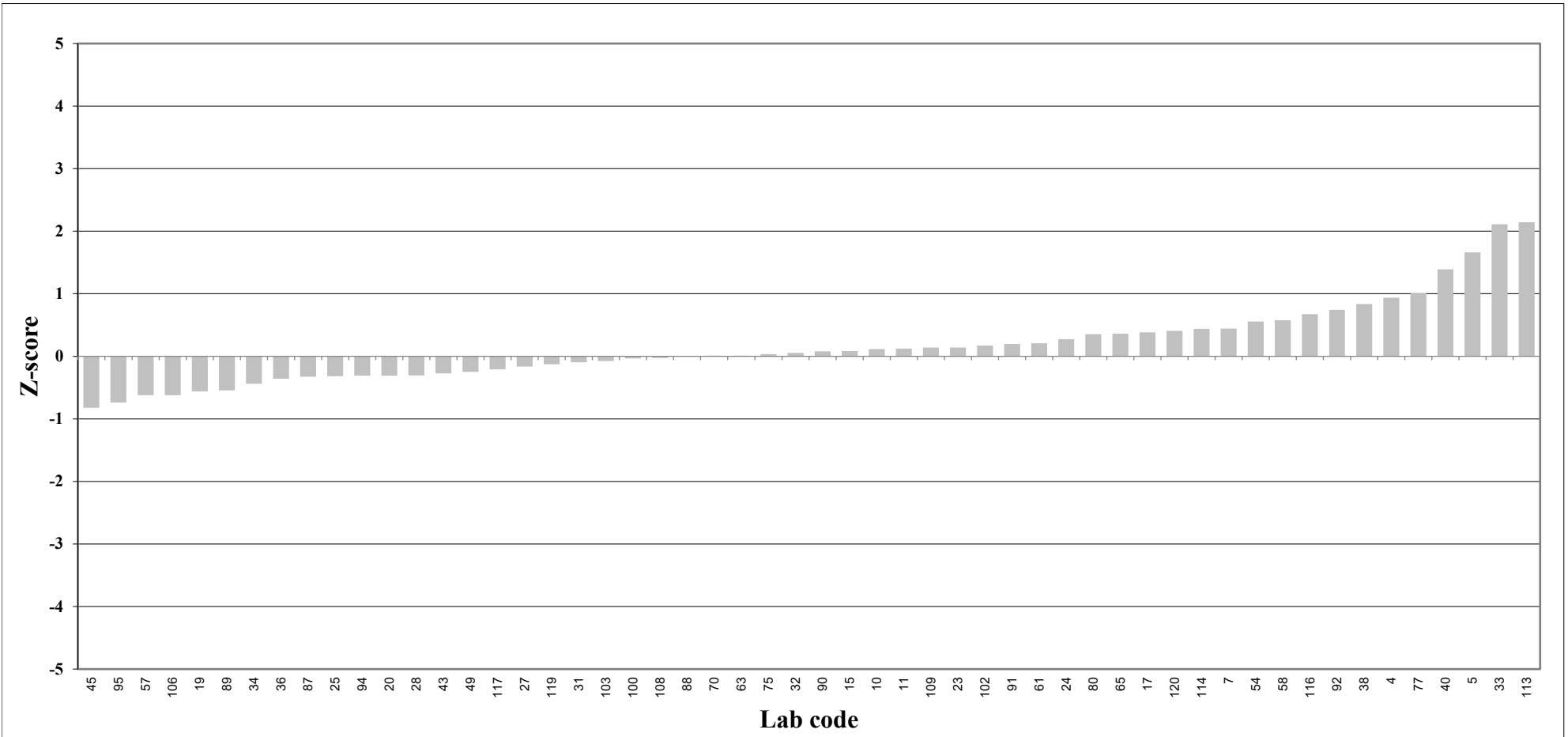
Z-score Brown meat, fresh weight; sum indicator PCB
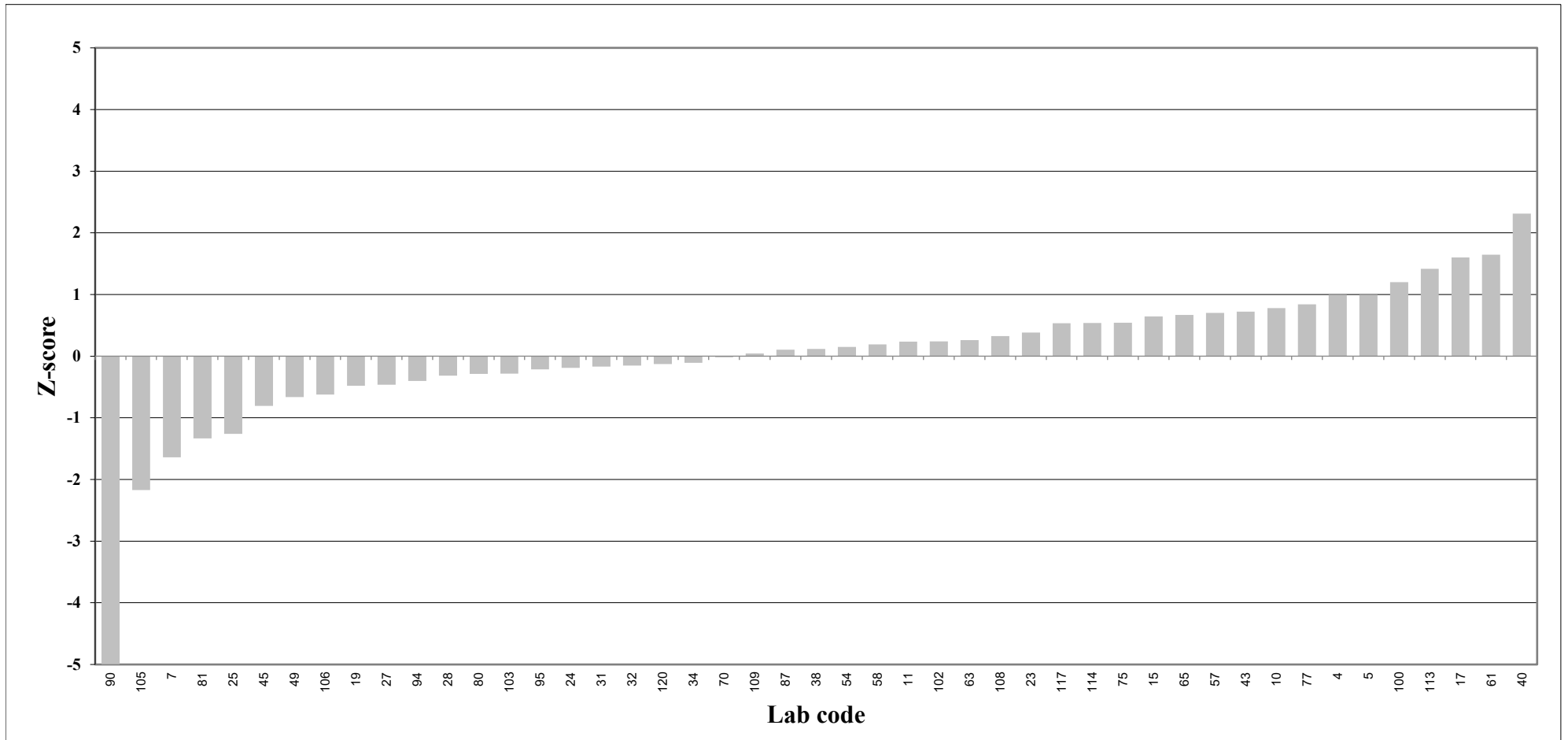
Z-score Brown meat, fresh weight; sum PBDE without PBDE-209
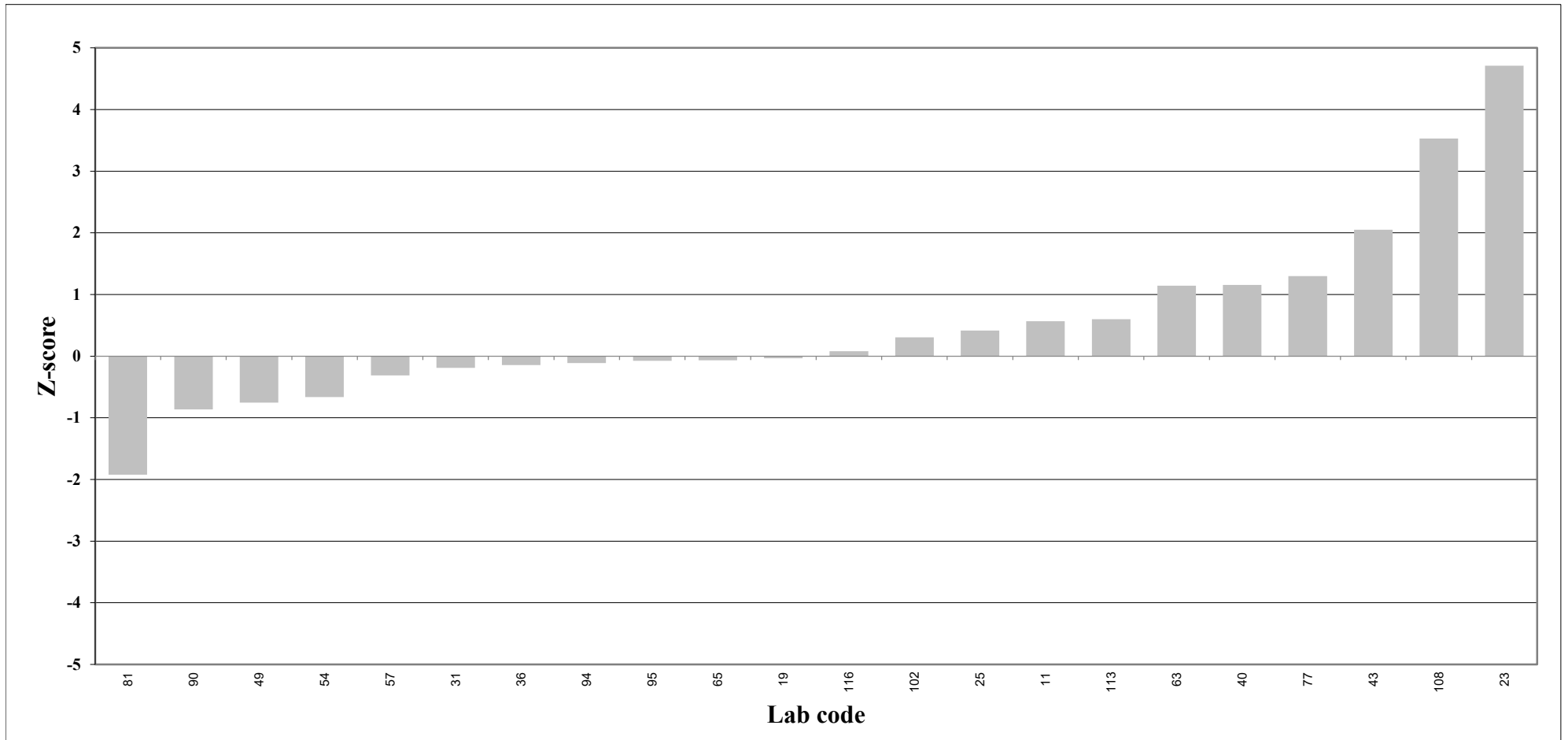
Z-score Brown meat, lipid weight; total TEQ
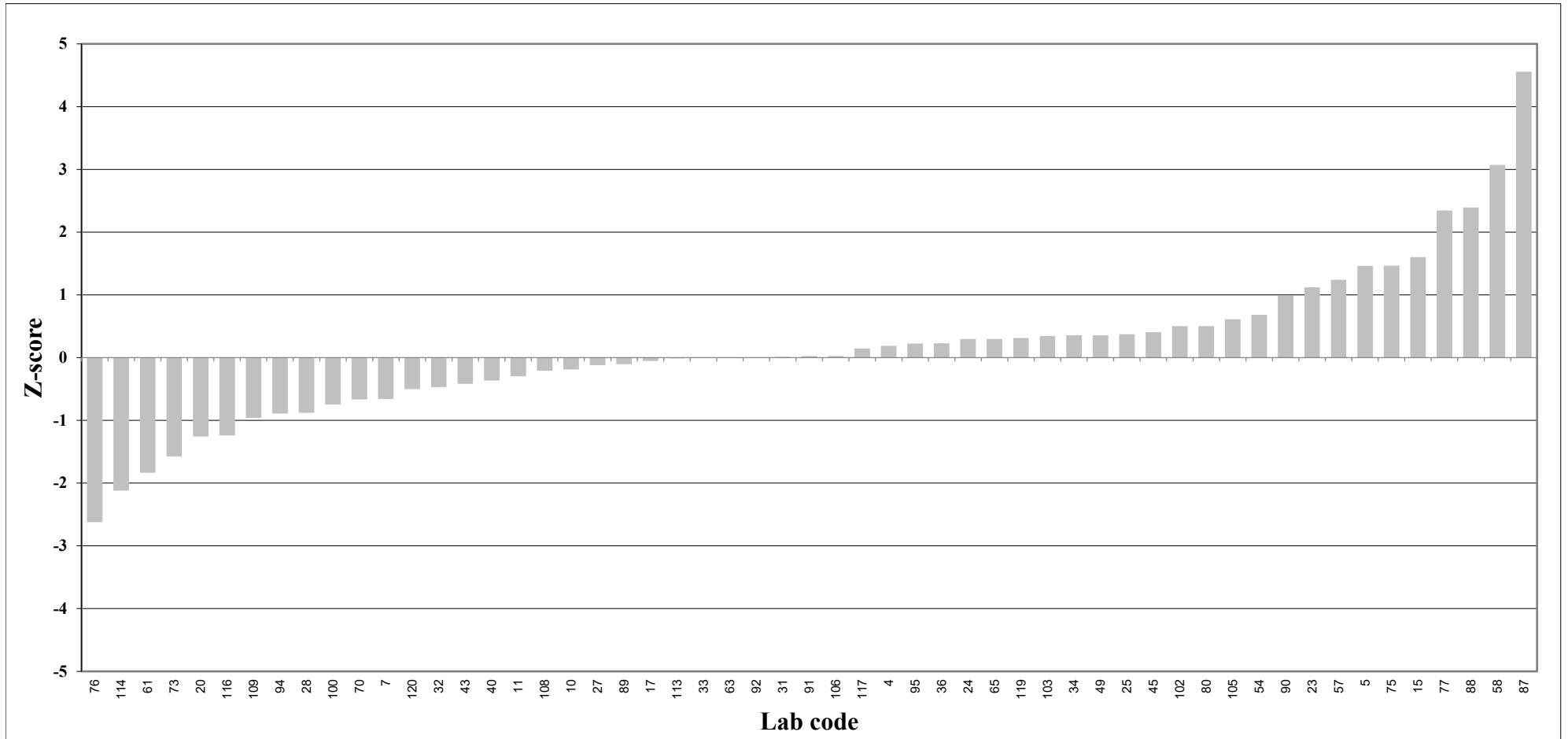
Z-score Brown meat, lipid weight; PCDD/PCDF TEQ
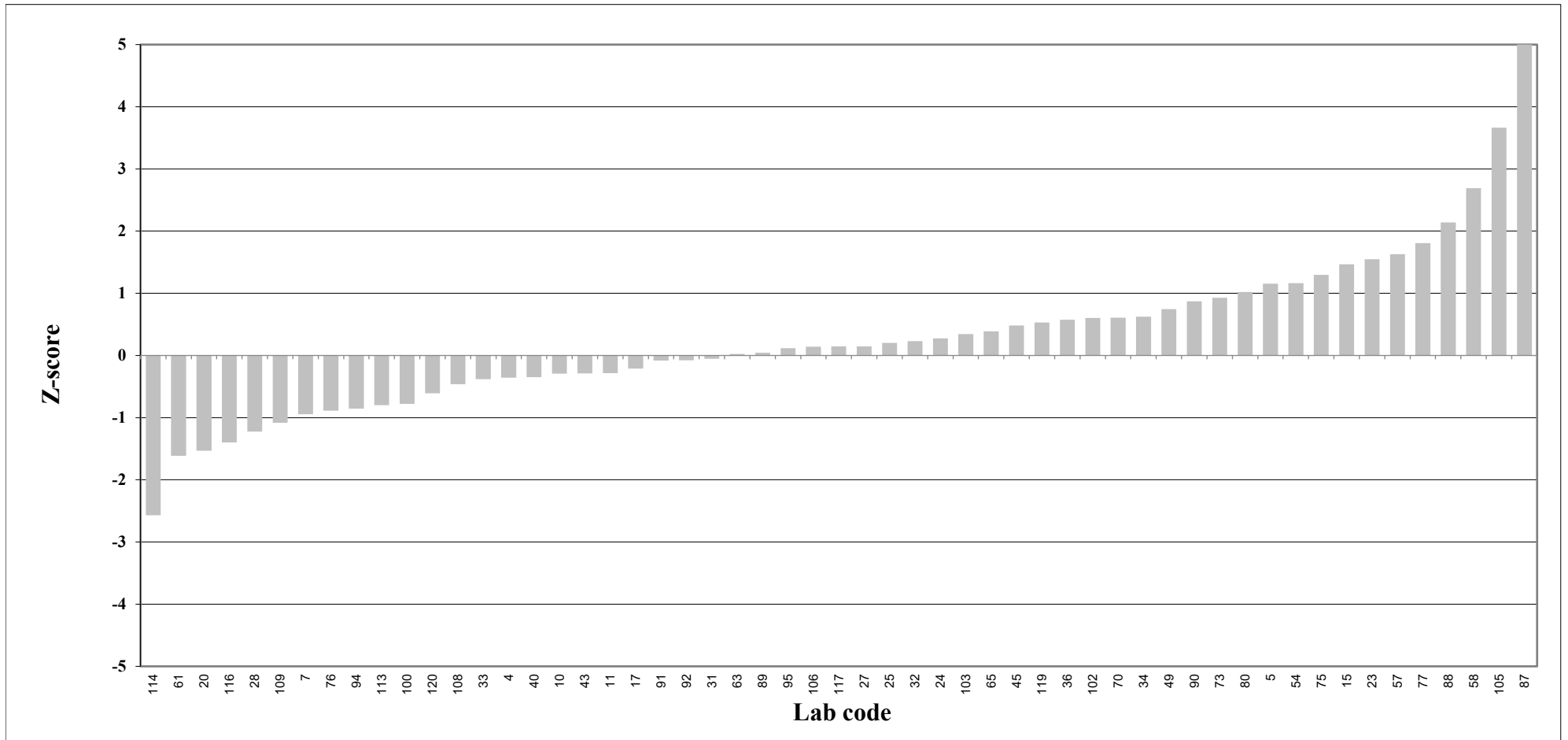
Z-score Brown meat, lipid weight; non-ortho PCB TEQ

Z-score Brown meat, lipid weight; mono-ortho PCB TEQ

Z-score Brown meat, lipid weight; sum indicator PCB

Z-score (y-axis) versus Lab code (x-axis): 90, 105, 7, 81, 25, 94, 28, 45, 27, 120, 109, 95, 49, 87, 106, 11, 32, 63, 24, 80, 31, 10, 23, 103, 70, 54, 102, 108, 34, 5, 65, 43, 100, 61, 117, 17, 58, 57, 4, 40, 75, 113, 15, 77, 114
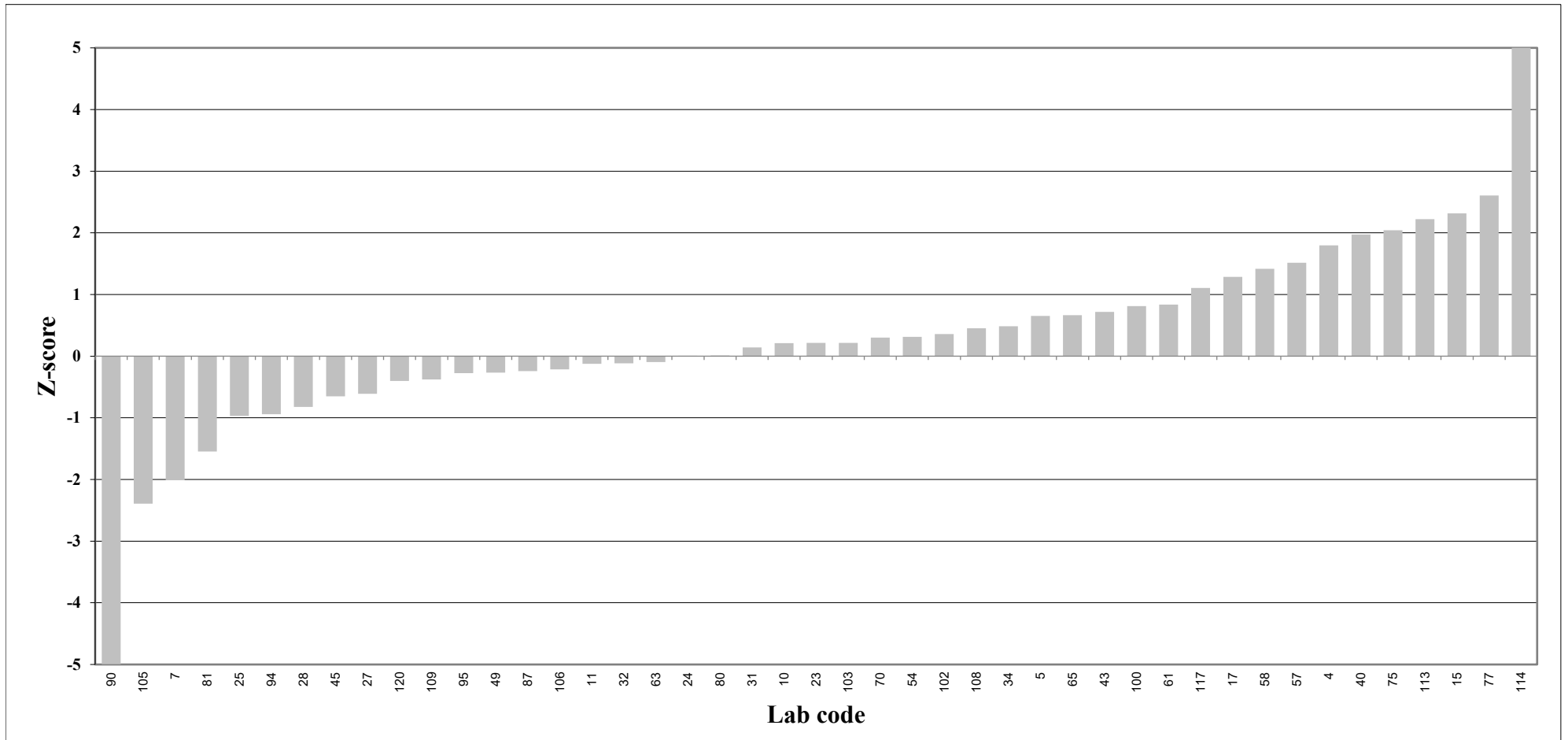
Z-score Brown meat, lipid weight; sum PBDE without BDE-209

Appendix 1:

Presentation of results
for analyte solution

Appendix 1: Presentation of results: Analyte solution

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

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

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.
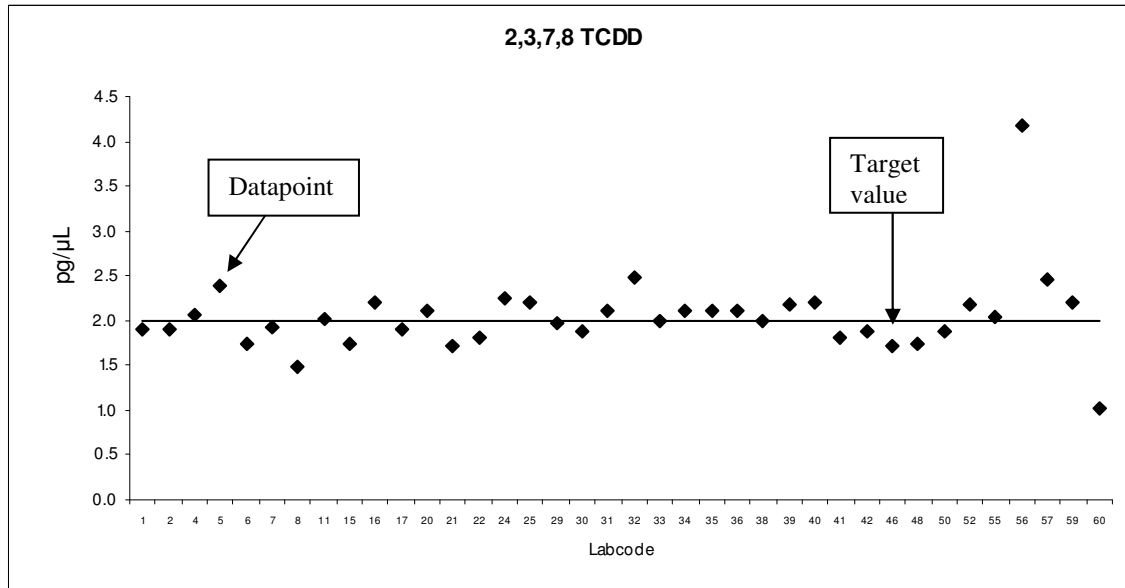
Z-Scores of individual congeners

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 ± 20% from the consensus value.

Analyte solution

Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	2,1	0,24		92	1,8	-0,48	
7	2,0	0,0020		94	1,9	-0,21	
10	2,1	0,12		95	2,0	0,093	
11	2,2	0,52		100	2,0	-0,13	
12	2,0	-0,0030		102	2,1	0,29	
15	2,0	-0,0070		103	2,3	0,66	
17	2,3	0,62		106	2,0	-0,0070	
20	2,1	0,19		109	1,9	-0,27	
23	2,1	0,32		110	1,9	-0,28	
24	2,0	-0,0020		113	2,0	-0,097	
25	1,6	-0,93		114	2,1	0,15	
28	1,8	-0,53		115	1,9	-0,15	
31	2,0	0,028		116	2,1	0,25	
32	2,1	0,31		118	1,9	-0,17	
33	2,0	-0,097		119	2,1	0,29	
34	2,0	0,10		120	1,9	-0,29	
36	2,1	0,12					
37	2,0	-0,11					
38	2,0	0,035					
40	1,7	-0,68					
42	1,9	-0,16					
44	2,0	-0,057					
45	2,0	0,033					
48	2,0	-0,0070					
49	1,9	-0,31					
54	2,2	0,57					
56	1,8	-0,55					
57	2,0	-0,074					
58	2,1	0,32					
61	2,1	0,29					
63	2,0	-0,084					
64	2,1	0,28					
65	2,2	0,57					
70	0,0000019	-5,0	Outlier				
71	2,0	0,022					
73	2,0	-0,082					
75	2,0	0,068					
76	2,1	0,18					
80	2,2	0,47					
84	1,9	-0,20					
87	2,0	-0,027					
88	2,0	0,040					
89	1,9	-0,26					
90	1,8	-0,46					
91	2,0	0,093					

Consenus statistics	
Consensus median, pg/g	2,0
Median all values pg/g	2,0
Consensus mean, pg/g	2,0
Standard deviation, pg/g	0,13
Relative standard deviation, %	6,3
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0

2,3,7,8 TCDD
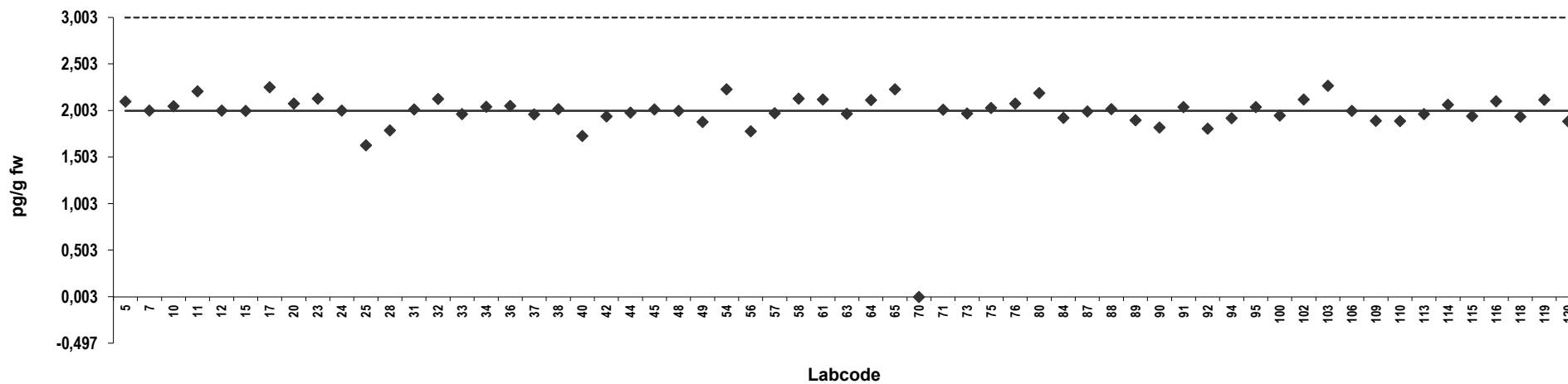
Z-score: 2,3,7,8 TCDD
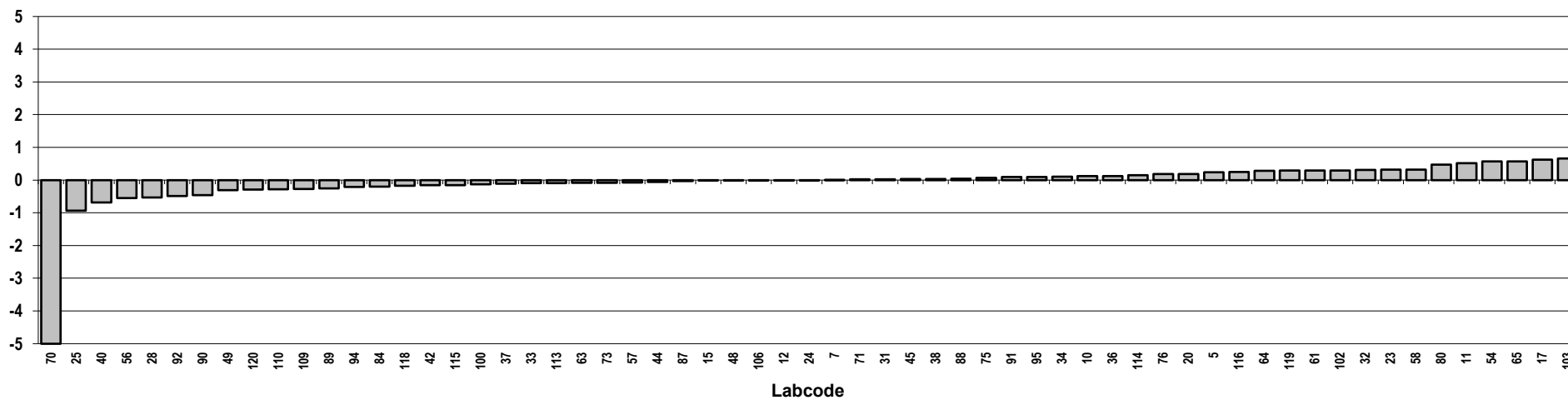
Analyte solution
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	5,3	0,28		92	5,5	0,53	
7	4,8	-0,19		94	5,2	0,20	
10	4,7	-0,30		95	5,7	0,70	
11	5,3	0,30		100	4,9	-0,058	
12	5,0	0,015		102	5,1	0,073	
15	5,1	0,10		103	5,6	0,65	
17	5,0	-0,029		106	4,3	-0,66	
20	5,0	-0,011		109	4,9	-0,061	
23	5,2	0,16		110	4,8	-0,20	
24	5,0	0,0075		113	5,0	0,027	
25	4,9	-0,12		114	5,6	0,58	
28	5,3	0,29		115	5,0	-0,0085	
31	5,0	0,036		116	4,9	-0,11	
32	5,8	0,82		118	5,6	0,57	
33	5,0	0,027		119	5,1	0,15	
34	5,1	0,063		120	4,8	-0,16	
36	4,7	-0,31					
37	5,0	-0,048					
38	4,9	-0,060					
40	4,8	-0,20					
42	4,7	-0,33					
44	4,5	-0,48					
45	5,0	0,0094					
48	4,9	-0,098					
49	4,7	-0,33					
54	4,4	-0,57					
56	5,1	0,093					
57	5,0	0,051					
58	5,0	-0,018					
61	5,0	-0,0075					
63	5,1	0,095					
64	5,2	0,25					
65	5,3	0,29					
70	0,0000052	-5,0	Outlier				
71	5,0	0,047					
73	4,9	-0,12					
75	5,2	0,15					
76	4,8	-0,17					
80	5,3	0,34					
84	4,9	-0,13					
87	4,8	-0,24					
88	5,1	0,071					
89	4,8	-0,20					
90	4,5	-0,47					
91	4,9	-0,088					

Consenus statistics	
Consensus median, pg/g	5,0
Median all values pg/g	5,0
Consensus mean, pg/g	5,0
Standard deviation, pg/g	0,29
Relative standard deviation, %	5,9
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0
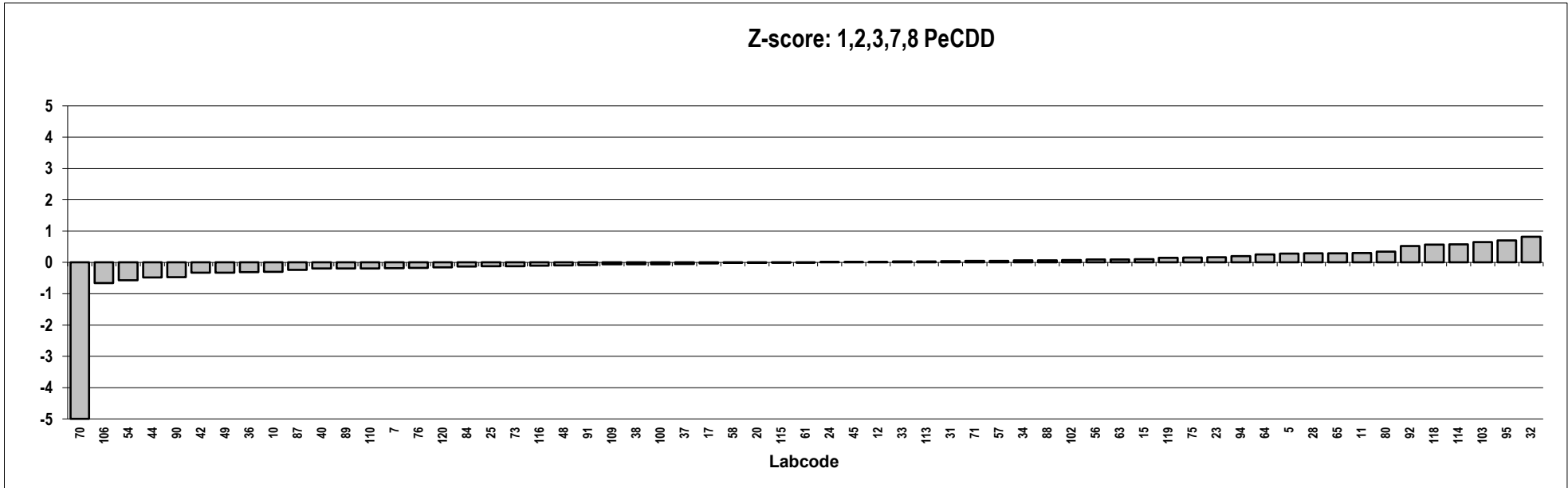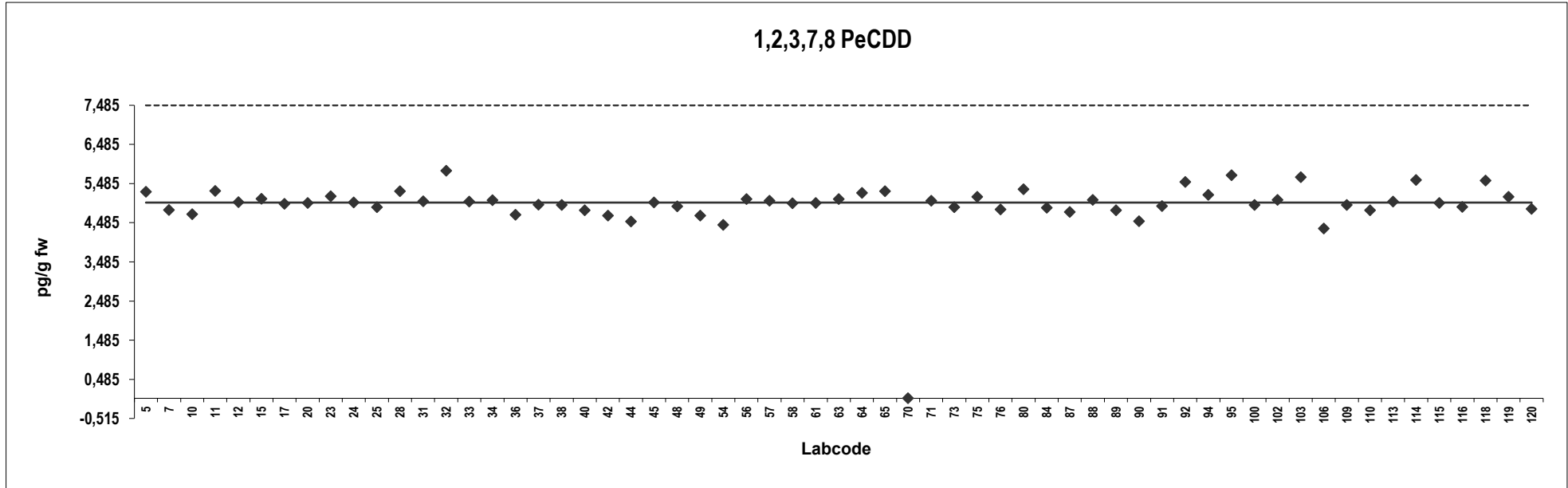
1,2,3,7,8 PeCDD

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

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	5,1	0,16		92	4,9	-0,13	
7	5,2	0,21		94	5,2	0,22	
10	4,7	-0,25		95	5,4	0,39	
11	5,3	0,31		100	4,9	-0,039	
12	5,0	0,017		102	4,9	-0,039	
15	5,1	0,12		103	5,2	0,20	
17	4,9	-0,031		106	5,1	0,13	
20	4,9	-0,10		109	4,6	-0,40	
23	5,9	0,97		110	4,3	-0,72	
24	5,0	0,018		113	5,0	0,00	
25	4,6	-0,41		114	5,0	0,049	
28	4,7	-0,29		115	4,8	-0,19	
31	5,0	0,015		116	4,8	-0,18	
32	5,0	-0,0068		118	5,2	0,23	
33	5,0	0,00		119	5,2	0,18	
34	5,1	0,13		120	4,9	-0,10	
36	4,6	-0,37					
37	5,1	0,15					
38	4,7	-0,23					
40	4,8	-0,18					
42	4,7	-0,33					
44	4,9	-0,059					
45	5,0	0,027					
48	4,8	-0,18					
49	5,2	0,20					
54	5,0	0,041					
56	6,5	1,6					
57	4,5	-0,43					
58	5,6	0,58					
61	5,0	-0,0088					
63	4,7	-0,33					
64	5,0	0,035					
65	5,4	0,43					
70	0,0000045	-5,0	Outlier				
71	5,0	0,010					
73	4,8	-0,20					
75	4,9	-0,099					
76	4,6	-0,35					
80	5,0	0,041					
84	4,9	-0,077					
87	4,5	-0,46					
88	5,2	0,23					
89	5,0	0,021					
90	4,3	-0,68					
91	5,1	0,072					

Consensus statistics	
Consensus median, pg/g	5,0
Median all values pg/g	5,0
Consensus mean, pg/g	5,0
Standard deviation, pg/g	0,35
Relative standard deviation, %	7,0
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0
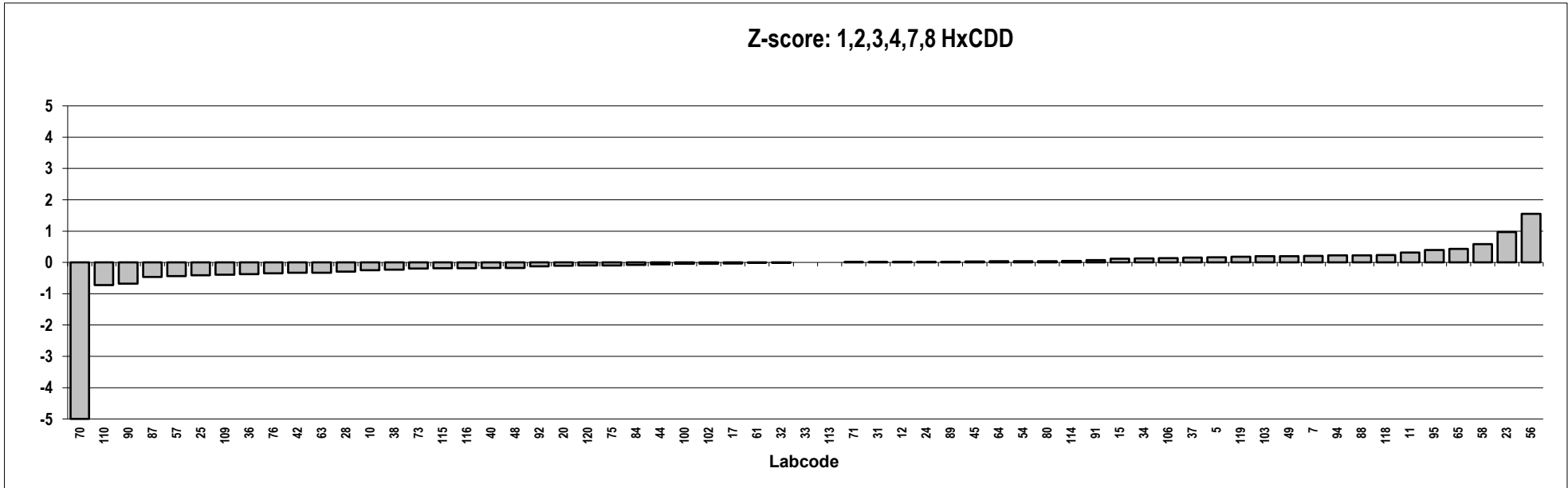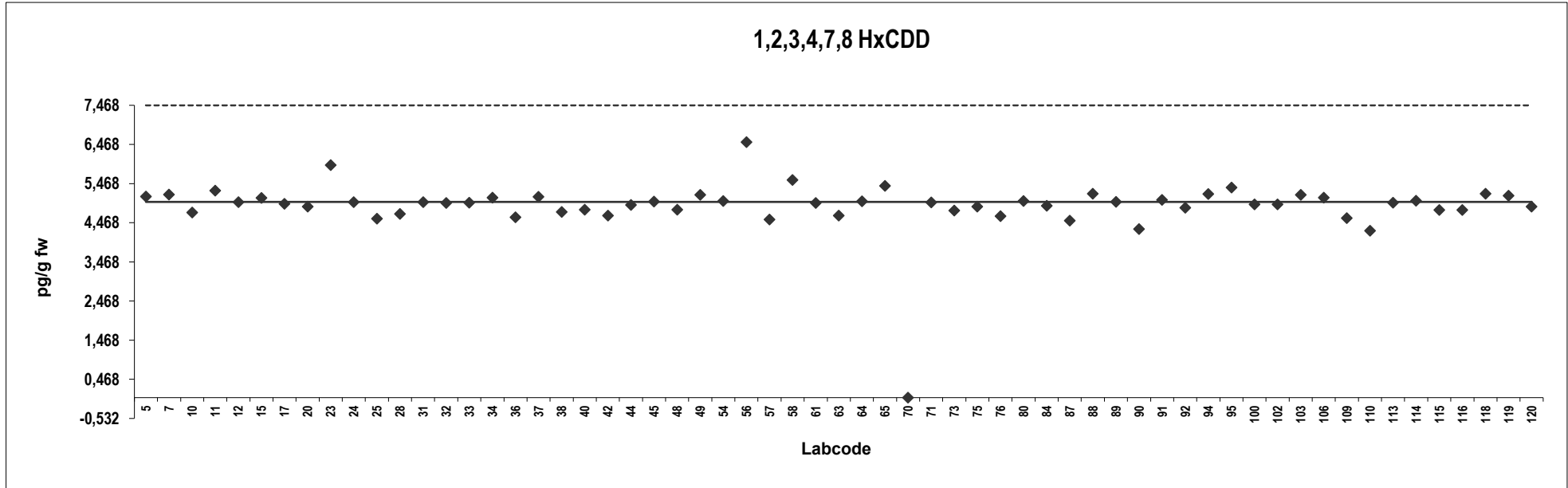
1,2,3,4,7,8 HxCDD

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

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	5,0	0,015		92	4,4	-0,51	
7	5,1	0,13		94	5,2	0,25	
10	5,2	0,21		95	4,5	-0,42	
11	5,2	0,26		100	5,0	0,035	
12	5,0	0,025		102	4,9	-0,015	
15	4,8	-0,16		103	5,6	0,62	
17	4,9	-0,046		106	5,0	0,015	
20	5,0	0,069		109	5,1	0,11	
23	5,6	0,65		110	4,1	-0,88	
24	5,0	0,047		113	4,8	-0,15	
25	5,7	0,70		114	5,0	0,014	
28	4,7	-0,24		115	5,0	0,030	
31	5,2	0,24		116	4,2	-0,75	
32	5,9	0,91		118	4,7	-0,28	
33	4,8	-0,15		119	5,1	0,14	
34	4,9	-0,014		120	4,8	-0,12	
36	4,7	-0,27					
37	5,0	0,075					
38	4,7	-0,30					
40	4,8	-0,21					
42	4,5	-0,50					
44	4,9	-0,096					
45	5,0	0,057					
48	4,8	-0,16					
49	4,9	-0,026					
54	4,8	-0,14					
56	5,6	0,70					
57	4,7	-0,31					
58	5,3	0,37					
61	5,6	0,66					
63	5,0	0,065					
64	5,1	0,14					
65	5,3	0,37					
70	0,0000044	-5,0	Outlier				
71	5,0	0,044					
73	5,1	0,13					
75	5,1	0,12					
76	4,6	-0,36					
80	4,4	-0,54					
84	4,9	-0,046					
87	4,4	-0,61					
88	4,7	-0,25					
89	4,8	-0,16					
90	4,0	-0,96					
91	4,9	-0,036					

Consenus statistics	
Consensus median, pg/g	5,0
Median all values pg/g	4,9
Consensus mean, pg/g	4,9
Standard deviation, pg/g	0,37
Relative standard deviation, %	7,4
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0
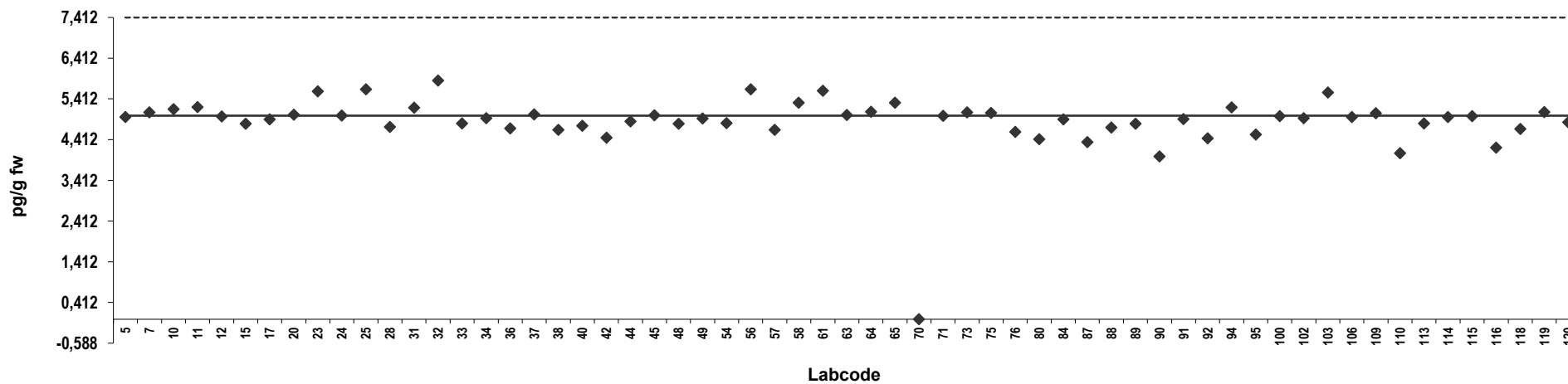
1,2,3,6,7,8 HxCDD

Z-score: 1,2,3,6,7,8 HxCDD
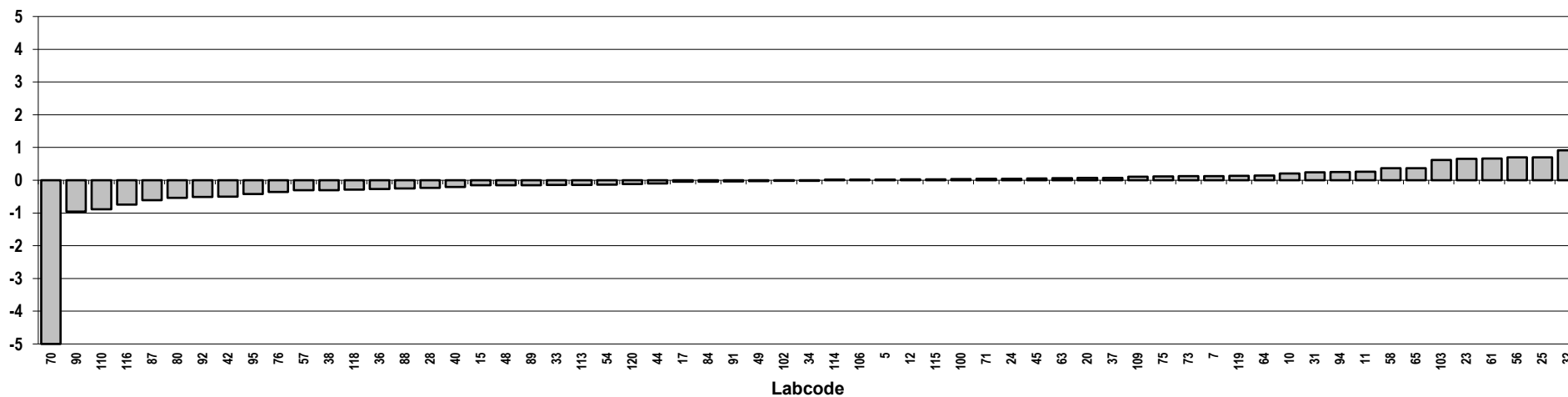
Analyte solution
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	4,9	-0,13		92	4,7	-0,30	
7	5,1	0,054		94	5,2	0,20	
10	6,0	0,99		95	5,2	0,22	
11	5,1	0,059		100	5,1	0,069	
12	5,0	0,00075		102	5,0	0,019	
15	5,1	0,099		103	5,7	0,75	
17	5,3	0,28		106	4,9	-0,11	
20	5,1	0,089		109	5,0	-0,0011	
23	5,5	0,47		110	4,5	-0,53	
24	5,0	0,0022		113	5,0	0,013	
25	6,4	1,3		114	5,1	0,070	
28	4,8	-0,20		115	5,0	0,047	
31	5,4	0,43		116	4,7	-0,29	
32	5,5	0,54		118	4,8	-0,24	
33	5,0	0,0015		119	5,1	0,11	
34	5,5	0,48		120	4,9	-0,12	
36	4,8	-0,23					
37	4,7	-0,27					
38	4,9	-0,11					
40	4,1	-0,92					
42	4,5	-0,48					
44	4,9	-0,12					
45	5,0	-0,0049					
48	4,9	-0,10					
49	4,9	-0,13					
54	5,8	0,77					
56	5,8	0,79					
57	4,9	-0,058					
58	5,1	0,099					
61	4,7	-0,30					
63	4,8	-0,15					
64	4,9	-0,089					
65	4,9	-0,061					
70	0,0000045	-5,0	Outlier				
71	5,0	-0,0093					
73	5,0	0,019					
75	4,9	-0,10					
76	5,0	0,018					
80	5,0	-0,00075					
84	4,8	-0,18					
87	4,7	-0,28					
88	5,1	0,14					
89	4,9	-0,10					
90	4,4	-0,57					
91	5,1	0,11					

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	0,37
Relative standard deviation, %	7,4
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0

1,2,3,7,8,9 HxCDD
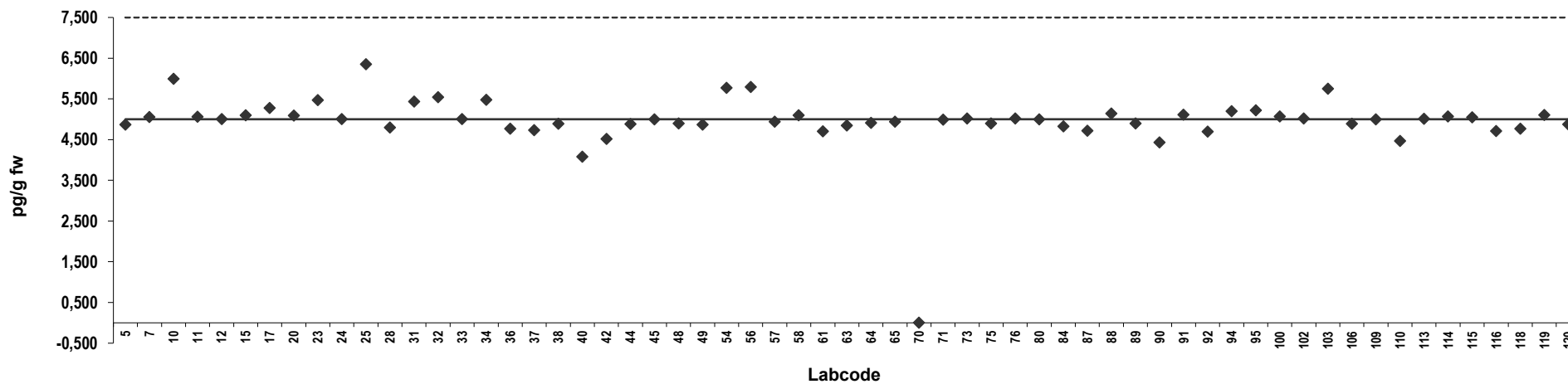
Z-score: 1,2,3,7,8,9 HxCDD
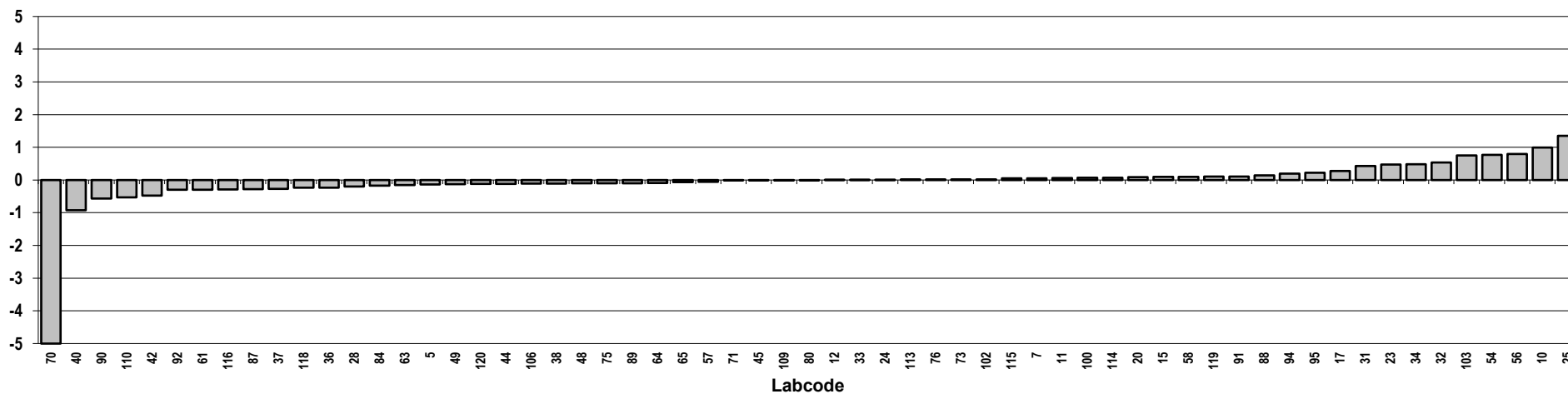
Analyte solution
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	5,1	0,14		92	4,8	-0,16	
7	5,3	0,27		94	5,0	0,00	
10	5,1	0,080		95	5,1	0,11	
11	5,1	0,050		100	5,0	-0,030	
12	5,0	-0,0075		102	4,9	-0,070	
15	5,0	0,00		103	5,4	0,43	
17	5,0	0,00		106	5,1	0,050	
20	4,9	-0,069		109	4,8	-0,20	
23	5,5	0,45		110	4,3	-0,66	
24	5,0	0,0070		113	5,0	0,0051	
25	5,1	0,060		114	5,3	0,29	
28	4,7	-0,30		115	5,0	0,012	
31	4,9	-0,090		116	4,7	-0,35	
32	5,7	0,75		118	5,4	0,42	
33	5,0	0,0051		119	5,1	0,052	
34	5,0	-0,0051		120	5,0	-0,039	
36	4,7	-0,32					
37	5,2	0,19					
38	4,8	-0,25					
40	3,9	-1,1					
42	4,6	-0,39					
44	5,1	0,060					
45	5,0	0,034					
48	4,8	-0,20					
49	4,8	-0,23					
54	4,4	-0,57					
56	5,8	0,79					
57	4,7	-0,30					
58	5,3	0,28					
61	10	5,5	Outlier				
63	4,5	-0,52					
64	4,9	-0,098					
65	5,6	0,59					
70	0,0000045	-5,0	Outlier				
71	5,1	0,062					
73	4,8	-0,16					
75	5,0	0,010					
76	4,7	-0,29					
80	4,9	-0,14					
84	4,9	-0,067					
87	4,5	-0,48					
88	5,1	0,14					
89	5,3	0,30					
90	4,3	-0,68					
91	5,1	0,080					

Consenus statistics

Consensus median, pg/g	5,0
Median all values pg/g	5,0
Consensus mean, pg/g	5,0
Standard deviation, pg/g	0,33
Relative standard deviation, %	6,7
No. of values reported	61
No. of values removed	2
No. of reported non-detects	0

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

Z-score: 1,2,3,4,6,7,8 HpCDD
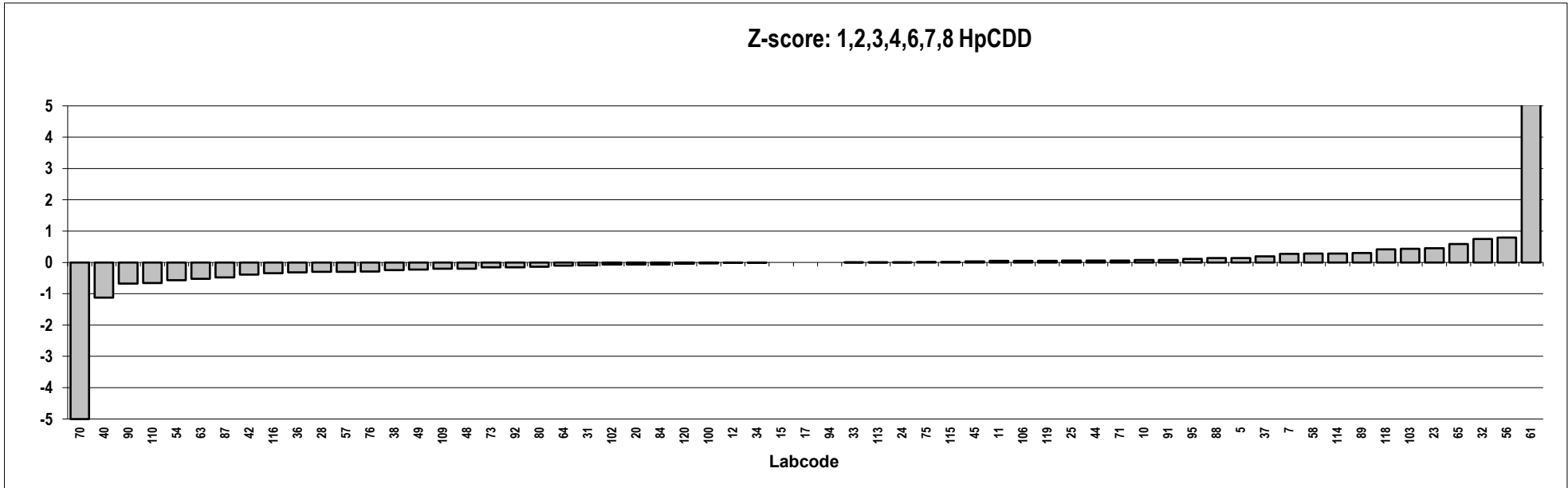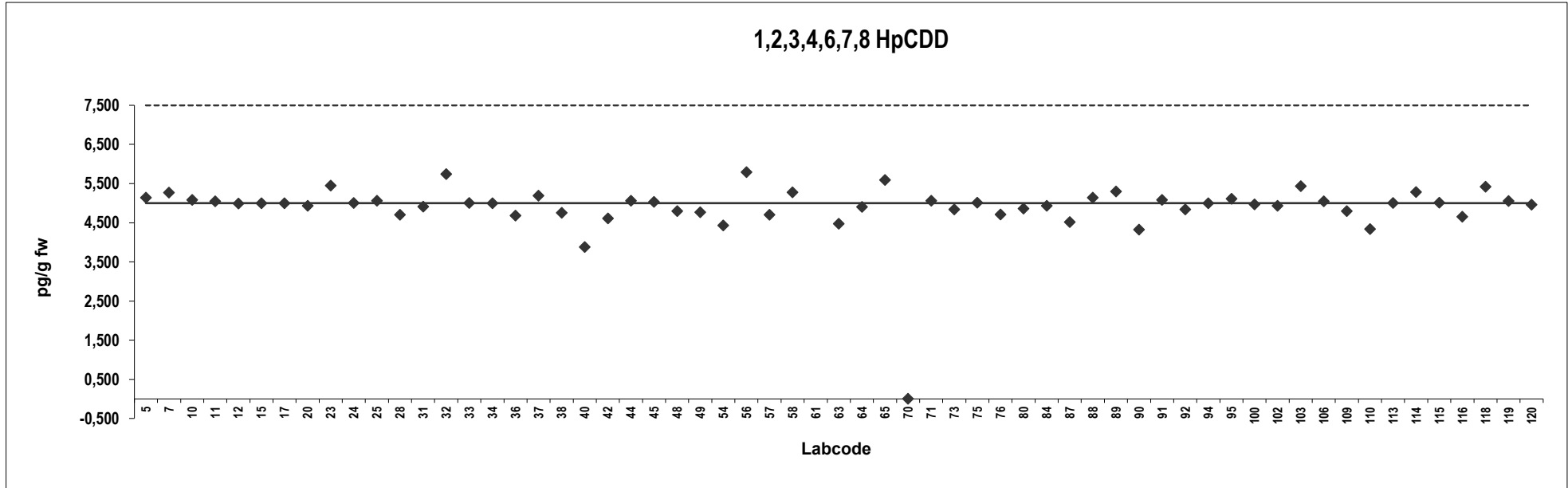
Analyte solution
Congener: OCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	9,8	0,0051		92	9,4	-0,21	
7	11	0,64		94	11	0,50	
10	10	0,14		95	8,5	-0,67	
11	10	0,25		100	10	0,068	
12	10	0,10		102	9,8	-0,0084	
15	10	0,093		103	11	0,47	
17	9,6	-0,12		106	9,8	-0,013	
20	9,9	0,039		109	9,2	-0,29	
23	10	0,25		110	8,7	-0,59	
24	10	0,093		113	9,9	0,037	
25	9,8	-0,0033		114	10	0,15	
28	9,3	-0,26		115	9,6	-0,11	
31	11	0,41		116	9,0	-0,40	
32	11	0,65		118	11	0,39	
33	9,9	0,037		119	9,8	-0,030	
34	9,2	-0,29		120	9,6	-0,092	
36	8,9	-0,44					
37	10	0,068					
38	9,6	-0,13					
40	8,5	-0,67					
42	9,2	-0,33					
44	9,8	-0,013					
45	10	0,14					
48	9,4	-0,21					
49	9,3	-0,26					
54	9,3	-0,27					
56	11	0,79					
57	9,8	-0,026					
58	11	0,58					
61	11	0,80					
63	9,5	-0,18					
64	11	0,37					
65	11	0,38					
70	0,0000089	-5,0	Outlier				
71	10	0,077					
73	5,0	-2,5					
75	10	0,20					
76	9,1	-0,36					
80	9,7	-0,085					
84	9,9	0,051					
87	9,0	-0,42					
88	9,8	0,0033					
89	9,5	-0,16					
90	8,7	-0,55					
91	10	0,073					

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	0,91
Relative standard deviation, %	9,3
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0

OCDD

pg/g fw

Labcode

Z-score: OCDD
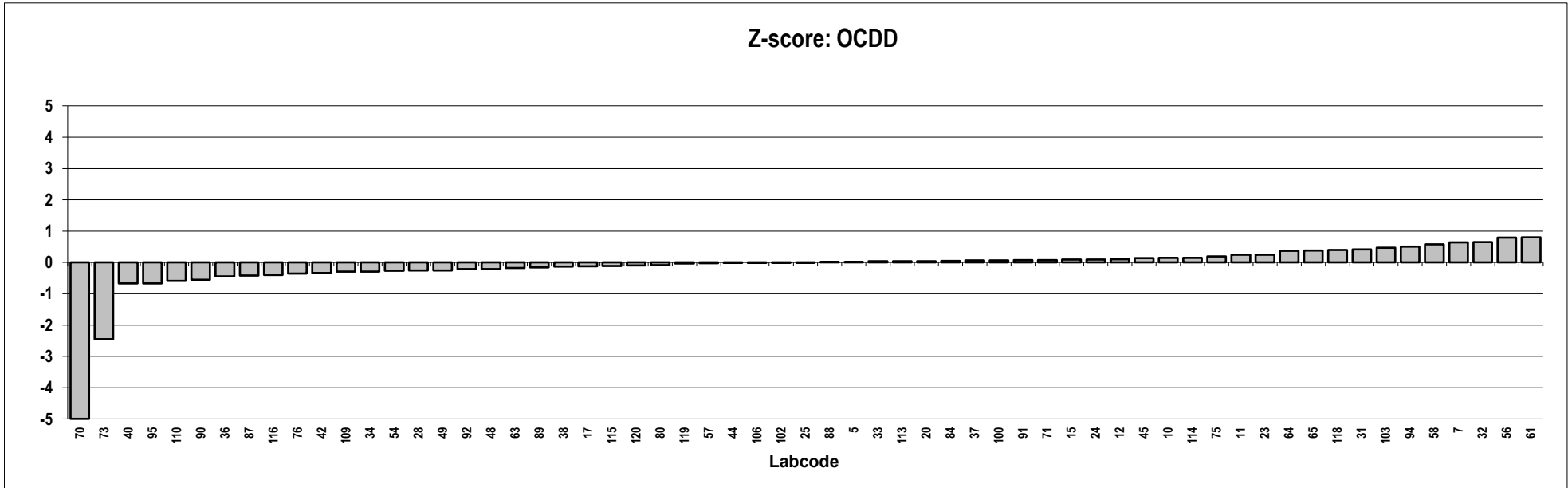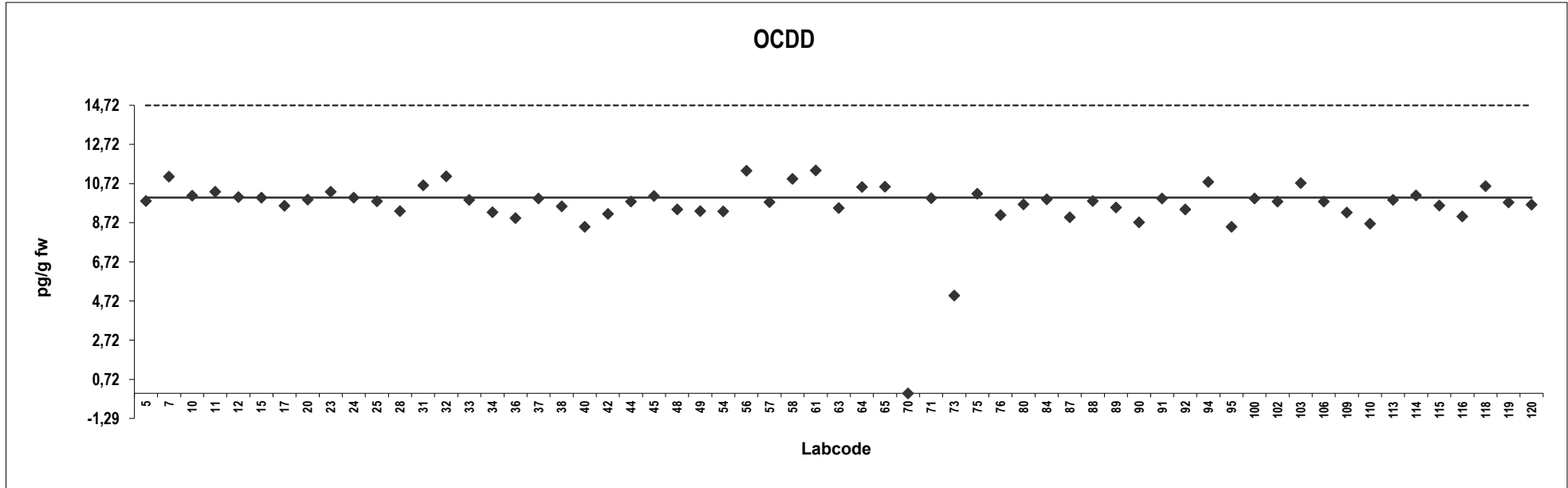
Labcode

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	1,9	-0,060		92	2,0	0,14	
7	2,2	0,48		94	2,0	-0,0079	
10	2,0	0,069		95	2,1	0,25	
11	2,0	0,17		100	2,1	0,27	
12	2,0	0,085		102	1,9	-0,084	
15	1,9	-0,16		103	2,3	0,89	
17	1,9	-0,20		106	2,2	0,53	
20	2,1	0,24		109	1,9	-0,15	
23	2,1	0,32		110	1,7	-0,67	
24	2,0	0,084		113	1,9	-0,054	
25	1,9	-0,11		114	2,1	0,32	
28	1,7	-0,62		115	1,9	-0,079	
31	2,0	0,00		116	1,9	-0,084	
32	2,4	1,0		118	1,9	-0,14	
33	1,9	-0,054		119	2,1	0,27	
34	2,0	-0,029		120	1,9	-0,092	
36	1,9	-0,25					
37	1,9	-0,084					
38	1,7	-0,57					
40	1,7	-0,59					
42	1,9	-0,29					
44	2,0	-0,0079					
45	2,0	0,13					
48	1,9	-0,16					
49	2,0	0,018					
54	2,1	0,30					
56	2,3	0,79					
57	1,7	-0,59					
58	2,0	0,16					
61	2,0	0,12					
63	2,1	0,27					
64	2,0	0,14					
65	2,3	0,76					
70	0,0000019	-5,0	Outlier				
71	2,0	0,12					
73	5,0	7,7	Outlier				
75	2,0	0,12					
76	1,9	-0,12					
80	2,1	0,27					
84	1,9	-0,044					
87	1,9	-0,28					
88	2,0	-0,0079					
89	2,1	0,35					
90	1,8	-0,37					
91	2,0	0,094					

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	0,13
Relative standard deviation, %	6,8
No. of values reported	61
No. of values removed	2
No. of reported non-detects	0
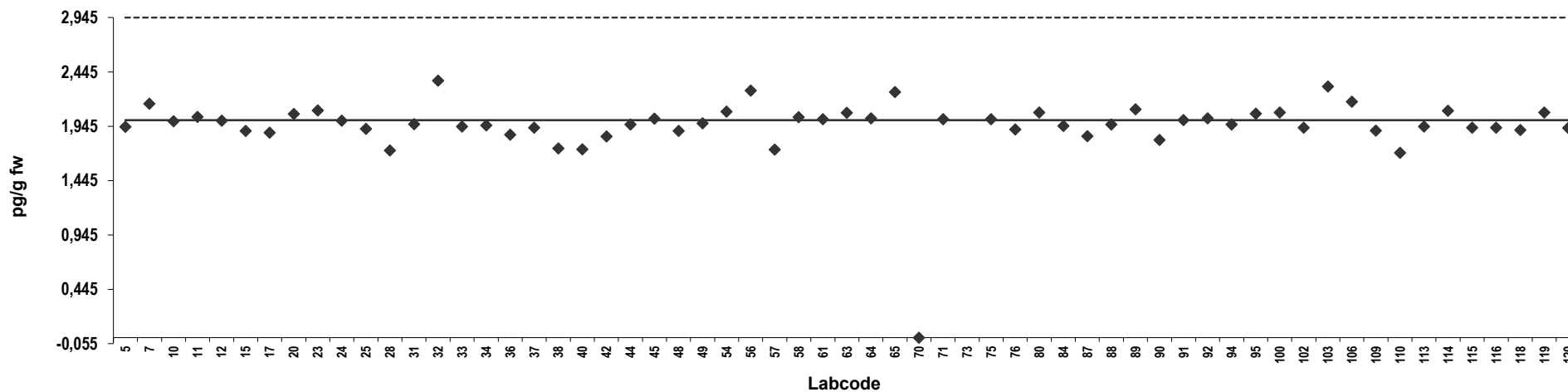
2,3,7,8 TCDF

Z-score: 2,3,7,8 TCDF
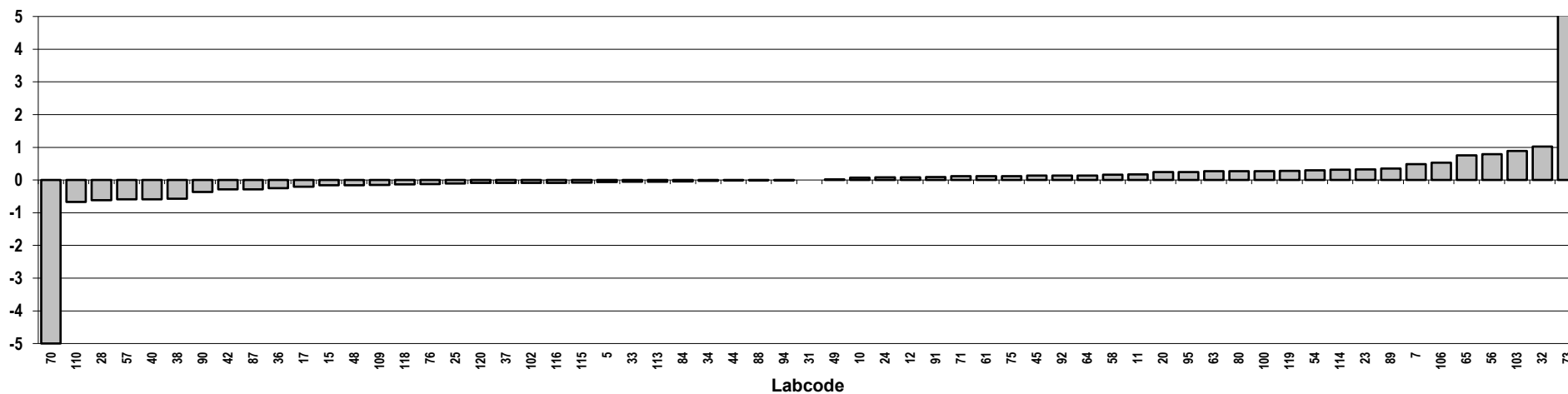
Analyte solution
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	5,3	0,36		92	4,8	-0,10	
7	4,9	-0,050		94	5,6	0,67	
10	5,1	0,13		95	5,4	0,42	
11	4,8	-0,13		100	5,0	0,040	
12	5,0	0,077		102	4,4	-0,51	
15	4,9	-0,041		103	5,4	0,44	
17	5,0	0,080		106	4,9	-0,00094	
20	4,8	-0,13		109	4,9	0,0047	
23	5,4	0,42		110	4,5	-0,49	
24	5,0	0,059		113	4,8	-0,18	
25	5,6	0,70		114	5,6	0,71	
28	4,7	-0,29		115	4,8	-0,10	
31	5,2	0,27		116	4,8	-0,12	
32	5,8	0,83		118	5,3	0,33	
33	4,8	-0,13		119	5,1	0,18	
34	4,9	-0,083		120	4,6	-0,31	
36	4,8	-0,11					
37	5,0	0,060					
38	4,9	-0,030					
40	4,5	-0,50					
42	4,6	-0,30					
44	4,9	-0,021					
45	5,0	0,071					
48	4,7	-0,24					
49	4,7	-0,28					
54	4,7	-0,26					
56	5,4	0,51					
57	4,9	0,00094					
58	5,2	0,27					
61	5,3	0,34					
63	4,7	-0,20					
64	5,0	0,058					
65	5,3	0,34					
70	0,0000050	-5,0	Outlier				
71	5,0	0,072					
73	5,0	0,0092					
75	5,0	0,090					
76	4,7	-0,23					
80	5,0	0,090					
84	4,8	-0,13					
87	4,3	-0,64					
88	4,6	-0,30					
89	4,7	-0,24					
90	4,4	-0,52					
91	5,0	0,040					

Consenus statistics

Consensus median, pg/g	4,9
Median all values pg/g	4,9
Consensus mean, pg/g	5,0
Standard deviation, pg/g	0,31
Relative standard deviation, %	6,3
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0

1,2,3,7,8 PeCDF

Z-score: 1,2,3,7,8 PeCDF
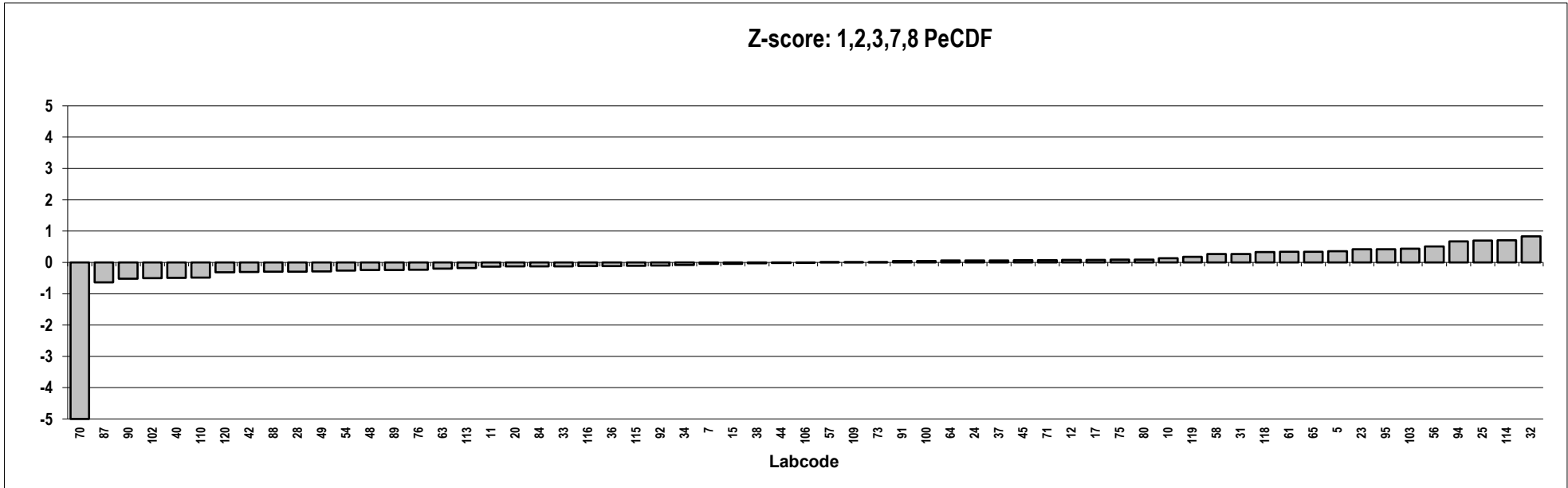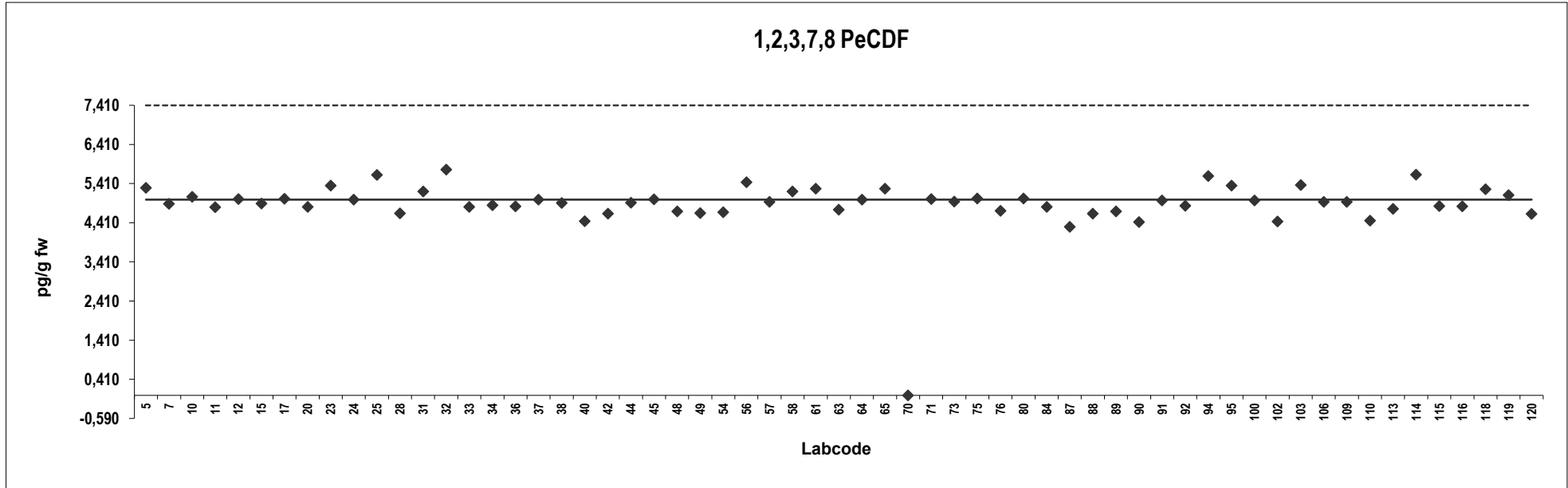
Analyte solution
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	4,6	-0,33		92	4,4	-0,45	
7	5,2	0,33		94	4,8	-0,082	
10	4,8	-0,12		95	4,8	-0,072	
11	5,2	0,30		100	5,0	0,092	
12	5,0	0,11		102	5,0	0,10	
15	4,9	0,020		103	5,1	0,19	
17	4,9	0,052		106	4,9	0,010	
20	5,2	0,35		109	4,8	-0,086	
23	5,2	0,33		110	4,2	-0,66	
24	5,0	0,11		113	4,6	-0,31	
25	4,0	-0,86		114	5,4	0,49	
28	4,2	-0,69		115	4,8	-0,040	
31	4,8	-0,067		116	4,2	-0,74	
32	5,1	0,18		118	4,8	-0,077	
33	4,7	-0,23		119	5,2	0,38	
34	5,0	0,13		120	4,8	-0,085	
36	4,7	-0,20					
37	4,8	-0,061					
38	4,2	-0,65					
40	4,4	-0,49					
42	4,6	-0,30					
44	4,9	0,00					
45	5,0	0,15					
48	4,8	-0,082					
49	5,0	0,10					
54	5,1	0,25					
56	5,0	0,15					
57	4,6	-0,27					
58	4,9	0,013					
61	4,8	-0,072					
63	4,8	-0,12					
64	5,0	0,16					
65	5,3	0,42					
70	0,0000041	-5,0	Outlier				
71	5,0	0,14					
73	9,7	4,9	Outlier				
75	4,9	0,010					
76	4,8	-0,095					
80	5,7	0,80					
84	4,8	-0,039					
87	4,4	-0,50					
88	5,0	0,13					
89	5,0	0,12					
90	4,2	-0,71					
91	4,9	0,041					

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	0,32
Relative standard deviation, %	6,6
No. of values reported	61
No. of values removed	2
No. of reported non-detects	0

2,3,4,7,8 PeCDF

Z-score: 2,3,4,7,8 PeCDF
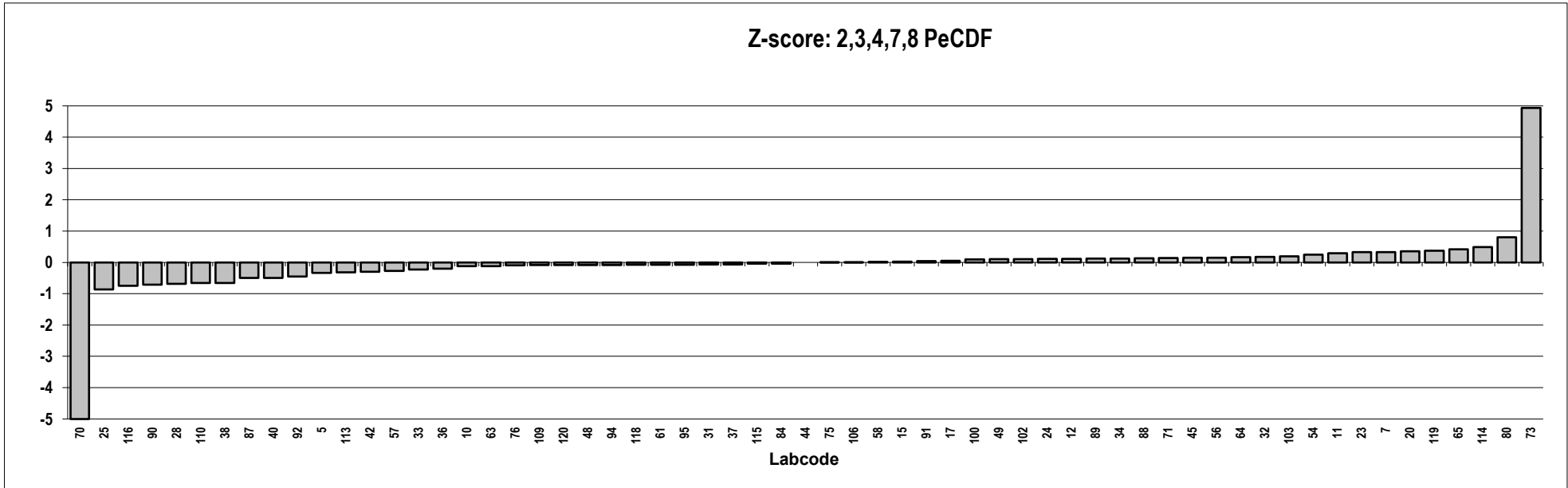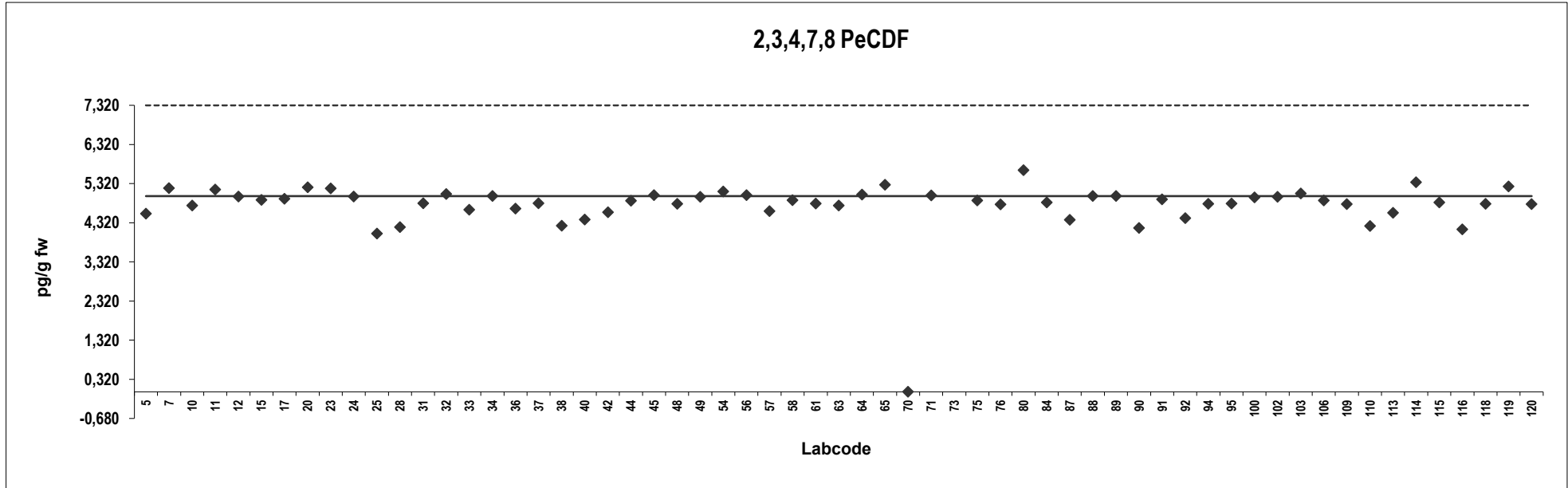
Analyte solution
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	4,9	-0,069		92	4,7	-0,27	
7	5,4	0,45		94	4,8	-0,20	
10	4,8	-0,17		95	5,2	0,24	
11	5,1	0,12		100	4,9	-0,10	
12	5,0	0,0014		102	4,9	-0,12	
15	5,0	0,00		103	5,5	0,54	
17	5,1	0,056		106	5,3	0,25	
20	5,0	-0,040		109	4,5	-0,46	
23	5,4	0,42		110	4,2	-0,81	
24	5,0	0,0030		113	4,8	-0,24	
25	5,0	0,00		114	5,5	0,49	
28	4,7	-0,28		115	5,0	-0,031	
31	5,2	0,20		116	4,4	-0,60	
32	5,5	0,48		118	5,1	0,10	
33	4,8	-0,24		119	5,1	0,14	
34	5,0	0,049		120	4,7	-0,33	
36	4,9	-0,14					
37	5,1	0,13					
38	4,6	-0,37					
40	4,1	-0,91					
42	4,7	-0,26					
44	4,9	-0,060					
45	5,0	-0,0046					
48	5,0	0,00					
49	5,0	-0,020					
54	5,4	0,35					
56	5,0	0,033					
57	4,7	-0,27					
58	5,3	0,26					
61	5,1	0,13					
63	5,0	-0,018					
64	5,0	0,0060					
65	5,8	0,81					
70	0,0000051	-5,0	Outlier				
71	5,0	0,011					
73	1,9	-3,1	Outlier				
75	5,1	0,090					
76	4,7	-0,32					
80	5,3	0,30					
84	4,9	-0,14					
87	4,6	-0,45					
88	4,7	-0,34					
89	5,0	0,00					
90	4,4	-0,61					
91	5,0	0,00					

Consenus statistics

Consensus median, pg/g	5,0
Median all values pg/g	5,0
Consensus mean, pg/g	5,0
Standard deviation, pg/g	0,32
Relative standard deviation, %	6,4
No. of values reported	61
No. of values removed	2
No. of reported non-detects	0

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

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

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	4,9	-0,10		92	4,8	-0,18	
7	5,2	0,22		94	5,0	0,025	
10	4,8	-0,17		95	5,3	0,35	
11	5,0	0,055		100	4,9	-0,035	
12	5,0	0,038		102	5,0	0,025	
15	4,9	-0,075		103	5,5	0,48	
17	5,2	0,19		106	5,1	0,13	
20	4,9	-0,031		109	4,7	-0,31	
23	5,5	0,57		110	4,2	-0,75	
24	5,0	0,026		113	5,0	0,035	
25	4,5	-0,49		114	5,1	0,082	
28	4,5	-0,51		115	4,9	-0,059	
31	4,9	-0,030		116	4,6	-0,37	
32	5,6	0,66		118	4,8	-0,17	
33	5,0	0,035		119	5,2	0,20	
34	5,4	0,44		120	4,8	-0,14	
36	4,7	-0,23					
37	5,2	0,21					
38	4,5	-0,52					
40	4,5	-0,45					
42	4,8	-0,19					
44	5,0	0,015					
45	5,0	0,056					
48	4,9	-0,075					
49	4,4	-0,58					
54	4,9	-0,13					
56	5,8	0,84					
57	5,1	0,15					
58	5,1	0,15					
61	4,8	-0,17					
63	4,9	-0,088					
64	5,2	0,18					
65	5,6	0,64					
70	0,0000047	-5,0	Outlier				
71	5,0	0,033					
73	5,0	0,025					
75	5,1	0,075					
76	4,9	-0,11					
80	5,0	-0,015					
84	5,0	0,055					
87	4,5	-0,51					
88	4,9	-0,055					
89	4,9	-0,075					
90	4,6	-0,39					
91	5,0	0,025					

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	0,30
Relative standard deviation, %	6,1
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0

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

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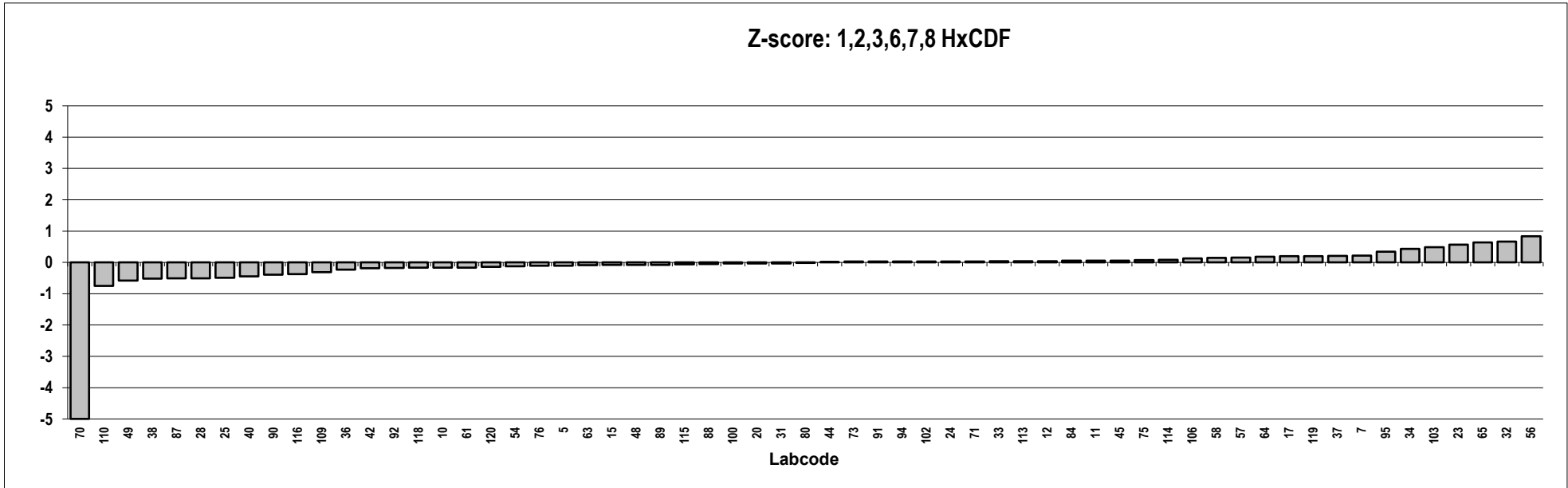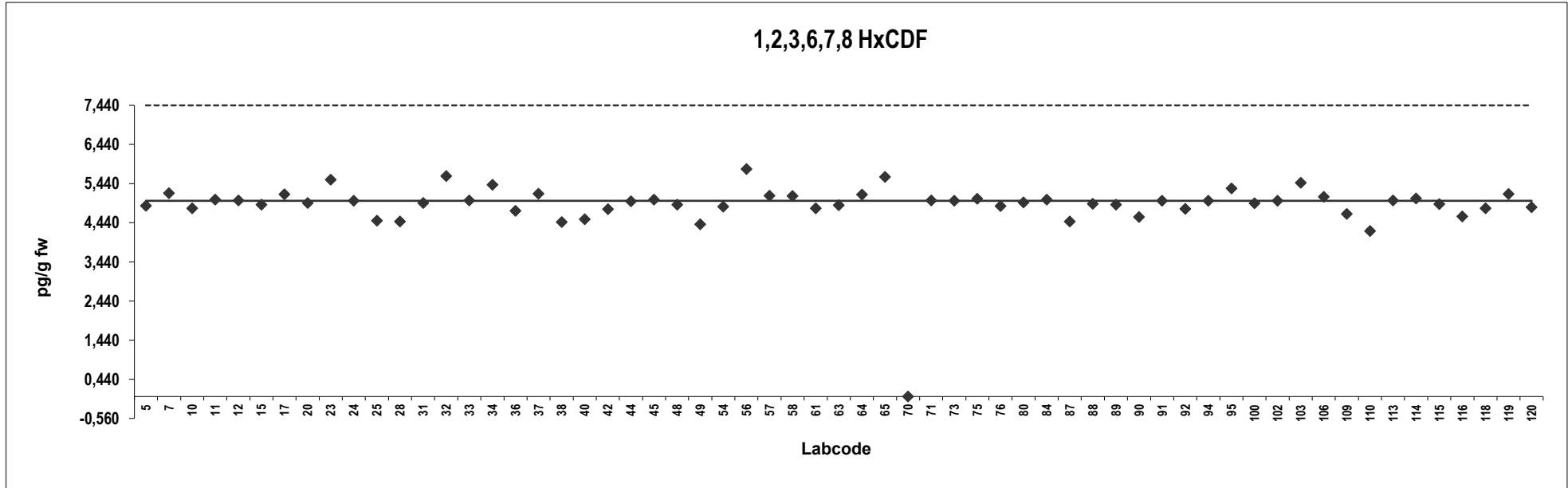
Analyte solution

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	4,8	-0,24		92	4,6	-0,36	
7	5,4	0,45		94	3,6	-1,4	
10	5,4	0,39		95	5,2	0,18	
11	5,0	0,040		100	5,0	-0,040	
12	5,0	0,0040		102	5,0	-0,030	
15	5,0	0,010		103	5,5	0,54	
17	5,1	0,070		106	5,2	0,17	
20	5,0	0,0026		109	4,7	-0,27	
23	5,1	0,10		110	4,2	-0,76	
24	5,0	0,014		113	4,8	-0,21	
25	4,4	-0,63		114	5,3	0,32	
28	4,4	-0,56		115	4,7	-0,28	
31	4,9	-0,071		116	4,4	-0,57	
32	5,0	0,039		118	4,9	-0,12	
33	4,8	-0,21		119	5,1	0,092	
34	5,2	0,20		120	4,8	-0,19	
36	4,9	-0,084					
37	5,3	0,26					
38	4,5	-0,48					
40	4,6	-0,38					
42	4,8	-0,22					
44	4,8	-0,18					
45	5,0	0,048					
48	4,7	-0,29					
49	5,1	0,11					
54	4,8	-0,21					
56	5,1	0,12					
57	4,8	-0,19					
58	5,0	0,046					
61	4,9	-0,070					
63	5,0	-0,0026					
64	5,0	0,034					
65	5,8	0,79					
70	0,0000041	-5,0	Outlier				
71	5,0	0,011					
73	5,0	0,040					
75	5,1	0,071					
76	4,6	-0,38					
80	4,8	-0,24					
84	5,0	0,026					
87	4,5	-0,46					
88	5,3	0,28					
89	5,2	0,21					
90	4,4	-0,54					
91	5,1	0,061					

Consenus statistics	
Consensus median, pg/g	5,0
Median all values pg/g	5,0
Consensus mean, pg/g	4,9
Standard deviation, pg/g	0,34
Relative standard deviation, %	6,9
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0
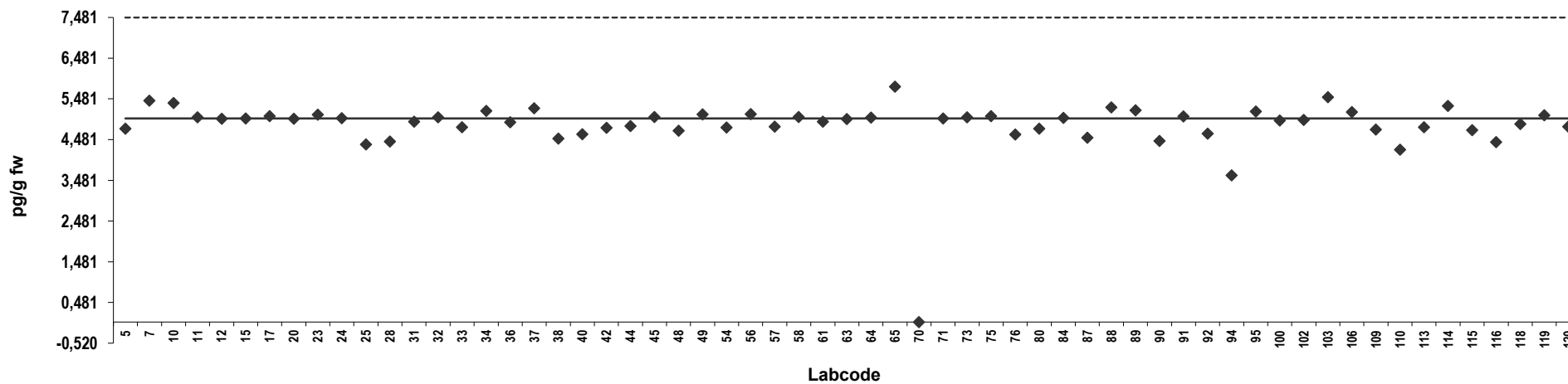
2,3,4,6,7,8 HxCDF

Z-score: 2,3,4,6,7,8 HxCDF
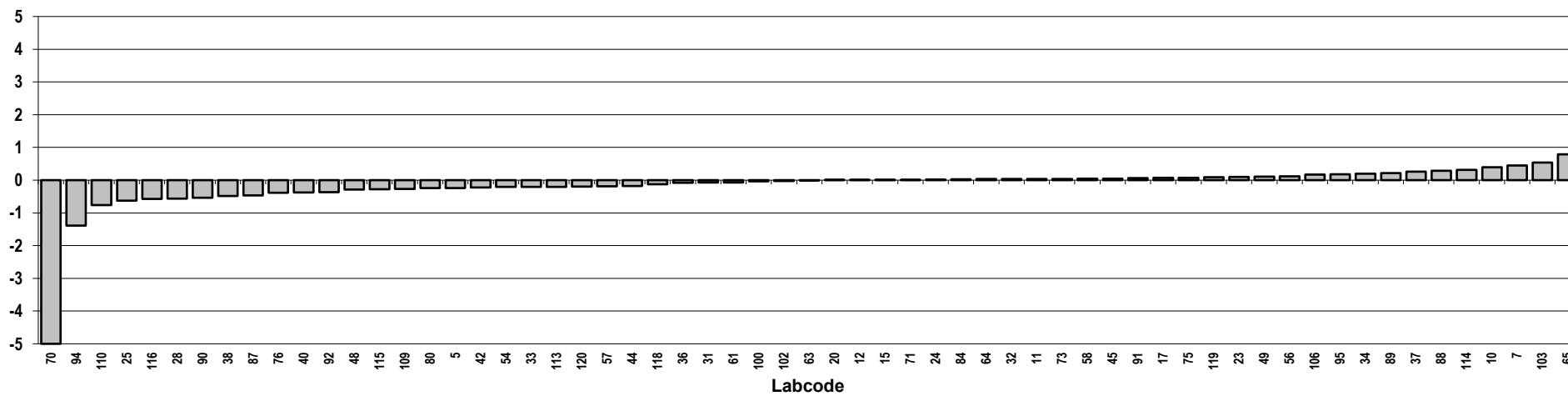
Analyte solution
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	4,9	-0,10		92	4,8	-0,18	
7	5,3	0,26		94	4,8	-0,20	
10	5,7	0,69		95	5,3	0,32	
11	5,3	0,33		100	5,1	0,049	
12	5,0	0,012		102	5,0	-0,00050	
15	5,0	-0,00050		103	5,8	0,82	
17	5,0	-0,044		106	5,2	0,17	
20	5,1	0,11		109	4,7	-0,28	
23	5,0	0,019		110	4,6	-0,40	
24	5,0	0,00050		113	5,0	0,047	
25	4,9	-0,070		114	5,3	0,33	
28	4,5	-0,55		115	5,0	-0,042	
31	5,0	-0,036		116	4,7	-0,31	
32	5,6	0,64		118	5,4	0,40	
33	5,0	0,047		119	4,8	-0,15	
34	5,4	0,38		120	4,7	-0,29	
36	4,9	-0,088					
37	5,1	0,14					
38	4,7	-0,34					
40	4,6	-0,41					
42	4,5	-0,51					
44	5,0	0,0095					
45	5,0	-0,0044					
48	5,0	-0,00050					
49	5,3	0,31					
54	5,2	0,19					
56	5,1	0,10					
57	5,0	-0,043					
58	5,6	0,62					
61	5,1	0,059					
63	5,1	0,092					
64	5,0	0,042					
65	5,4	0,38					
70	0,0000051	-5,0	Outlier				
71	5,0	-0,014					
73	5,1	0,069					
75	5,0	0,029					
76	4,9	-0,13					
80	5,0	-0,040					
84	4,9	-0,083					
87	4,7	-0,33					
88	4,6	-0,35					
89	4,5	-0,50					
90	4,7	-0,27					
91	5,1	0,049					

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	0,29
Relative standard deviation, %	5,8
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0

1,2,3,7,8,9 HxCDF
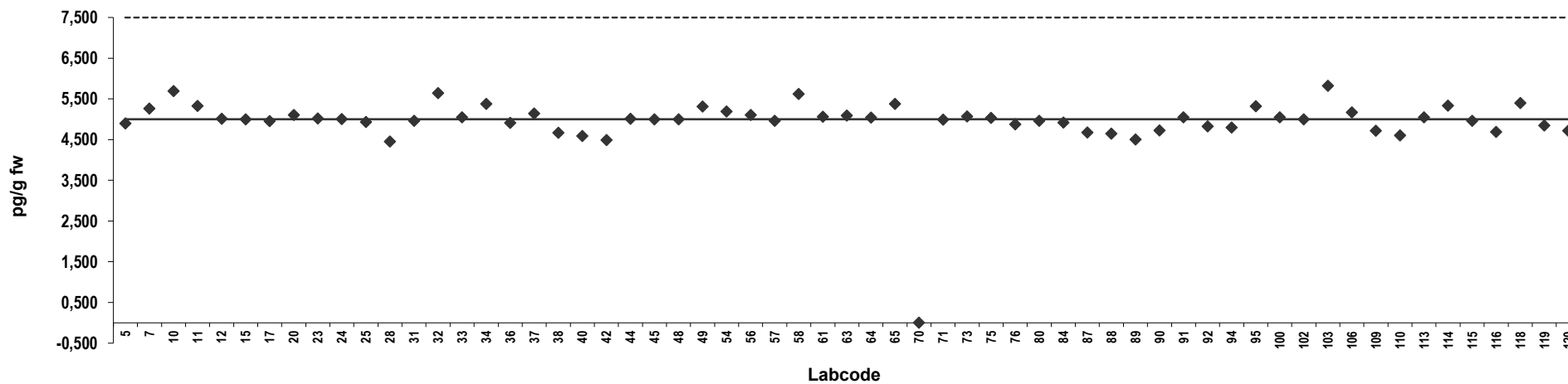
Z-score: 1,2,3,7,8,9 HxCDF
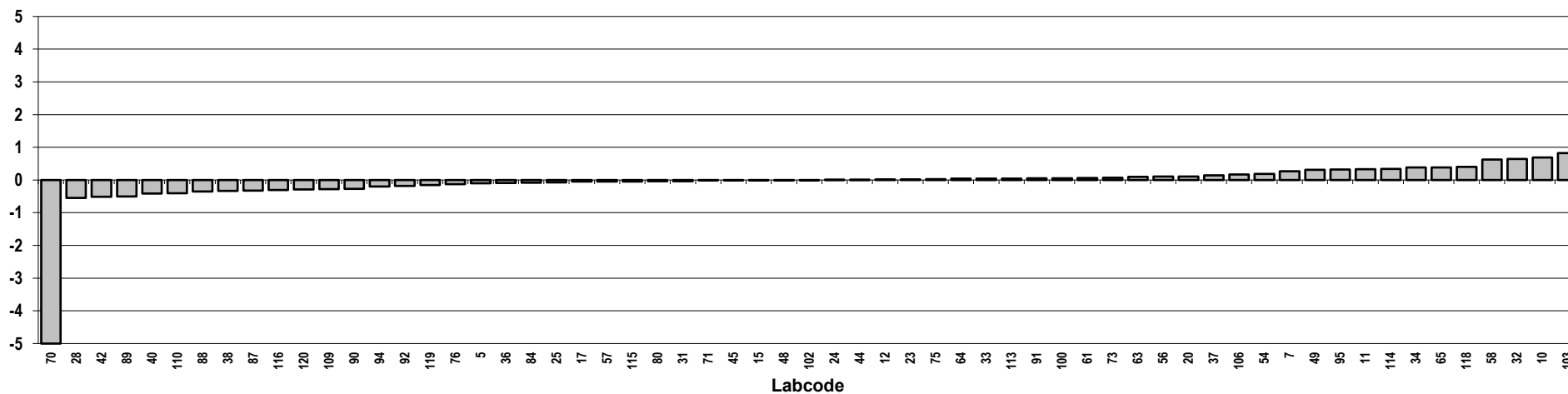
Analyte solution
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	4,7	-0,16		92	4,8	-0,063	
7	5,1	0,14		94	6,2	1,3	
10	4,9	-0,010		95	5,4	0,49	
11	4,8	-0,16		100	4,9	0,031	
12	5,0	0,12		102	4,9	-0,051	
15	4,9	-0,010		103	5,4	0,50	
17	4,8	-0,082		106	5,2	0,26	
20	5,1	0,21		109	4,7	-0,23	
23	5,5	0,55		110	4,0	-0,96	
24	5,0	0,10		113	5,0	0,13	
25	4,8	-0,11		114	5,0	0,12	
28	4,6	-0,30		115	4,7	-0,22	
31	5,4	0,52		116	5,2	0,26	
32	5,5	0,61		118	5,4	0,50	
33	5,0	0,13		119	5,2	0,34	
34	5,0	0,11		120	4,8	-0,16	
36	4,6	-0,34					
37	5,1	0,16					
38	4,7	-0,18					
40	4,1	-0,85					
42	4,9	0,00					
44	4,9	-0,051					
45	5,0	0,084					
48	4,7	-0,21					
49	4,7	-0,25					
54	4,8	-0,13					
56	5,7	0,84					
57	4,6	-0,28					
58	5,4	0,52					
61	9,7	4,8	Outlier				
63	4,8	-0,089					
64	5,2	0,30					
65	5,7	0,85					
70	0,0000042	-5,0	Outlier				
71	5,1	0,16					
73	4,9	-0,020					
75	5,0	0,081					
76	4,9	-0,041					
80	4,9	-0,020					
84	4,9	-0,0085					
87	4,5	-0,38					
88	5,0	0,079					
89	4,9	-0,010					
90	4,4	-0,51					
91	5,0	0,13					

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	0,37
Relative standard deviation, %	7,4
No. of values reported	61
No. of values removed	2
No. of reported non-detects	0

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

Z-score: 1,2,3,4,6,7,8 HpCDF
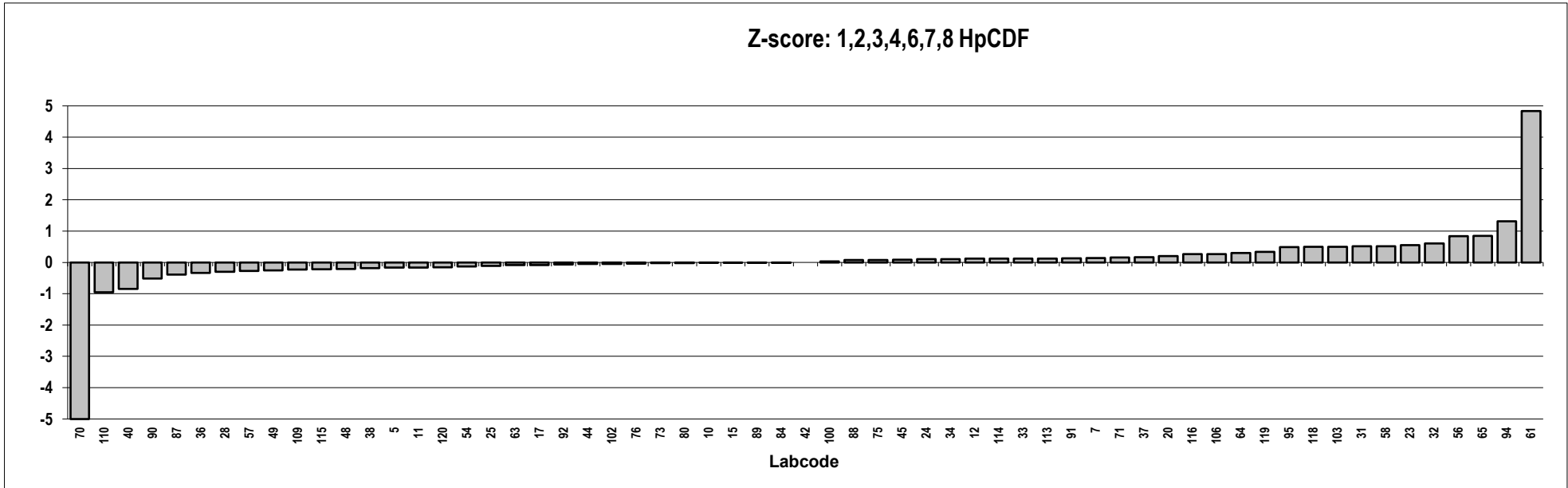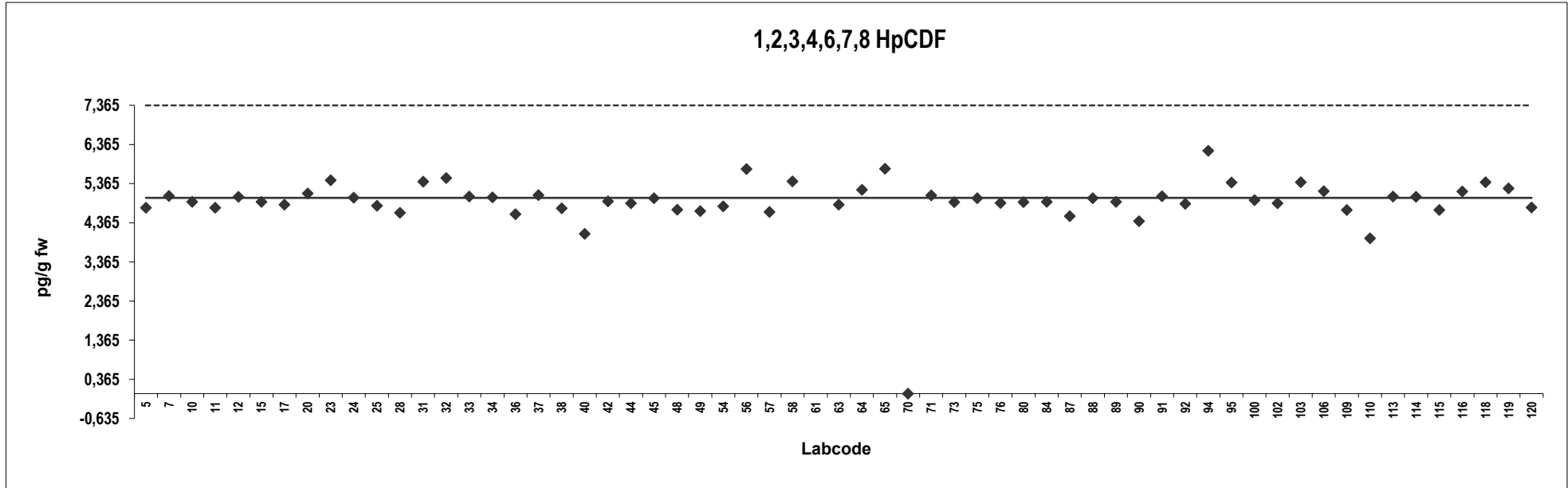
Analyte solution
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	4,7	-0,28		92	4,8	-0,13	
7	5,2	0,23		94	4,2	-0,77	
10	4,7	-0,23		95	4,9	-0,075	
11	5,3	0,30		100	5,0	0,025	
12	5,0	0,028		102	4,7	-0,28	
15	5,0	0,036		103	5,3	0,34	
17	5,4	0,43		106	5,1	0,086	
20	5,0	0,053		109	4,6	-0,36	
23	5,0	0,076		110	4,1	-0,87	
24	5,0	0,039		113	5,0	0,00	
25	5,0	0,0053		114	5,0	0,068	
28	4,1	-0,86		115	4,8	-0,16	
31	4,8	-0,18		116	4,5	-0,51	
32	5,4	0,43		118	5,3	0,37	
33	5,0	0,00		119	5,0	0,0084	
34	4,8	-0,14		120	4,5	-0,46	
36	5,0	0,086					
37	5,3	0,33					
38	4,6	-0,39					
40	4,6	-0,39					
42	4,5	-0,47					
44	5,0	-0,0047					
45	5,0	0,034					
48	4,8	-0,17					
49	4,8	-0,17					
54	5,3	0,32					
56	6,5	1,5					
57	4,7	-0,28					
58	4,7	-0,22					
61	11	6,5	Outlier				
63	5,1	0,12					
64	5,1	0,11					
65	5,3	0,29					
70	0,0000043	-5,0	Outlier				
71	5,0	0,037					
73	5,0	-0,015					
75	4,9	-0,075					
76	4,7	-0,25					
80	5,2	0,19					
84	5,0	0,032					
87	4,5	-0,45					
88	4,7	-0,25					
89	4,6	-0,37					
90	4,3	-0,63					
91	5,0	0,015					

Consensus statistics

Consensus median, pg/g	5,0
Median all values pg/g	5,0
Consensus mean, pg/g	4,9
Standard deviation, pg/g	0,36
Relative standard deviation, %	7,4
No. of values reported	61
No. of values removed	2
No. of reported non-detects	0

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

Z-score: 1,2,3,4,7,8,9 HpCDF
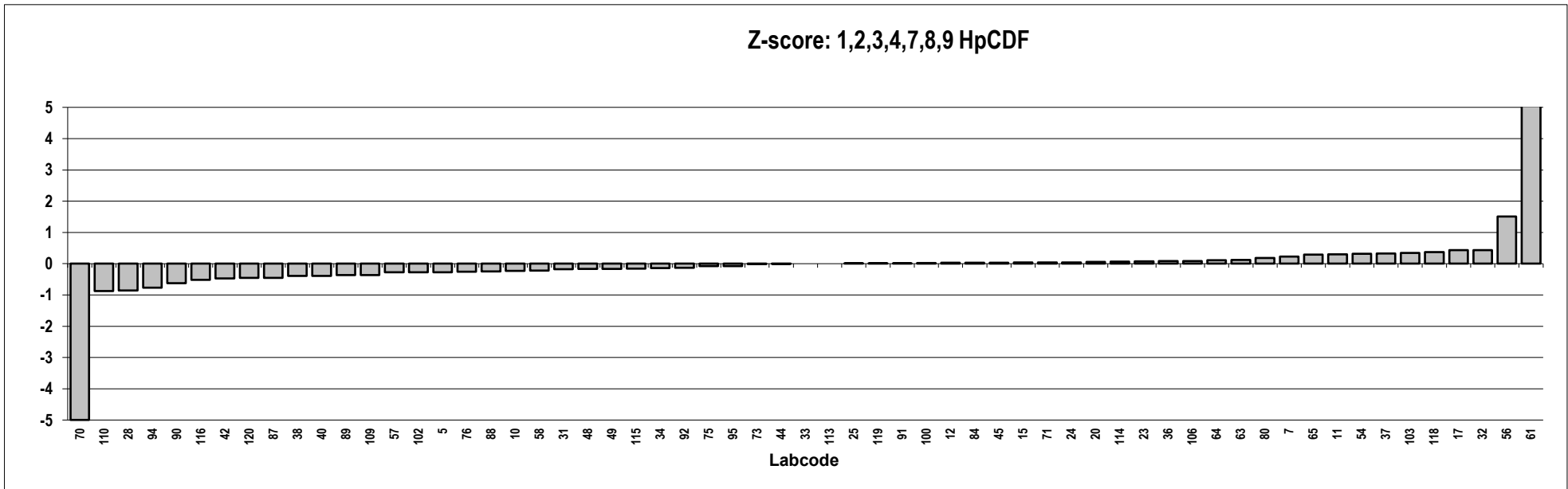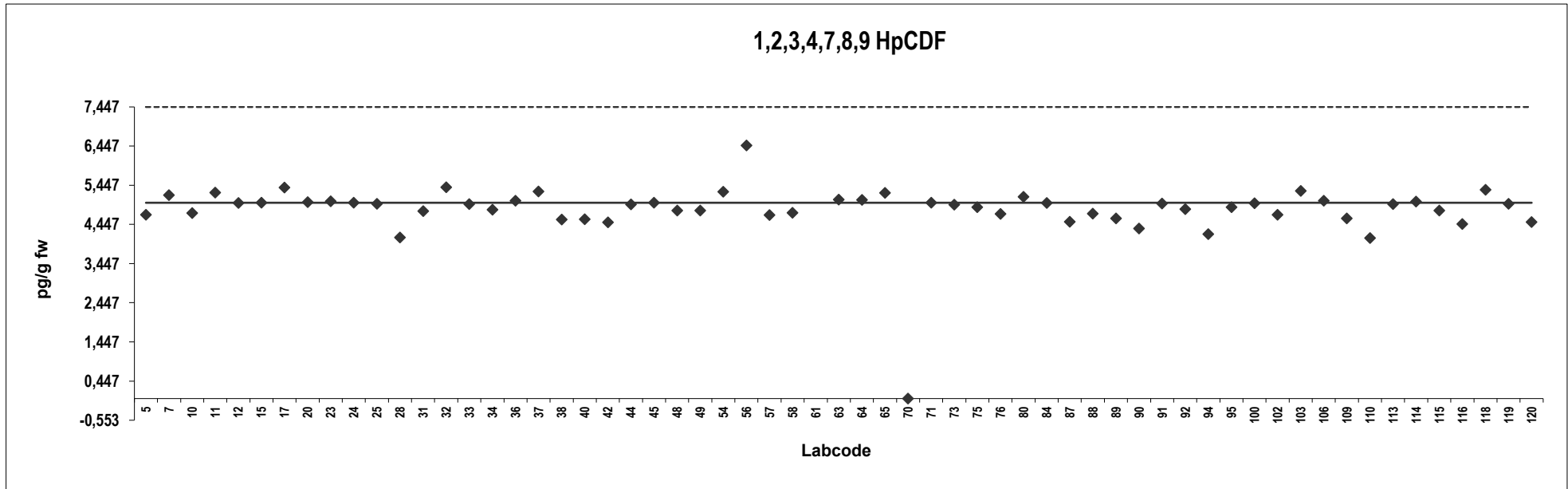
Analyte solution
Congener: OCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	11	0,37		92	9,3	-0,35	
7	8,7	-0,61		94	8,4	-0,78	
10	9,8	-0,091		95	10	0,020	
11	11	0,42		100	10	0,12	
12	10	0,019		102	9,6	-0,18	
15	10	0,020		103	11	0,36	
17	10	0,13		106	10	0,19	
20	10	-0,0012		109	9,2	-0,36	
23	10	0,17		110	8,4	-0,81	
24	10	0,021		113	9,6	-0,20	
25	9,4	-0,29		114	11	0,29	
28	8,3	-0,82		115	9,7	-0,13	
31	10	0,0077		116	9,5	-0,23	
32	12	0,89		118	11	0,64	
33	9,6	-0,20		119	9,8	-0,06	
34	10	0,22		120	9,6	-0,16	
36	8,5	-0,76					
37	10	0,10					
38	9,0	-0,50					
40	8,7	-0,65					
42	8,9	-0,53					
44	9,9	-0,011					
45	10	0,039					
48	9,9	-0,031					
49	10	0,11					
54	9,5	-0,24					
56	10	0,19					
57	9,4	-0,26					
58	11	0,54					
61	12	0,86					
63	10	0,00050					
64	10	0,072					
65	11	0,49					
70	0,0000087	-5,0	Outlier				
71	10	0,020					
73	10	-0,00050					
75	10	0,070					
76	9,1	-0,42					
80	10	0,10					
84	10	0,11					
87	9,5	-0,25					
88	9,1	-0,46					
89	9,5	-0,23					
90	8,1	-0,94					
91	10	0,020					

Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	9,8
Standard deviation, pg/g	0,77
Relative standard deviation, %	7,9
No. of values reported	61
No. of values removed	1
No. of reported non-detects	0

OCDF

Z-score: OCDF
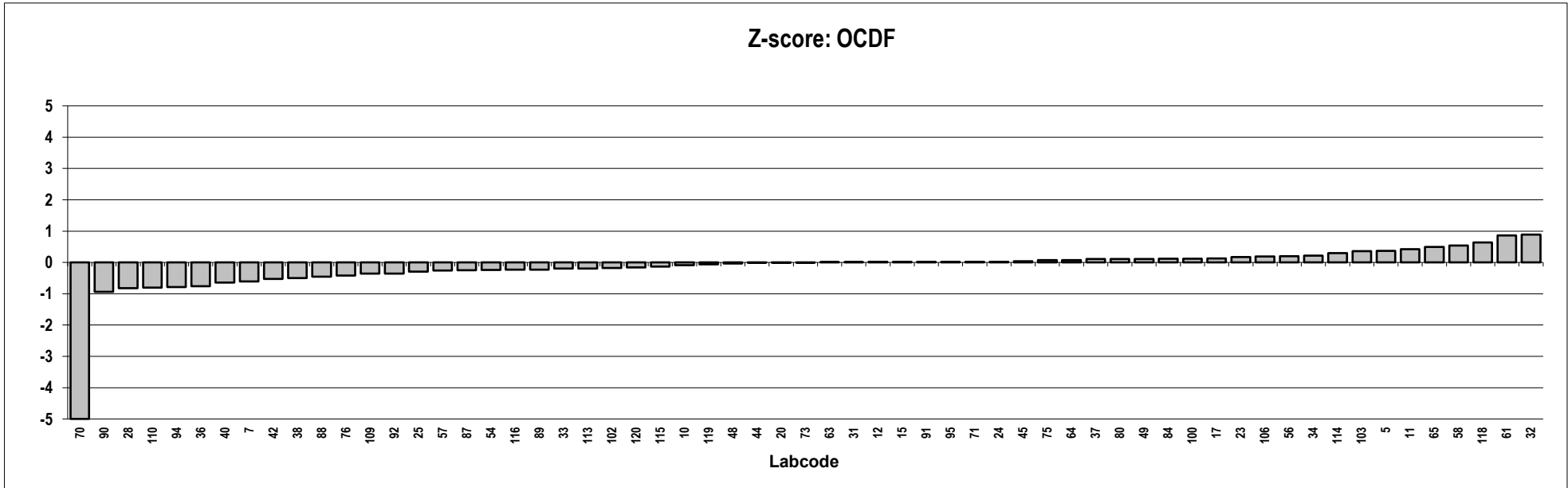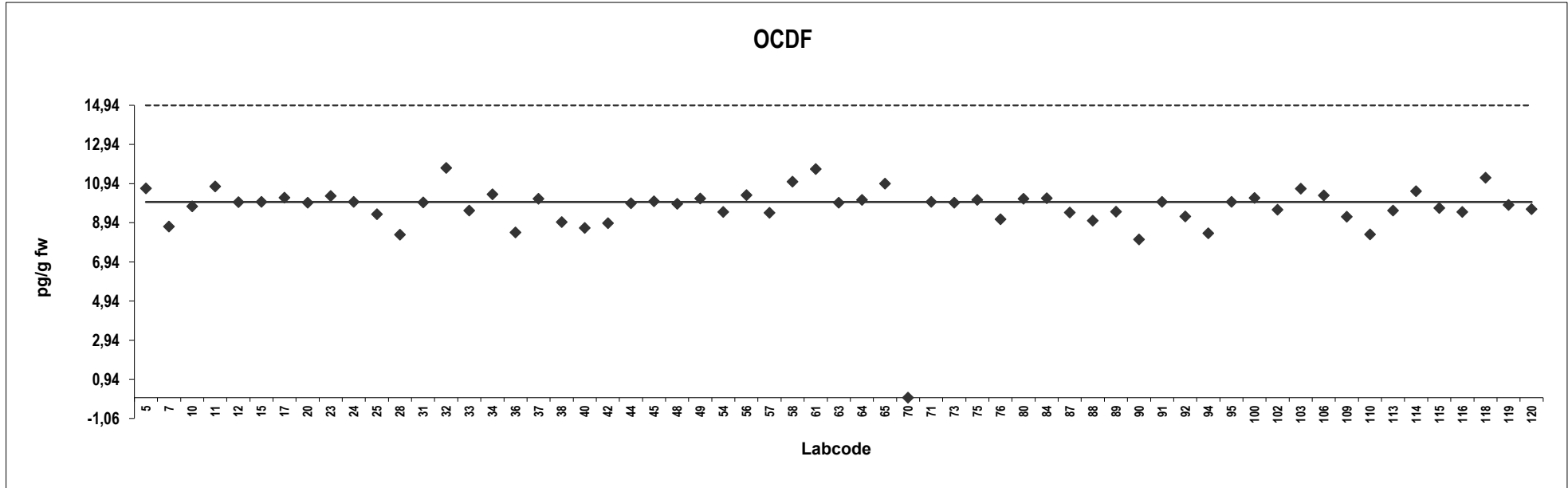
Analyte solution
Congener: PCB 77

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	8,1	-0,94		91	11	0,35	
7	9,1	-0,43		92	9,0	-0,51	
10	10	0,00		94	9,8	-0,10	
11	10	0,15		95	8,9	-0,54	
12	10	0,00060		100	10	0,20	
15	9,9	-0,045		102	11	0,40	
17	11	0,35		103	9,0	-0,49	
20	10	0,085		106	9,4	-0,28	
23	9,6	-0,19		109	10	0,034	
24	10	0,016		110	8,7	-0,65	
25	9,7	-0,13		113	9,9	-0,060	
28	10	0,10		114	11	0,37	
31	11	0,49		115	11	0,63	
32	9,3	-0,35		116	9,4	-0,31	
33	9,9	-0,060		118	9,7	-0,16	
34	10	0,13		119	9,6	-0,21	
36	7,8	-1,1		120	9,6	-0,19	
37	10	0,035					
38	9,7	-0,13					
40	10	0,00					
42	11	0,25					
44	9,2	-0,39					
45	10	0,061					
48	9,8	-0,10					
49	9,9	-0,057					
54	11	0,74					
56	11	0,42					
57	9,6	-0,19					
58	9,9	-0,055					
61	10	0,0050					
63	9,3	-0,36					
64	10	0,24					
65	10	0,24					
70	0,0095	-5,0	Outlier				
71	10	0,030					
73	10	0,010					
75	10	0,050					
76	11	0,26					
77	9,9	-0,045					
80	10	0,11					
84	10	-0,013					
87	10	0,030					
88	10	0,0060					
89	100	45	Outlier				
90	9,7	-0,15					

Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	9,9
Standard deviation, pg/g	0,66
Relative standard deviation, %	6,7
No. of values reported	62
No. of values removed	2
No. of reported non-detects	0

PCB 77

Z-score: PCB 77
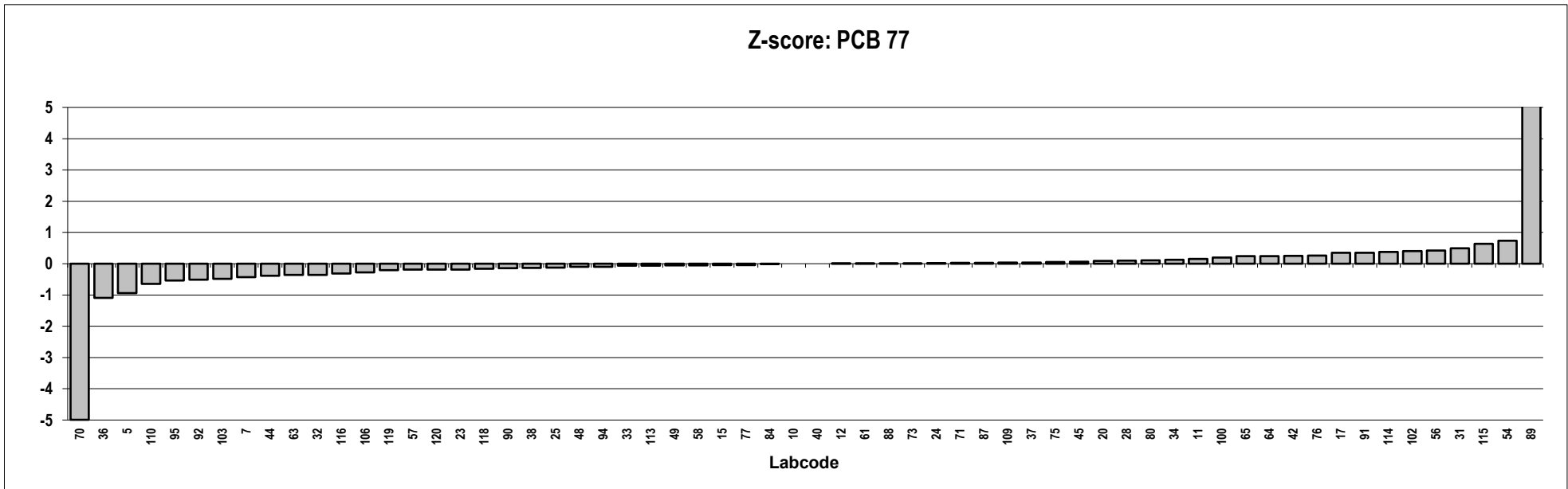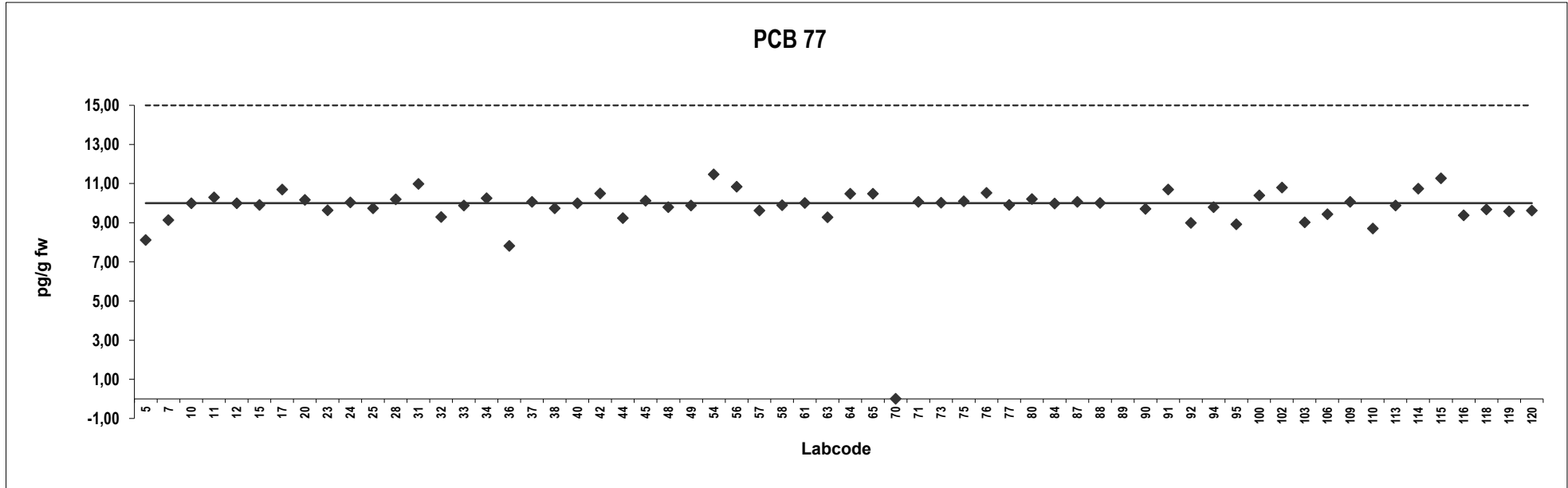
Analyte solution

Congener: PCB 126

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	9,4	-0,31		91	9,9	-0,040	
7	9,1	-0,44		92	8,7	-0,62	
10	11	0,31		94	10	0,0049	
11	10	0,0049		95	8,8	-0,60	
12	10	0,00		100	10	0,11	
15	10	0,21		102	10	0,055	
17	10	0,080		103	9,7	-0,16	
20	10	0,19		106	9,4	-0,30	
23	10	0,21		109	10	0,015	
24	11	0,33		110	8,2	-0,90	
25	11	0,51		113	9,9	-0,046	
28	11	0,46		114	10	0,013	
31	10	-0,0049		115	9,9	-0,070	
32	9,6	-0,18		116	10	0,027	
33	9,9	-0,046		118	9,4	-0,31	
34	9,9	-0,066		119	9,6	-0,19	
36	8,2	-0,91		120	9,6	-0,20	
37	9,5	-0,25					
38	9,8	-0,11					
40	9,9	-0,045					
42	10	0,21					
44	9,1	-0,46					
45	10	0,038					
48	10	0,0049					
49	8,7	-0,64					
54	12	0,79					
56	10	0,19					
57	9,6	-0,18					
58	9,7	-0,17					
61	10	0,17					
63	9,2	-0,39					
64	11	0,52					
65	11	0,66					
70	0,0098	-5,0	Outlier				
71	10	-0,0053					
73	10	0,015					
75	11	0,26					
76	10	0,051					
77	9,9	-0,035					
80	10	0,12					
84	9,0	-0,50					
87	9,7	-0,15					
88	10	0,080					
89	11	0,52					
90	10	0,0016					

Consensus statistics	
Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	9,9
Standard deviation, pg/g	0,67
Relative standard deviation, %	6,7
No. of values reported	62
No. of values removed	1
No. of reported non-detects	0

PCB 126

Z-score: PCB 126
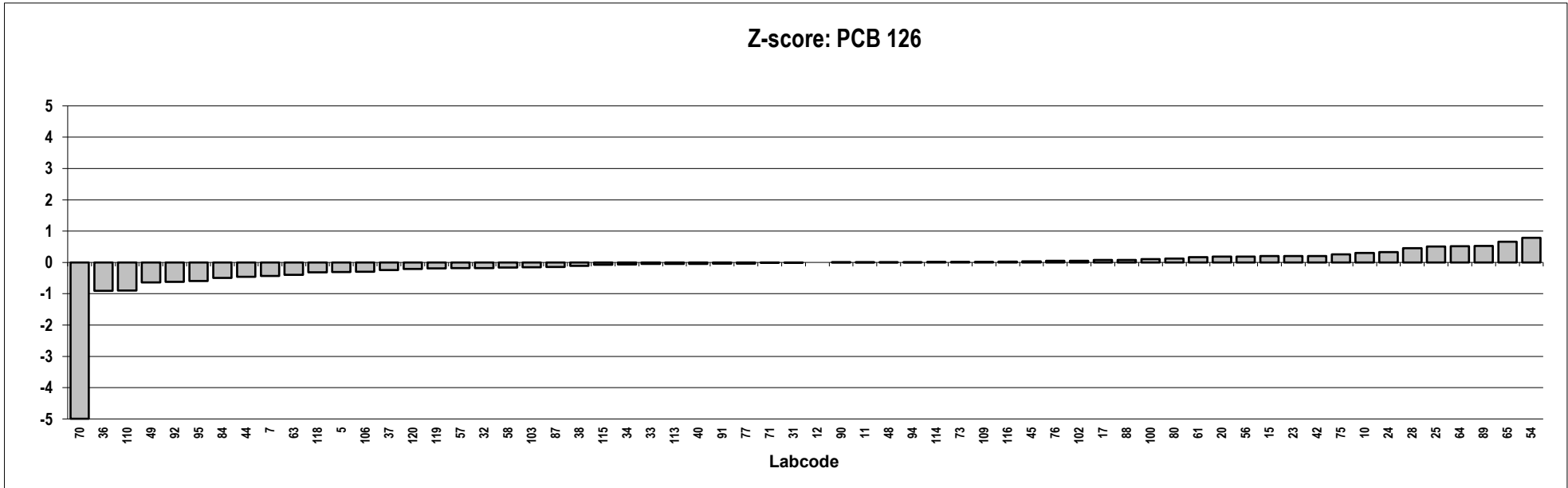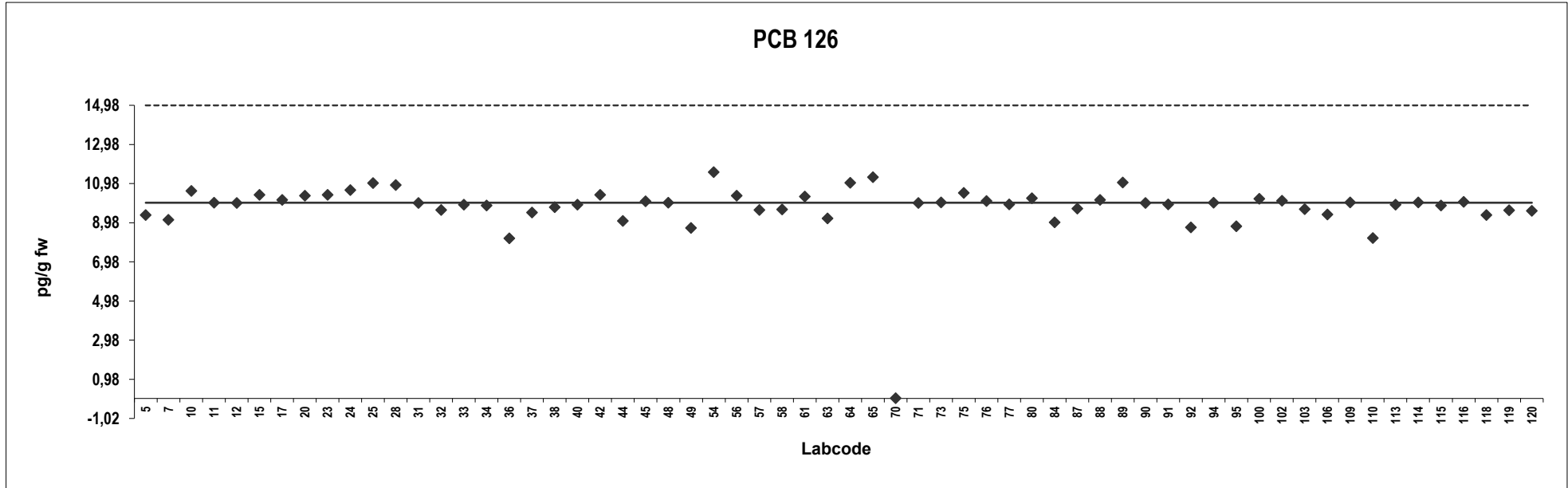
Analyte solution
Congener: PCB 169

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	10	0,27		91	10	0,21	
7	9,0	-0,45		92	9,1	-0,41	
10	10	0,11		94	10	0,061	
11	10	0,11		95	9,1	-0,39	
12	10	0,051		100	9,8	-0,056	
15	10	0,11		102	10	0,11	
17	10	0,26		103	8,8	-0,55	
20	9,6	-0,16		106	8,8	-0,57	
23	9,3	-0,27		109	10	0,10	
24	10	0,17		110	7,8	-1,1	
25	9,0	-0,47		113	9,5	-0,22	
28	11	0,31		114	9,8	-0,033	
31	9,7	-0,075		115	9,8	-0,018	
32	9,4	-0,23		116	10	0,11	
33	9,5	-0,22		118	9,7	-0,10	
34	9,9	0,0025		119	9,5	-0,21	
36	8,3	-0,82		120	9,9	-0,0020	
37	9,6	-0,13					
38	9,5	-0,18					
40	9,7	-0,091					
42	11	0,36					
44	9,9	-0,010					
45	10	0,067					
48	10	0,061					
49	9,2	-0,34					
54	12	0,90					
56	9,5	-0,19					
57	10	0,20					
58	9,9	0,00					
61	9,7	-0,081					
63	10	0,18					
64	11	0,52					
65	9,9	-0,015					
70	0,010	-5,0	Outlier				
71	10	0,055					
73	10	0,071					
75	10	0,16					
76	11	0,54					
77	10	0,26					
80	10	0,26					
84	9,4	-0,25					
87	9,9	0,025					
88	11	0,43					
89	10	0,19					
90	9,7	-0,086					

Consenus statistics	
Consensus median, pg/g	9,9
Median all values pg/g	9,9
Consensus mean, pg/g	9,8
Standard deviation, pg/g	0,63
Relative standard deviation, %	6,4
No. of values reported	62
No. of values removed	1
No. of reported non-detects	0

PCB 169

Z-score: PCB 169
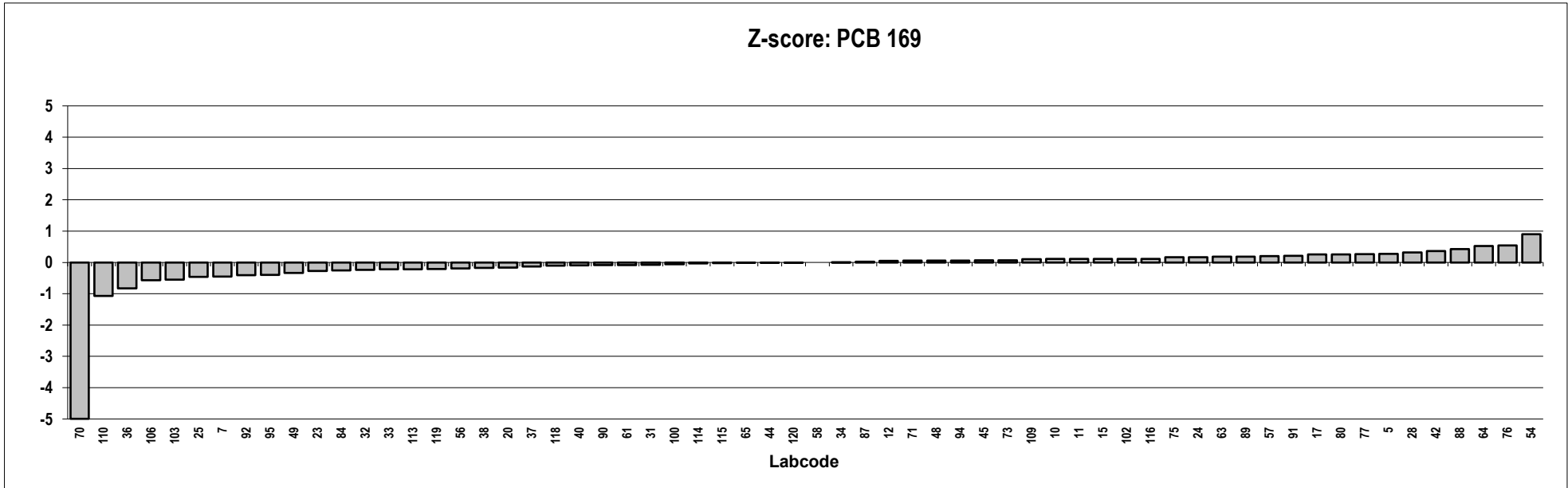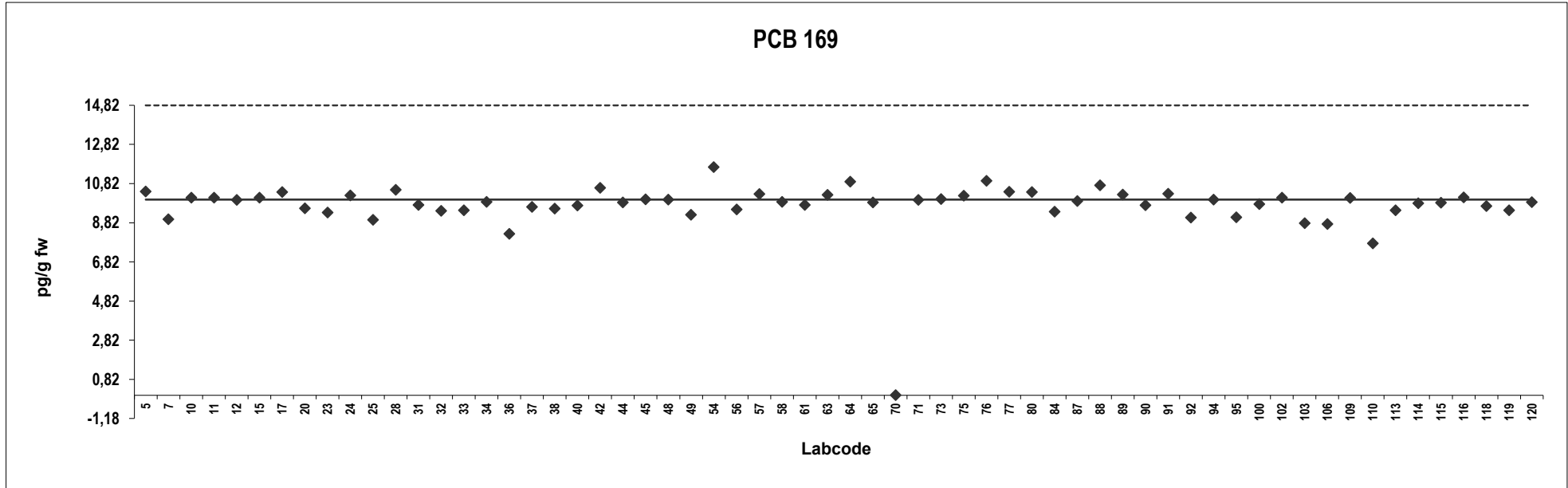
Analyte solution
Congener: PCB 81

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	8,3	-0,83		91	11	0,32	
7	9,5	-0,24		92	9,0	-0,47	
10	10	0,17		94	9,6	-0,18	
11	10	0,021		95	9,0	-0,50	
12	10	0,026		100	10	0,071	
15	9,8	-0,069		102	9,9	-0,044	
17	11	0,34		103	9,7	-0,11	
20	10	0,091		106	9,7	-0,15	
23	10	0,12		109	11	0,32	
24	10	0,0079		110	8,1	-0,95	
25	9,0	-0,49		113	9,1	-0,42	
28	10	0,12		114	10	0,15	
31	10	0,14		115	11	0,30	
32	9,9	-0,026		116	9,7	-0,11	
33	9,4	-0,30		118	9,6	-0,18	
34	9,9	-0,0059		119	9,5	-0,24	
36	8,2	-0,90		120	9,7	-0,14	
37	9,8	-0,079					
38	9,1	-0,41					
40	10	0,12					
42	11	0,42					
44	9,3	-0,32					
45	10	0,053					
48	10	0,021					
49	10	0,11					
54	11	0,67					
56	12	1,3					
57	10	0,12					
58	9,9	-0,019					
61	10	0,081					
63	10	0,071					
64	10	0,26					
65	11	0,42					
70	0,0098	-5,0	Outlier				
71	10	-0,0038					
73	10	0,091					
75	9,8	-0,079					
76	10	0,10					
77	11	0,27					
80	9,6	-0,16					
84	9,6	-0,20					
87	9,5	-0,23					
88	10	0,088					
89	10	0,00					
90	9,9	-0,014					

Consenus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	9,9
Standard deviation, pg/g	0,69
Relative standard deviation, %	6,9
No. of values reported	62
No. of values removed	1
No. of reported non-detects	0

PCB 81

Z-score: PCB 81
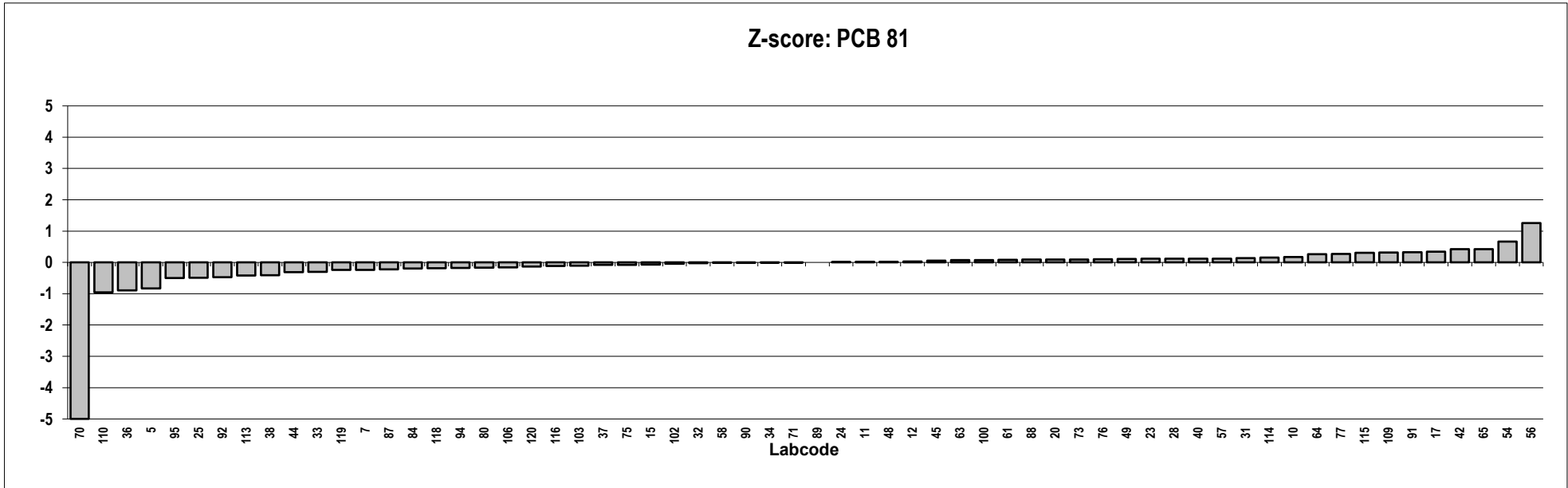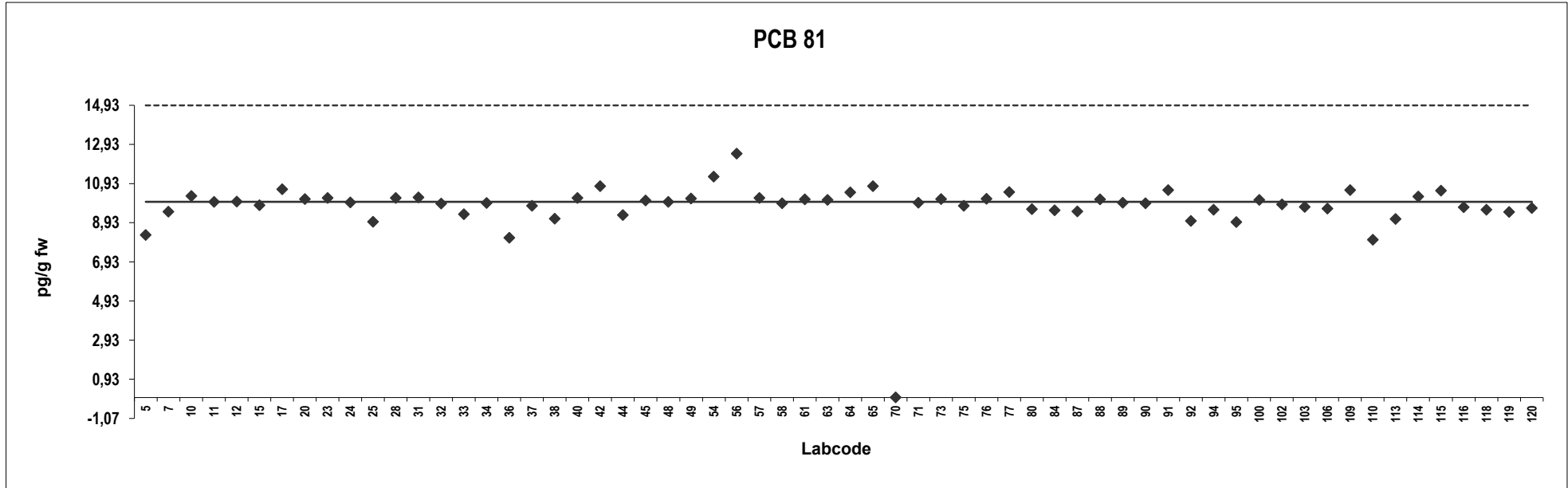
Analyte solution
Congener: PCB 105

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	102	0,11		94	98	-0,096	
7	102	0,099		95	95	-0,24	
10	94	-0,27		100	104	0,21	
11	110	0,53		102	94	-0,31	
12	98	-0,081		103	100	-0,00045	
15	98	-0,11		106	94	-0,31	
17	115	0,76		109	105	0,29	
20	104	0,20		110	97	-0,15	
23	95	-0,23		113	103	0,17	
24	104	0,21		114	99	-0,036	
25	103	0,14		115	97	-0,12	
28	106	0,31		116	96	-0,19	
31	101	0,057		118	108	0,40	
32	106	0,33		119	98	-0,10	
33	103	0,17		120	100	-0,0017	
34	100	0,00					
36	83	-0,85					
37	99	-0,034					
38	105	0,27					
40	99	-0,036					
42	86	-0,70					
44	98	-0,11					
45	100	0,019					
48	98	-0,086					
49	100	0,016					
54	106	0,31					
57	93	-0,32					
61	92	-0,36					
63	100	0,027					
64	101	0,079					
65	115	0,76					
70	0,094	-5,0	Outlier				
71	98	-0,10					
73	101	0,042					
75	98	-0,11					
76	99	-0,040					
77	104	0,23					
80	98	-0,11					
84	98	-0,071					
87	94	-0,30					
88	104	0,19					
89	122	1,1					
90	100	0,0085					
91	105	0,26					
92	103	0,14					

Consenus statistics

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	6,3
Relative standard deviation, %	6,3
No. of values reported	60
No. of values removed	1
No. of reported non-detects	0

PCB 105

Z-score: PCB 105
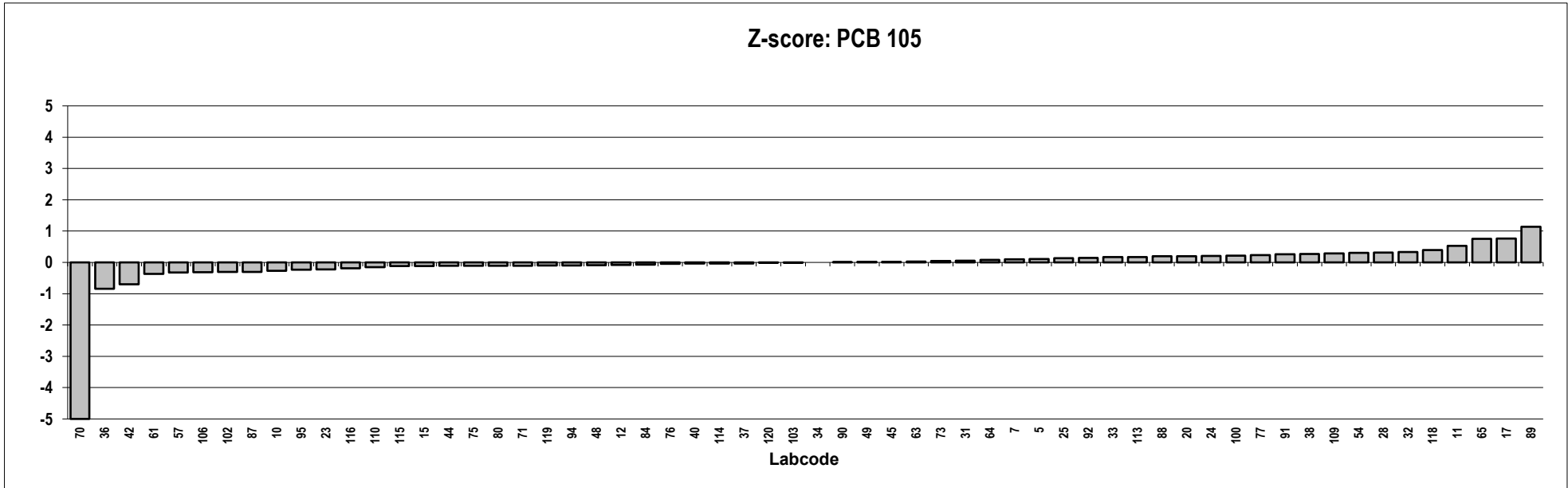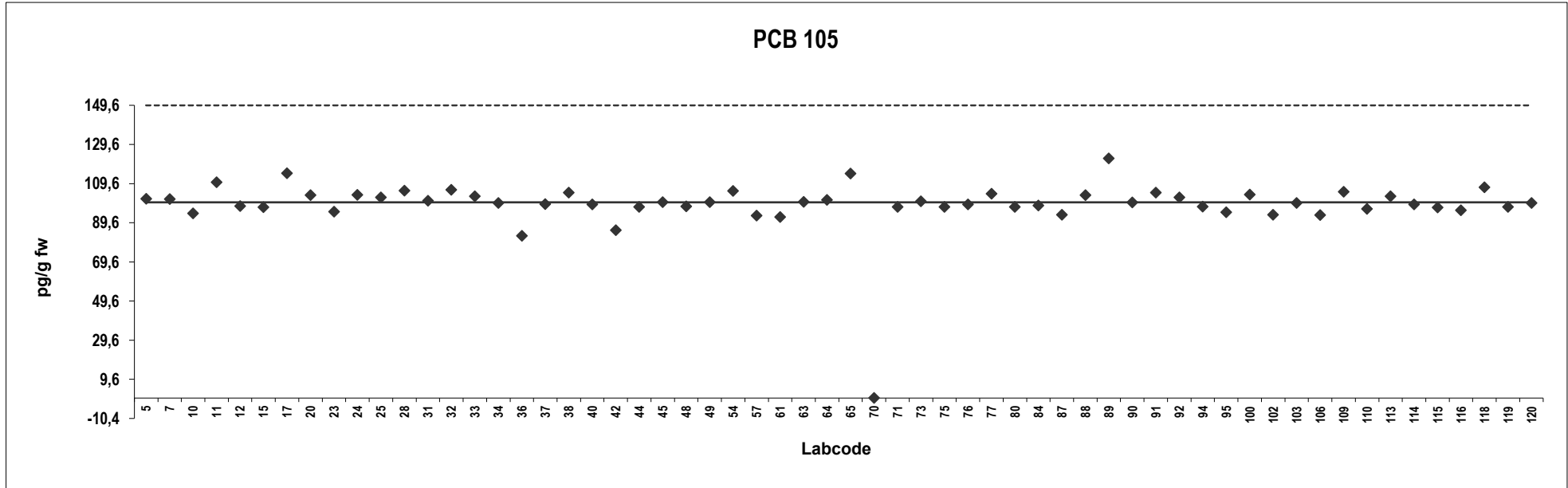
Analyte solution
Congener: PCB 114

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	97	-0,11		94	92	-0,39	
7	137	1,9		95	96	-0,17	
10	101	0,075		100	102	0,13	
11	109	0,50		102	96	-0,17	
12	100	0,028		103	97	-0,14	
15	97	-0,14		106	98	-0,095	
17	115	0,79		109	102	0,12	
20	97	-0,14		110	98	-0,10	
23	95	-0,23		113	96	-0,16	
24	103	0,16		114	98	-0,075	
25	100	0,00		115	102	0,10	
28	113	0,68		116	98	-0,088	
31	100	0,043		118	105	0,27	
32	117	0,86		119	98	-0,092	
33	96	-0,16		120	100	0,0049	
34	100	0,025					
36	86	-0,67					
37	98	-0,075					
38	95	-0,22					
40	101	0,075					
42	88	-0,60					
44	97	-0,13					
45	100	0,029					
48	99	-0,025					
49	102	0,14					
54	107	0,40					
57	93	-0,32					
61	88	-0,58					
63	100	0,023					
64	102	0,15					
65	116	0,81					
70	0,096	-5,0	Outlier				
71	98	-0,062					
73	100	0,036					
75	96	-0,16					
76	106	0,35					
77	100	0,030					
80	105	0,26					
84	101	0,061					
87	98	-0,086					
88	98	-0,083					
89	105	0,30					
90	95	-0,24					
91	96	-0,20					
92	101	0,095					

Consenus statistics	
Consensus median, pg/g	100
Median all values pg/g	99
Consensus mean, pg/g	100
Standard deviation, pg/g	7,7
Relative standard deviation, %	7,6
No. of values reported	60
No. of values removed	1
No. of reported non-detects	0

PCB 114

Z-score: PCB 114
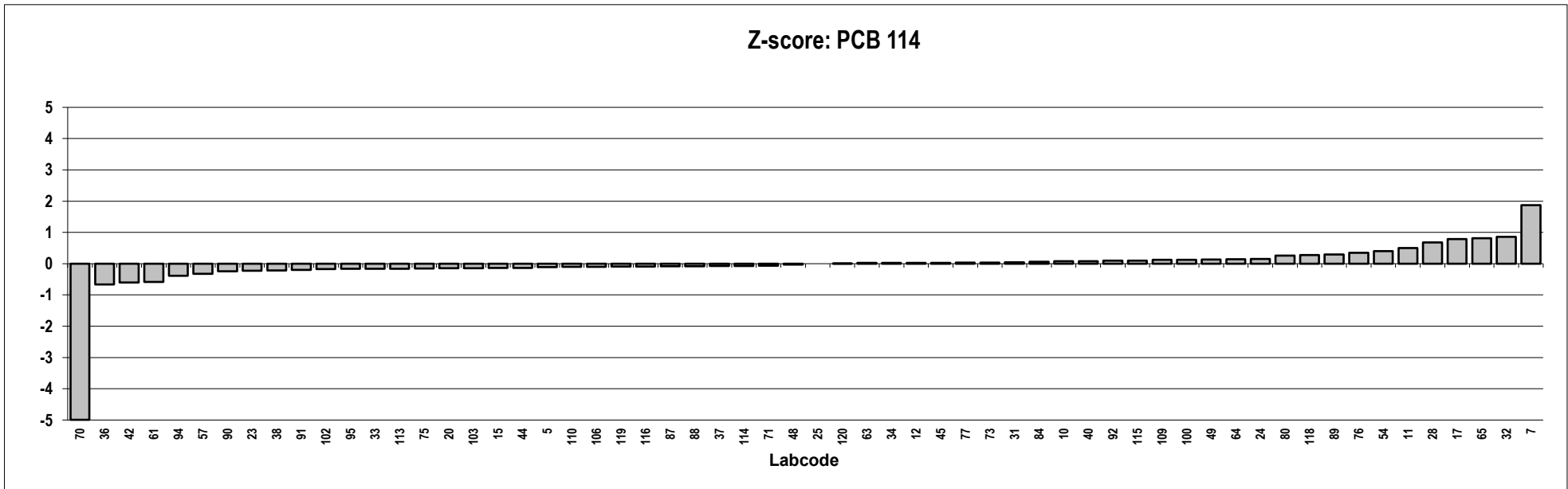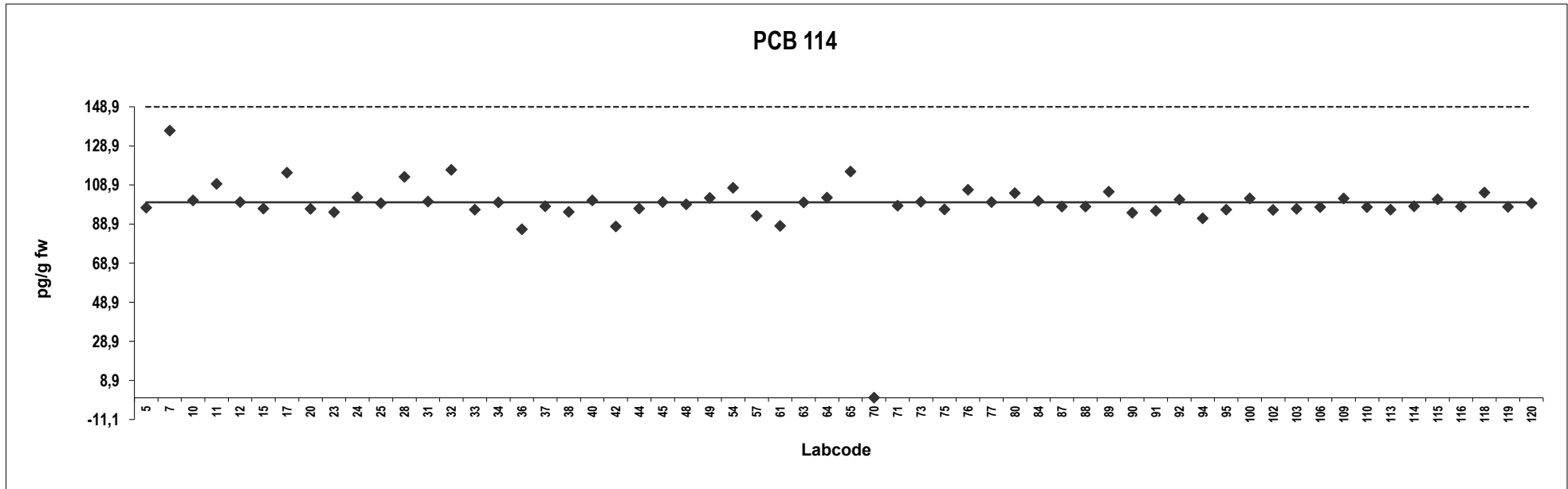
Analyte solution
Congener: PCB 118

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	107	0,28		94	101	-0,0020	
7	101	-0,0020		95	97	-0,20	
10	97	-0,18		100	105	0,21	
11	111	0,50		102	96	-0,25	
12	98	-0,14		103	97	-0,21	
15	101	0,0079		106	93	-0,41	
17	111	0,49		109	92	-0,43	
20	101	0,032		110	99	-0,10	
23	102	0,058		113	103	0,13	
24	104	0,14		114	120	0,95	
25	106	0,27		115	101	0,00040	
28	112	0,55		116	102	0,048	
31	99	-0,089		118	105	0,19	
32	109	0,38		119	99	-0,10	
33	103	0,13		120	100	-0,058	
34	99	-0,11					
36	80	-1,0					
37	100	-0,057					
38	101	0,018					
40	100	-0,042					
42	83	-0,87					
44	98	-0,16					
45	100	-0,036					
48	100	-0,042					
49	96	-0,22					
54	101	0,00					
57	91	-0,50					
61	86	-0,73					
63	99	-0,11					
64	101	0,029					
65	115	0,68					
70	0,096	-5,0	Outlier				
71	101	-0,010					
73	100	-0,038					
75	102	0,058					
76	108	0,36					
77	105	0,20					
80	104	0,16					
84	102	0,059					
87	92	-0,43					
88	103	0,10					
89	104	0,16					
90	95	-0,27					
91	101	0,0079					
92	104	0,14					

Consensus statistics

Consensus median, pg/g	101
Median all values pg/g	101
Consensus mean, pg/g	101
Standard deviation, pg/g	6,7
Relative standard deviation, %	6,7
No. of values reported	60
No. of values removed	1
No. of reported non-detects	0

PCB 118

Z-score: PCB 118
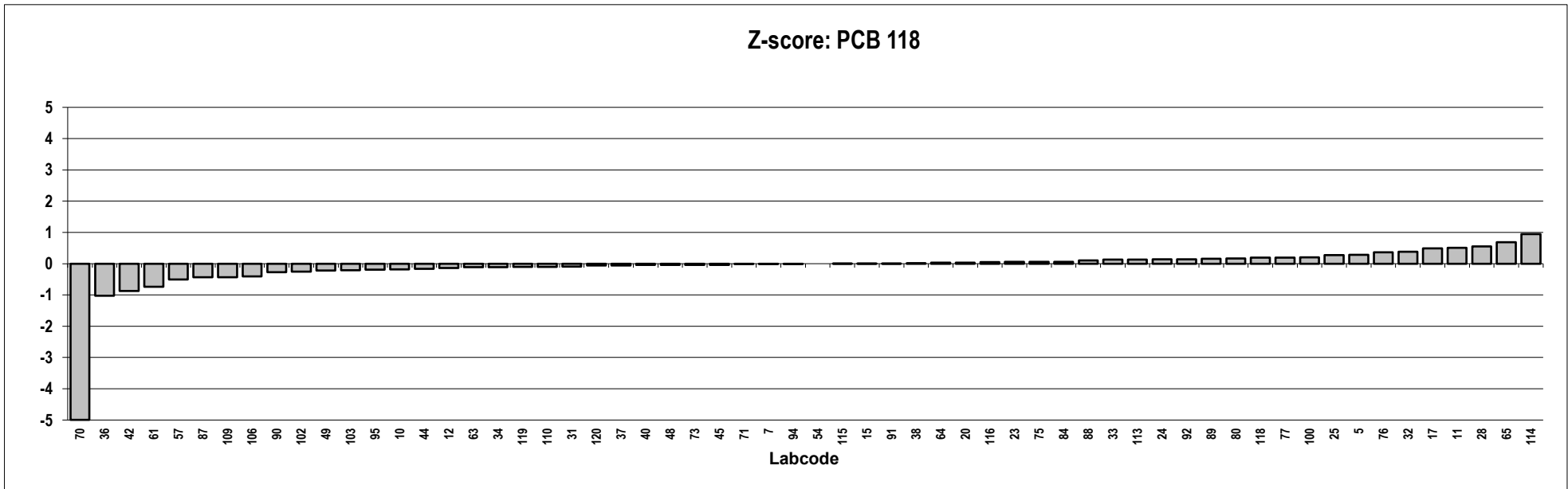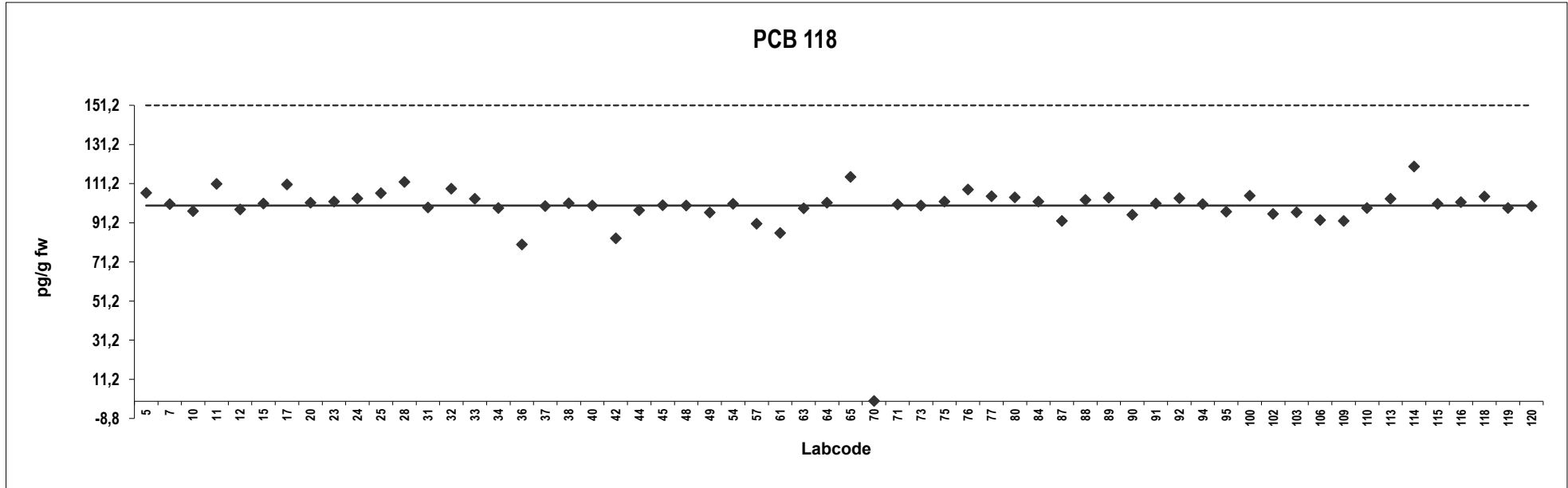
Analyte solution
Congener: PCB 123

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	103	0,11		94	97	-0,21	
7	114	0,62		95	96	-0,28	
10	100	-0,059		100	105	0,19	
11	111	0,47		102	101	-0,0098	
12	100	-0,062		103	104	0,14	
15	101	-0,0098		106	101	-0,035	
17	113	0,59		109	104	0,13	
20	102	0,050		110	98	-0,14	
23	96	-0,24		113	102	0,034	
24	102	0,054		114	110	0,43	
25	111	0,48		115	101	0,00	
28	120	0,93		116	106	0,23	
31	103	0,086		118	106	0,25	
32	107	0,26		119	101	-0,030	
33	102	0,030		120	99	-0,098	
34	99	-0,089					
36	79	-1,1					
37	100	-0,039					
38	105	0,16					
40	97	-0,21					
42	88	-0,66					
44	99	-0,092					
45	100	-0,050					
48	101	-0,0098					
49	99	-0,10					
54	106	0,22					
57	95	-0,28					
61	94	-0,38					
63	97	-0,19					
64	104	0,13					
65	115	0,66					
70	0,10	-5,0	Outlier				
71	100	-0,054					
73	100	-0,074					
75	102	0,040					
76	103	0,11					
77	105	0,16					
80	106	0,23					
84	99	-0,093					
87	93	-0,42					
88	102	0,018					
89	104	0,16					
90	98	-0,18					
91	101	-0,0098					
92	102	0,050					

Consenus statistics	
Consensus median, pg/g	101
Median all values pg/g	101
Consensus mean, pg/g	102
Standard deviation, pg/g	6,2
Relative standard deviation, %	6,1
No. of values reported	60
No. of values removed	1
No. of reported non-detects	0

PCB 123

Z-score: PCB 123
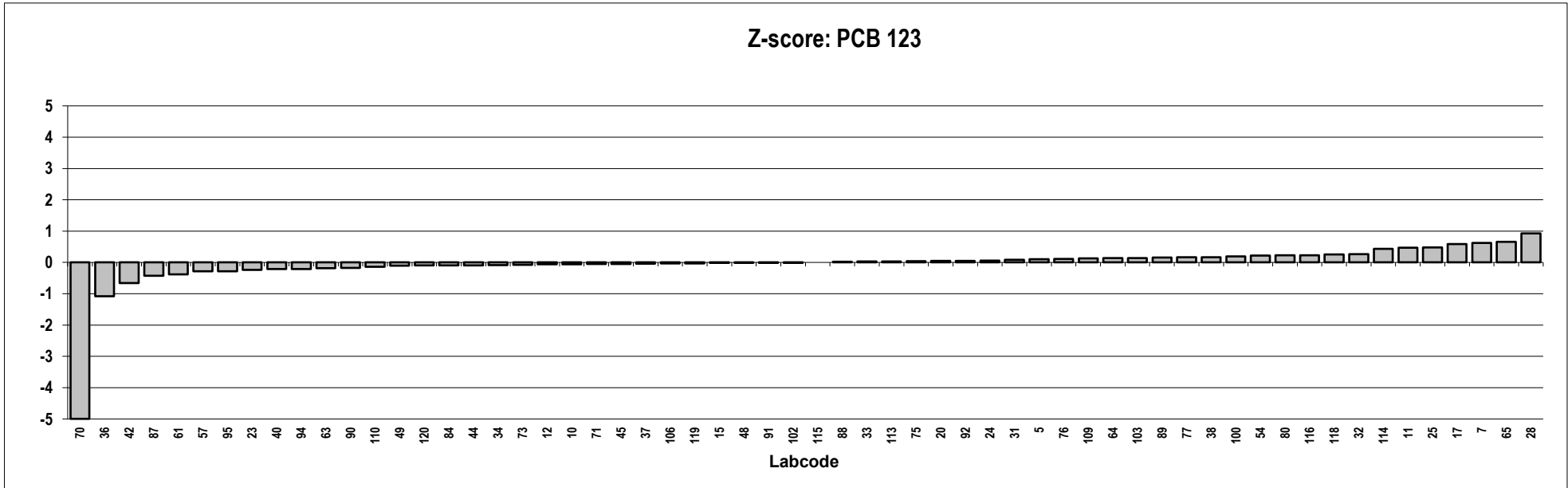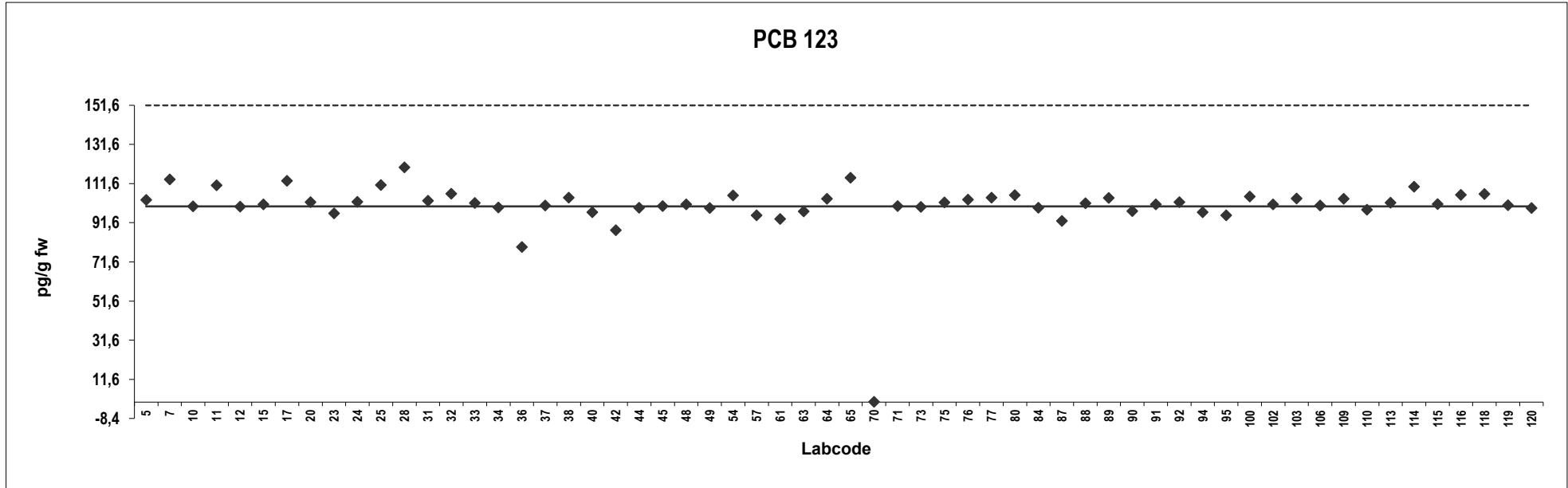
Analyte solution
Congener: PCB 156

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	104	0,17		94	99	-0,050	
7	105	0,22		95	93	-0,35	
10	106	0,29		100	103	0,14	
11	113	0,62		102	100	-0,010	
12	101	0,041		103	99	-0,061	
15	100	-0,015		106	100	0,0048	
17	117	0,83		109	94	-0,31	
20	97	-0,14		110	105	0,24	
23	98	-0,10		113	93	-0,35	
24	10	-4,5	Outlier	114	110	0,49	
25	86	-0,69		115	104	0,17	
28	106	0,29		116	113	0,65	
31	100	0,013		118	102	0,068	
32	108	0,37		119	98	-0,12	
33	95	-0,25		120	99	-0,041	
34	99	-0,042					
36	90	-0,53					
37	102	0,095					
38	100	-0,0083					
40	100	-0,010					
42	86	-0,72					
44	98	-0,11					
45	100	-0,0048					
48	101	0,040					
49	98	-0,11					
54	110	0,51					
57	94	-0,33					
61	102	0,098					
63	97	-0,14					
64	101	0,063					
65	100	-0,015					
70	0,19	-5,0	Outlier				
71	100	0,0083					
73	101	0,019					
75	104	0,19					
76	97	-0,15					
77	104	0,18					
80	105	0,24					
84	98	-0,13					
87	97	-0,17					
88	102	0,097					
89	108	0,38					
90	97	-0,18					
91	98	-0,11					
92	102	0,075					

Consenus statistics

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	101
Standard deviation, pg/g	5,8
Relative standard deviation, %	5,8
No. of values reported	60
No. of values removed	2
No. of reported non-detects	0
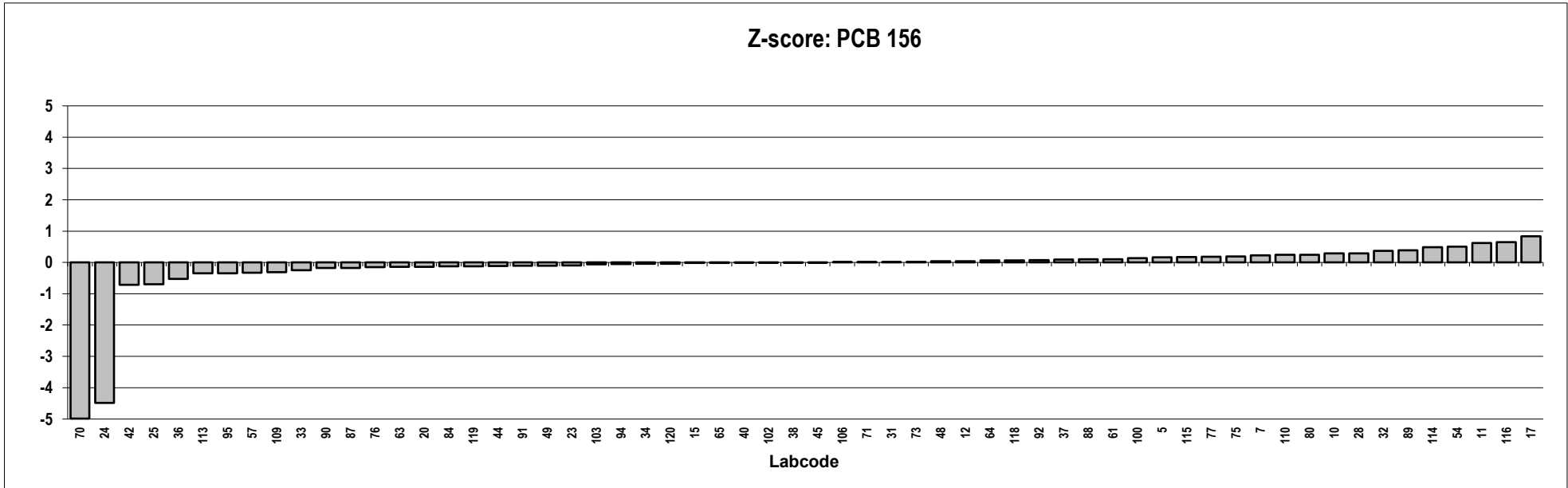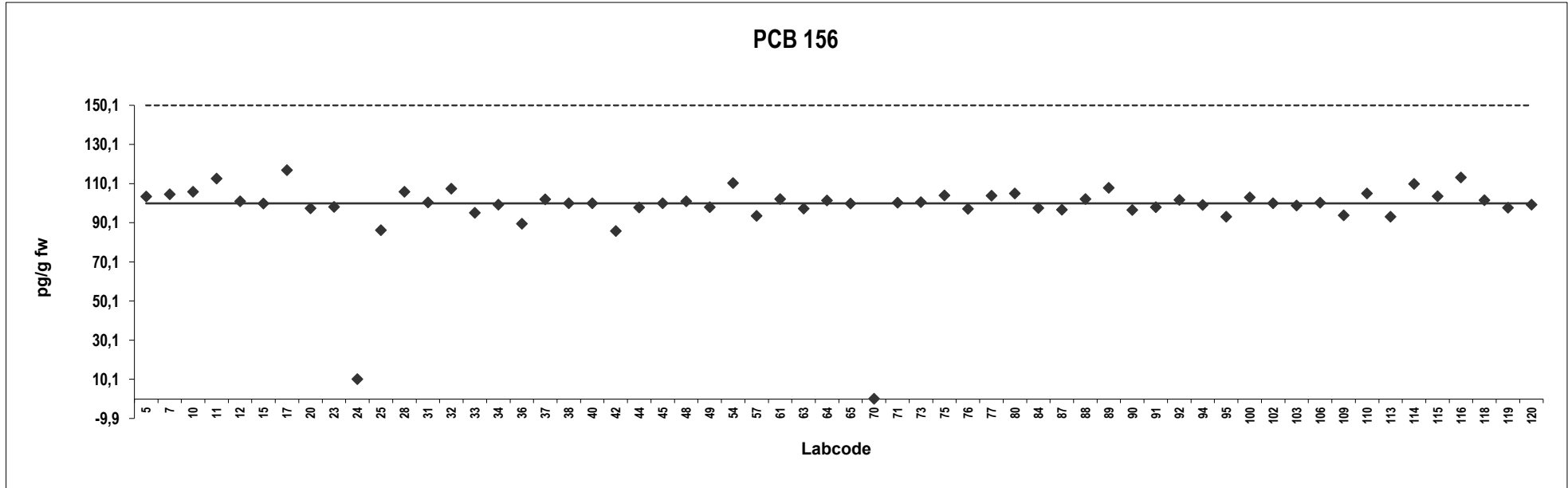
PCB 156

Analyte solution
Congener: PCB 157

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	102	0,098		94	105	0,27	
7	110	0,50		95	102	0,12	
10	104	0,21		100	101	0,058	
11	108	0,41		102	86	-0,70	
12	100	0,0065		103	96	-0,17	
15	103	0,16		106	107	0,35	
17	115	0,75		109	102	0,099	
20	100	0,00		110	96	-0,22	
23	97	-0,14		113	95	-0,26	
24	104	0,20		114	98	-0,092	
25	91	-0,43		115	102	0,092	
28	109	0,46		116	103	0,15	
31	98	-0,11		118	99	-0,041	
32	110	0,50		119	95	-0,24	
33	97	-0,16		120	99	-0,018	
34	99	-0,048					
36	86	-0,71					
37	99	-0,052					
38	99	-0,030					
40	101	0,058					
42	81	-0,93					
44	99	-0,053					
45	100	0,015					
48	101	0,058					
49	99	-0,032					
54	105	0,28					
57	90	-0,48					
61	99	-0,040					
63	93	-0,34					
64	103	0,18					
65	108	0,43					
70	0,19	-5,0	Outlier				
71	100	-0,012					
73	102	0,098					
75	104	0,21					
76	100	0,028					
77	101	0,058					
80	102	0,13					
84	98	-0,068					
87	94	-0,30					
88	96	-0,17					
89	122	1,1					
90	95	-0,25					
91	97	-0,15					
92	98	-0,091					

Consenus statistics

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	6,6
Relative standard deviation, %	6,6
No. of values reported	60
No. of values removed	1
No. of reported non-detects	0

PCB 157

pg/g fw

Labcode

Z-score: PCB 157
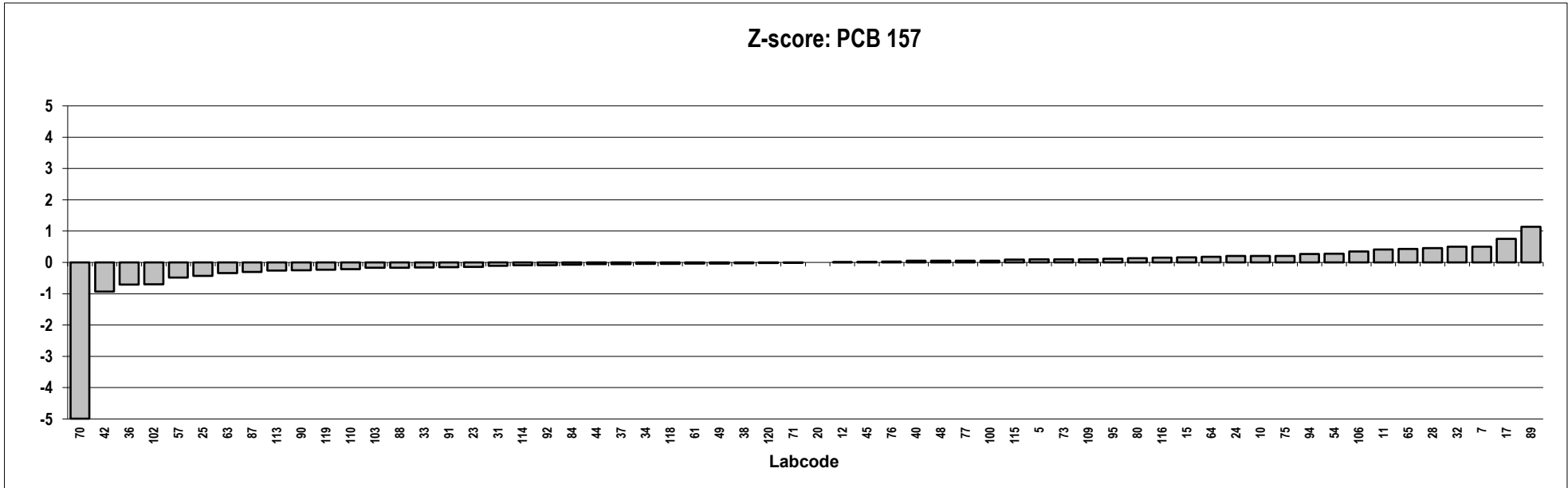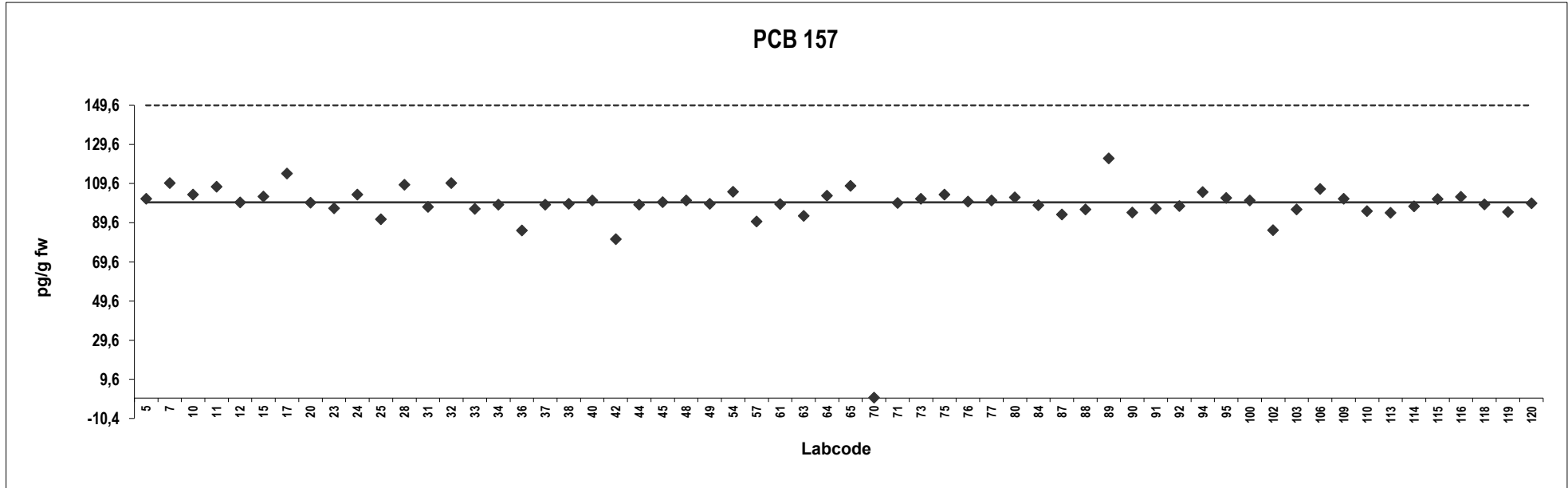
Labcode

Analyte solution
Congener: PCB 167

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	101	0,038		94	103	0,15	
7	109	0,46		95	95	-0,23	
10	103	0,14		100	104	0,19	
11	113	0,63		102	97	-0,15	
12	101	0,044		103	92	-0,39	
15	103	0,14		106	107	0,35	
17	113	0,67		109	95	-0,26	
20	97	-0,14		110	105	0,24	
23	100	-0,0050		113	95	-0,27	
24	99	-0,057		114	100	-0,0050	
25	85	-0,75		115	103	0,16	
28	115	0,74		116	105	0,23	
31	109	0,44		118	102	0,092	
32	111	0,53		119	98	-0,11	
33	98	-0,12		120	100	-0,024	
34	100	0,019					
36	85	-0,74					
37	101	0,045					
38	92	-0,41					
40	96	-0,20					
42	87	-0,65					
44	98	-0,11					
45	100	0,00					
48	100	-0,0050					
49	99	-0,050					
54	94	-0,29					
57	87	-0,63					
61	94	-0,30					
63	94	-0,29					
64	103	0,14					
65	106	0,31					
70	0,096	-5,0	Outlier				
71	102	0,082					
73	103	0,13					
75	100	-0,0050					
76	104	0,18					
77	107	0,33					
80	104	0,20					
84	94	-0,30					
87	95	-0,24					
88	96	-0,21					
89	115	0,73					
90	93	-0,35					
91	101	0,045					
92	100	0,019					

Consenus statistics

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	6,7
Relative standard deviation, %	6,7
No. of values reported	60
No. of values removed	1
No. of reported non-detects	0
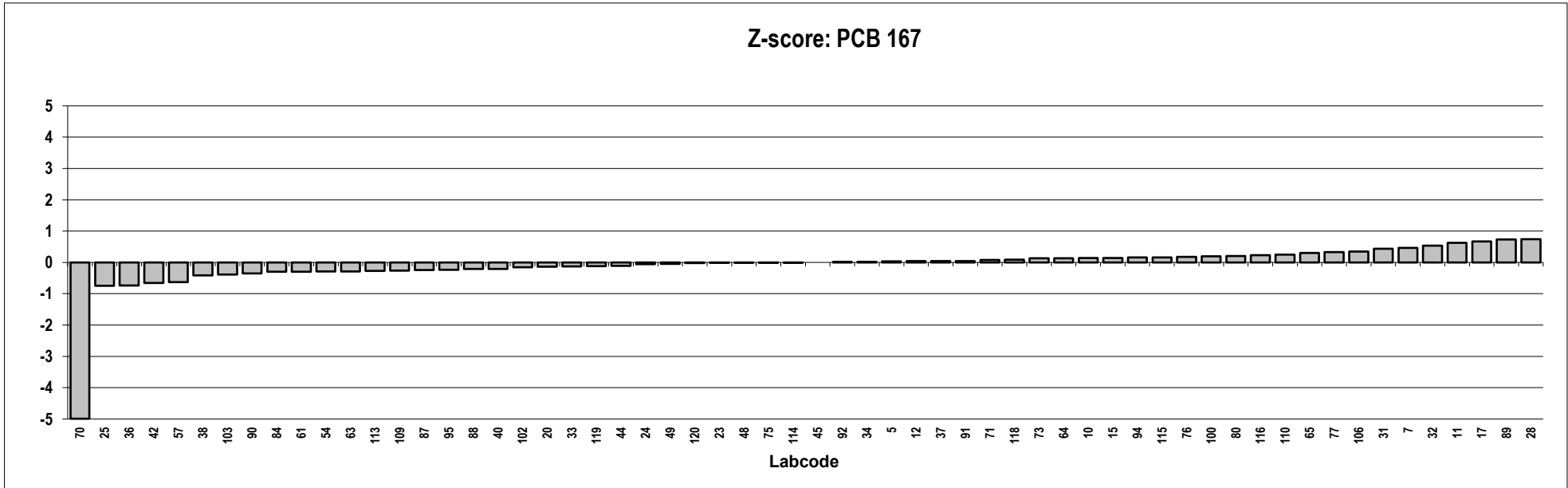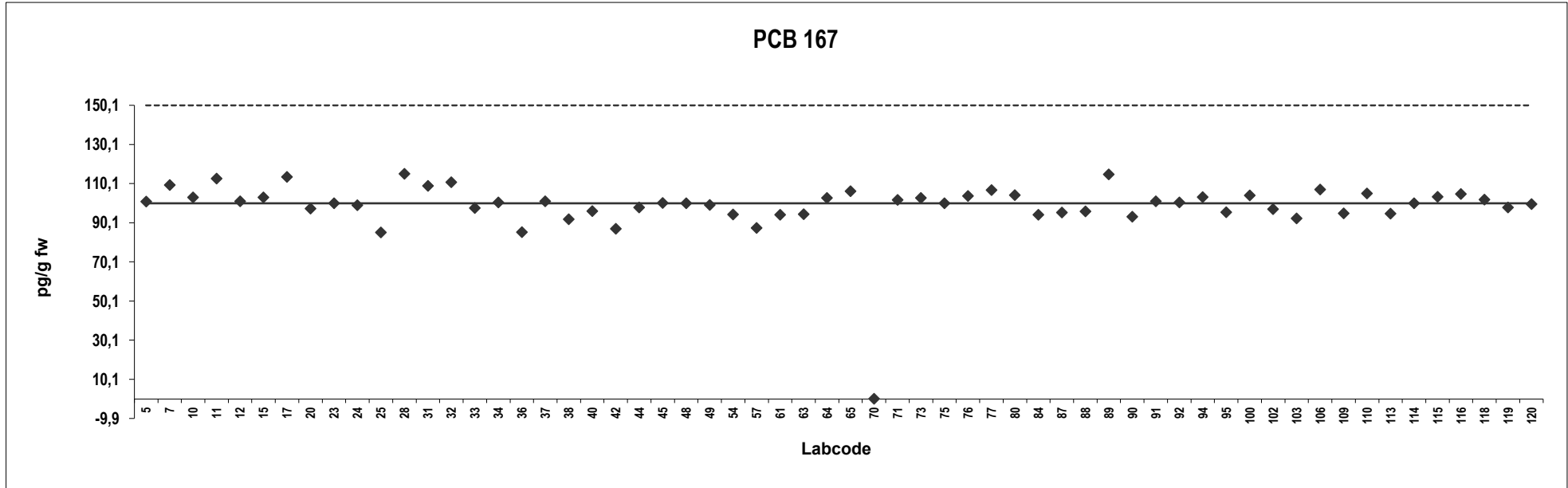
Analyte solution
Congener: PCB 189

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
5	106	0,29		94	103	0,16	
7	108	0,36		95	98	-0,14	
10	98	-0,11		100	104	0,19	
11	106	0,31		102	92	-0,39	
12	98	-0,11		103	100	0,0014	
15	102	0,088		106	107	0,33	
17	119	0,94		109	101	0,034	
20	98	-0,096		110	93	-0,35	
23	100	-0,012		113	99	-0,052	
24	104	0,17		114	100	-0,012	
25	100	-0,027		115	105	0,23	
28	111	0,54		116	98	-0,096	
31	110	0,48		118	100	0,010	
32	113	0,66		119	98	-0,12	
33	99	-0,079		120	99	-0,044	
34	100	-0,0084					
36	85	-0,75					
37	100	-0,037					
38	101	0,022					
40	98	-0,11					
42	89	-0,54					
44	100	-0,034					
45	100	-0,011					
48	100	-0,012					
49	101	0,054					
54	105	0,22					
57	102	0,10					
61	91	-0,44					
63	99	-0,085					
64	100	-0,011					
65	105	0,23					
70	0,094	-5,0	Outlier				
71	100	0,0017					
73	100	0,011					
75	102	0,088					
76	100	0,00					
77	104	0,19					
80	108	0,41					
84	101	0,038					
87	98	-0,13					
88	108	0,38					
89	98	-0,14					
90	98	-0,094					
91	99	-0,072					
92	103	0,15					

Consenus statistics

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	101
Standard deviation, pg/g	5,4
Relative standard deviation, %	5,4
No. of values reported	60
No. of values removed	1
No. of reported non-detects	0

PCB 189

Z-score: PCB 189
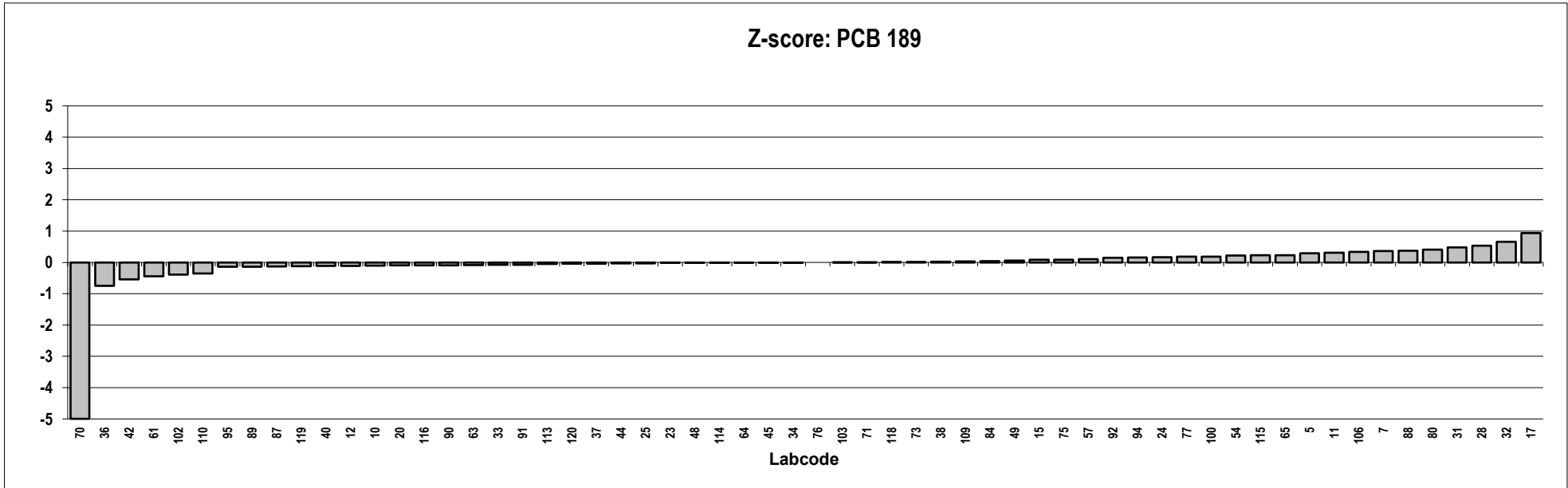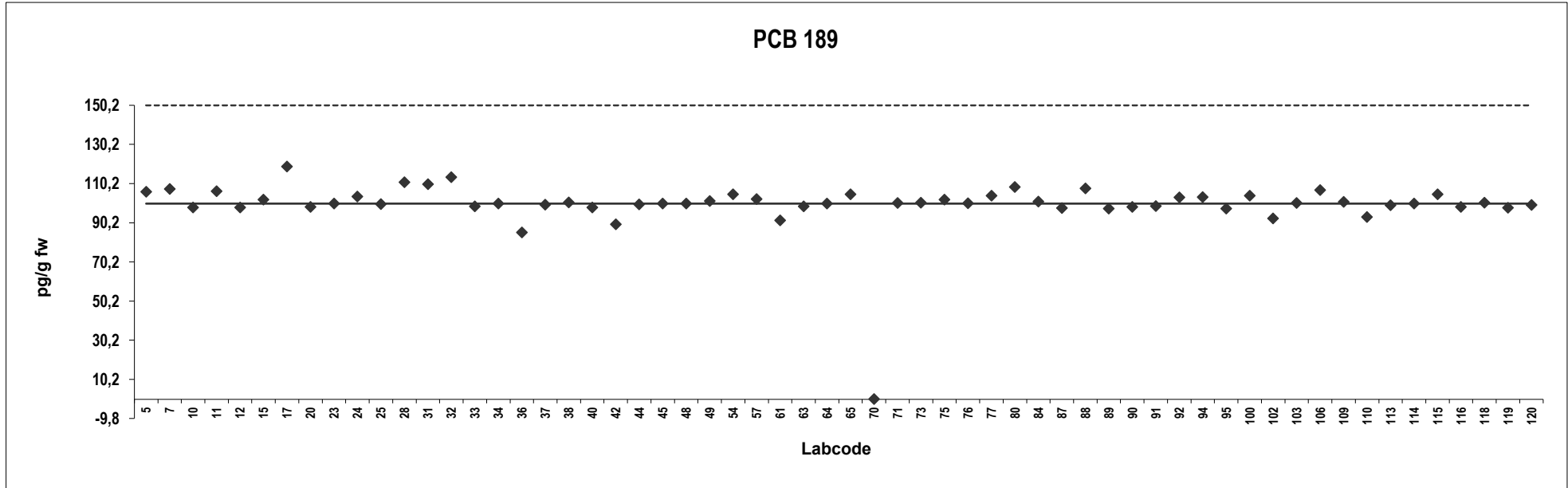
Analyte solution
Congener: PCB 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
7	98	0,015		109	94	-0,22	
10	88	-0,51		110	90	-0,38	
11	113	0,76		113	99	0,066	
12	100	0,11		114	100	0,11	
15	97	-0,066		115	105	0,37	
17	98	-0,0064		118	89	-0,48	
23	97	-0,051		120	97	-0,033	
24	99	0,060					
25	98	0,0051					
28	96	-0,087					
31	96	-0,075					
32	112	0,73					
34	102	0,22					
37	99	0,031					
38	97	-0,072					
40	79	-0,97					
42	82	-0,81					
44	98	-0,013					
45	100	0,11					
48	102	0,21					
49	95	-0,13					
54	94	-0,19					
57	91	-0,33					
58	103	0,24					
61	104	0,30					
63	103	0,28					
64	100	0,11					
65	99	0,068					
70	0,11	-5,0	Outlier				
71	99	0,079					
75	96	-0,077					
76	99	0,070					
77	98	0,00					
80	98	0,00					
81	95	-0,15					
84	98	-0,0057					
87	87	-0,54					
90	0,090	-5,0	Outlier				
94	99	0,036					
95	98	-0,010					
100	106	0,41					
102	94	-0,18					
103	0,044	-5,0	Outlier				
105	110	0,62					
106	88	-0,51					

Consenus statistics	
Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	98
Standard deviation, pg/g	6,5
Relative standard deviation, %	6,6
No. of values reported	52
No. of values removed	3
No. of reported non-detects	0

PCB 28

Z-score: PCB 28
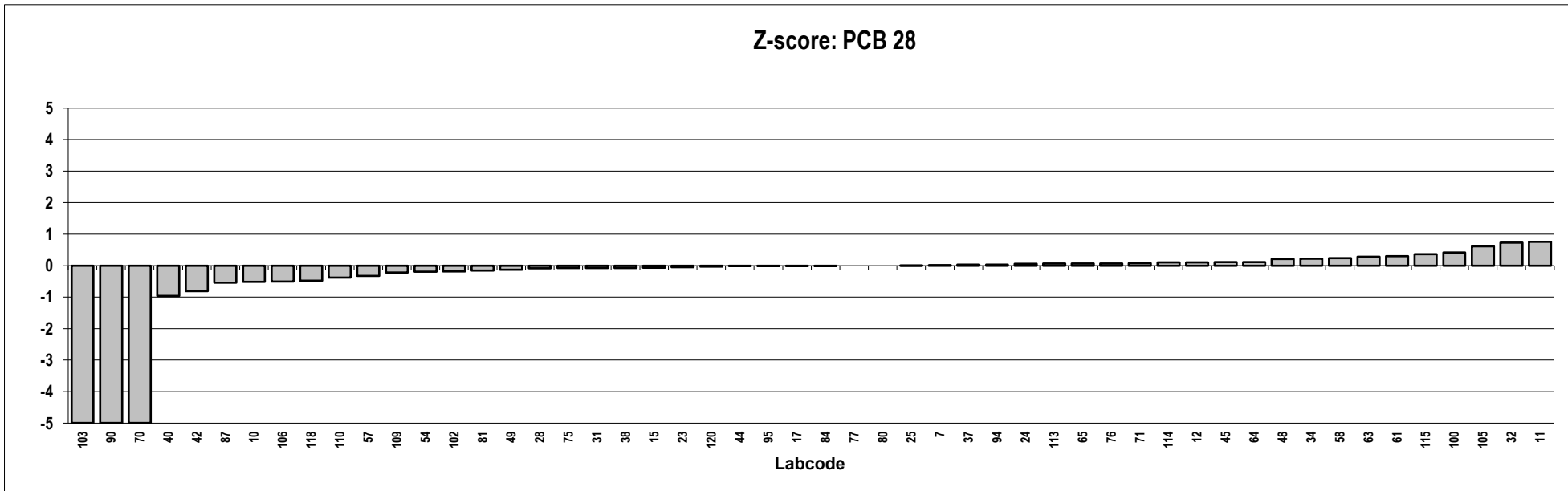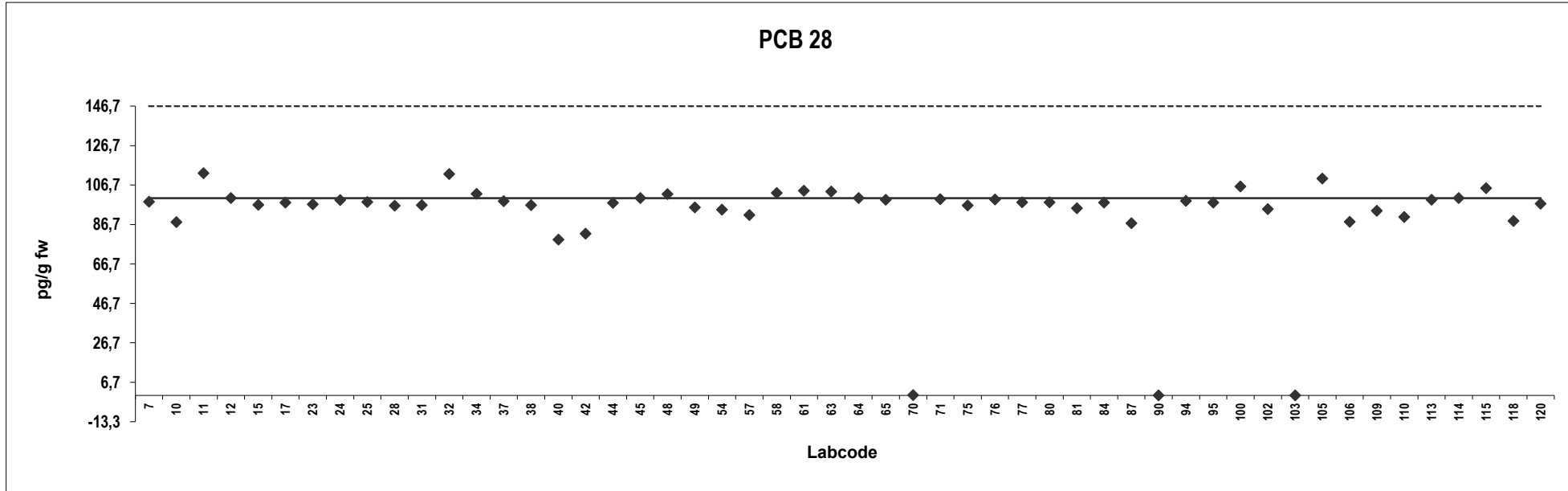
Analyte solution
Congener: PCB 52

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
7	90	-0,37		109	98	0,0067	
10	93	-0,22		110	96	-0,087	
11	112	0,75		113	101	0,17	
12	100	0,10		114	110	0,64	
15	97	-0,036		115	99	0,055	
17	103	0,26		118	89	-0,46	
23	95	-0,13		120	95	-0,12	
24	101	0,18					
25	80	-0,93					
28	85	-0,64					
31	109	0,56					
32	115	0,89					
34	100	0,13					
37	105	0,38					
38	92	-0,30					
40	78	-1,0					
42	81	-0,83					
44	98	0,032					
45	99	0,077					
48	102	0,23					
49	95	-0,13					
54	102	0,21					
57	91	-0,35					
58	105	0,40					
61	99	0,072					
63	100	0,13					
64	100	0,11					
65	92	-0,28					
70	0,12	-5,0	Outlier				
71	101	0,20					
75	97	-0,056					
76	104	0,33					
77	95	-0,14					
80	93	-0,23					
81	89	-0,45					
84	103	0,26					
87	90	-0,40					
90	0,10	-5,0	Outlier				
94	95	-0,14					
95	98	0,00					
100	97	-0,056					
102	97	-0,010					
103	0,087	-5,0	Outlier				
105	110	0,64					
106	97	-0,015					

Consenus statistics	
Consensus median, pg/g	98
Median all values pg/g	97
Consensus mean, pg/g	97
Standard deviation, pg/g	7,7
Relative standard deviation, %	7,9
No. of values reported	52
No. of values removed	3
No. of reported non-detects	0

PCB 52

Z-score: PCB 52
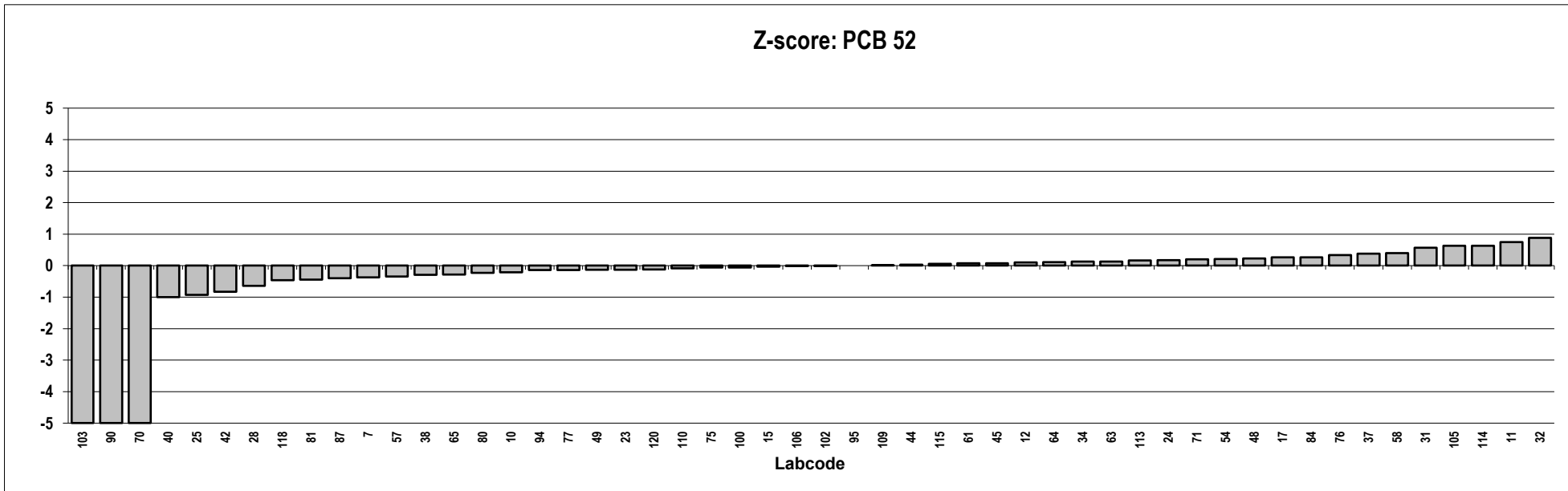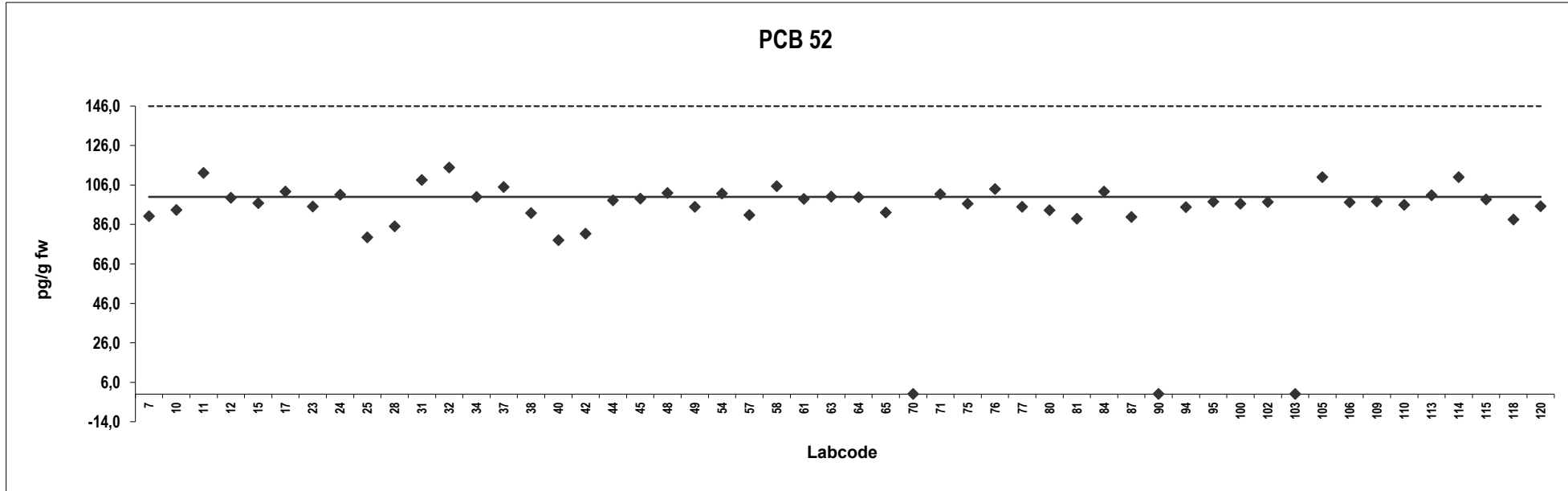
Analyte solution

Congener: PCB 101

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
7	98	-0,13		109	95	-0,27	
10	98	-0,11		110	106	0,27	
11	115	0,72		113	105	0,22	
12	100	-0,00057		114	110	0,47	
15	104	0,17		115	102	0,07	
17	105	0,20		118	82	-0,93	
23	101	0,025		120	95	-0,29	
24	101	0,046					
25	76	-1,2					
28	34	-3,3	Outlier				
31	108	0,38					
32	102	0,053					
34	100	0,00057					
37	106	0,27					
38	98	-0,12					
40	81	-0,97					
42	81	-0,96					
44	102	0,061					
45	99	-0,052					
48	102	0,075					
49	92	-0,42					
54	103	0,15					
57	98	-0,13					
58	105	0,22					
61	103	0,12					
63	97	-0,16					
64	100	-0,035					
65	93	-0,35					
70	0,10	-5,0	Outlier				
71	98	-0,10					
75	105	0,22					
76	109	0,43					
77	106	0,25					
80	95	-0,26					
81	94	-0,34					
84	105	0,22					
87	95	-0,25					
90	0,11	-5,0	Outlier				
94	98	-0,12					
95	96	-0,21					
100	96	-0,23					
102	101	0,025					
103	0,089	-5,0	Outlier				
105	110	0,47					
106	93	-0,38					

Consenus statistics

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	99
Standard deviation, pg/g	7,7
Relative standard deviation, %	7,8
No. of values reported	52
No. of values removed	4
No. of reported non-detects	0

PCB 101

Z-score: PCB 101
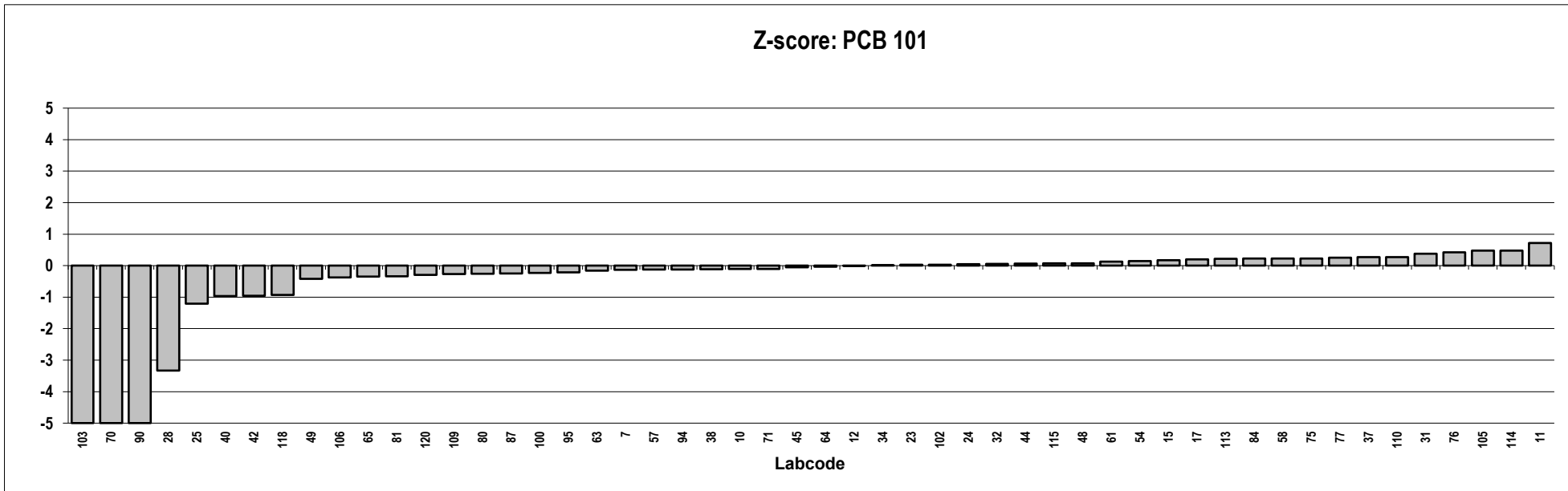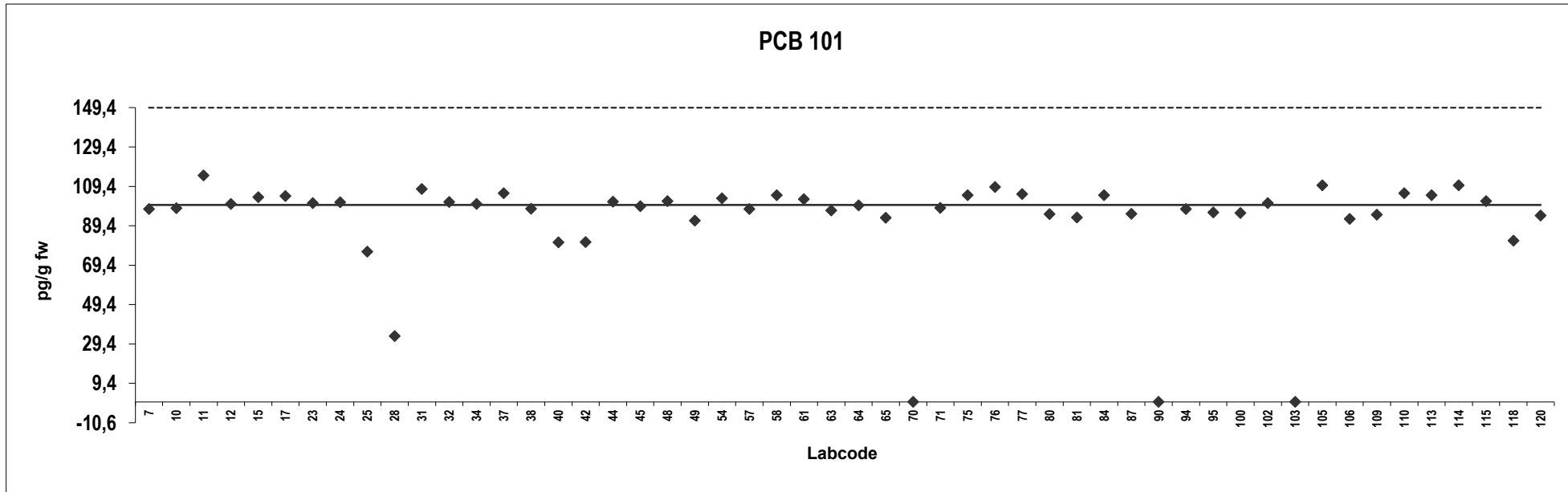
Analyte solution
Congener: PCB 138

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
7	74	-1,3		109	102	0,11	
10	99	-0,010		110	92	-0,37	
11	116	0,80		113	107	0,36	
12	99	-0,029		114	110	0,52	
15	105	0,27		115	98	-0,085	
17	127	1,4		118	83	-0,83	
23	97	-0,13		120	97	-0,15	
24	101	0,065					
25	86	-0,68					
28	90	-0,48					
31	109	0,47					
32	107	0,35					
34	103	0,19					
37	110	0,52					
38	95	-0,25					
40	90	-0,48					
42	84	-0,79					
44	96	-0,19					
45	99	-0,0092					
48	102	0,12					
49	89	-0,55					
54	105	0,28					
57	94	-0,30					
58	103	0,17					
61	111	0,58					
63	97	-0,12					
64	101	0,053					
65	89	-0,53					
70	0,11	-5,0	Outlier				
71	103	0,17					
75	106	0,32					
76	100	0,030					
77	94	-0,29					
80	96	-0,17					
81	89	-0,52					
84	109	0,50					
87	93	-0,33					
90	0,096	-5,0	Outlier				
94	100	0,00					
95	100	0,00					
100	105	0,27					
102	101	0,070					
103	0,087	-5,0	Outlier				
105	110	0,52					
106	99	-0,020					

Consenus statistics	
Consensus median, pg/g	100
Median all values pg/g	99
Consensus mean, pg/g	99
Standard deviation, pg/g	9,2
Relative standard deviation, %	9,3
No. of values reported	52
No. of values removed	3
No. of reported non-detects	0

PCB 138

Z-score: PCB 138
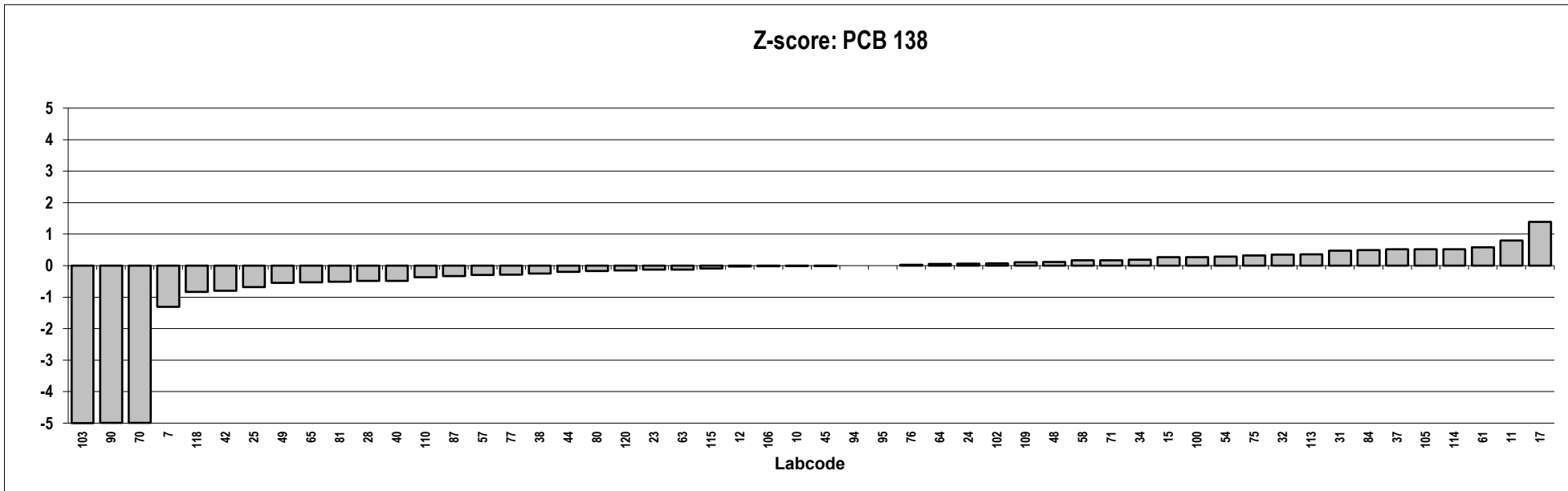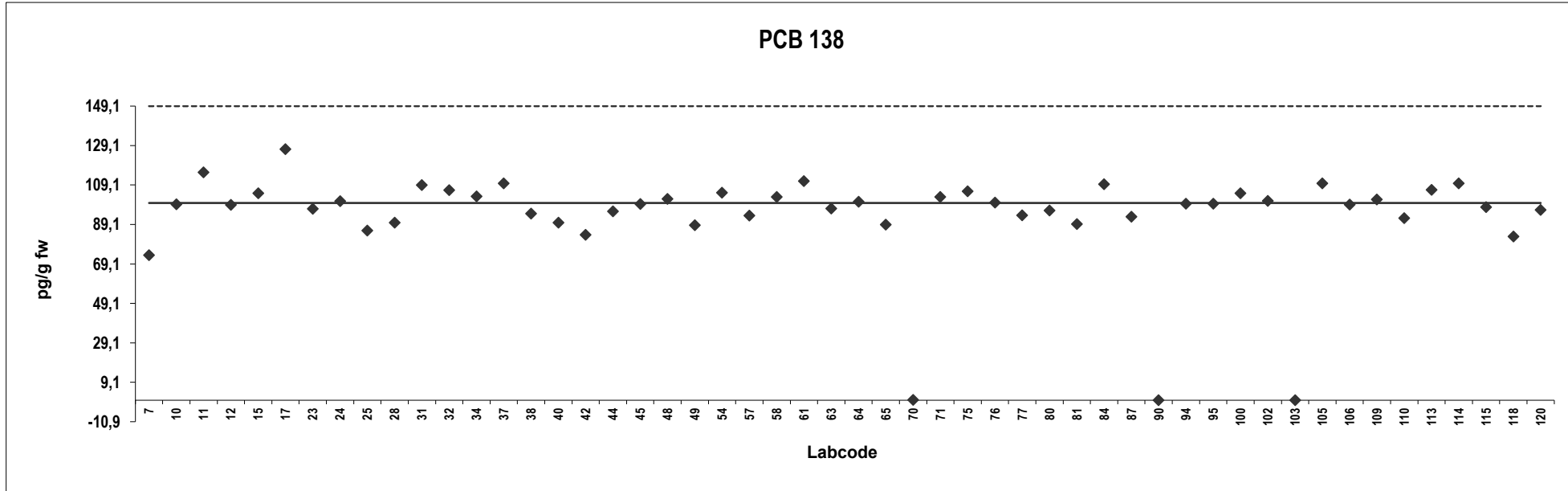
Analyte solution
Congener: PCB 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
7	89	-0,52		109	100	0,059	
10	106	0,34		110	98	-0,051	
11	114	0,73		113	101	0,090	
12	101	0,083		114	110	0,54	
15	98	-0,066		115	99	-0,031	
17	102	0,13		118	82	-0,89	
23	105	0,29		120	95	-0,20	
24	99	0,00					
25	82	-0,85					
28	106	0,34					
31	110	0,56					
32	108	0,42					
34	100	0,039					
37	111	0,59					
38	96	-0,17					
40	82	-0,87					
42	83	-0,83					
44	99	-0,015					
45	99	0,00066					
48	102	0,14					
49	85	-0,73					
54	104	0,26					
57	99	-0,010					
58	105	0,28					
61	107	0,42					
63	100	0,045					
64	100	0,049					
65	88	-0,58					
70	0,098	-5,0	Outlier				
71	100	0,046					
75	98	-0,071					
76	99	-0,032					
77	97	-0,091					
80	98	-0,056					
81	89	-0,51					
84	107	0,39					
87	97	-0,13					
90	0,094	-5,0	Outlier				
94	91	-0,42					
95	96	-0,17					
100	106	0,34					
102	98	-0,066					
103	0,091	-5,0	Outlier				
105	112	0,64					
106	98	-0,051					

Consenus statistics

Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	99
Standard deviation, pg/g	8,0
Relative standard deviation, %	8,0
No. of values reported	52
No. of values removed	3
No. of reported non-detects	0

PCB 153

Z-score: PCB 153
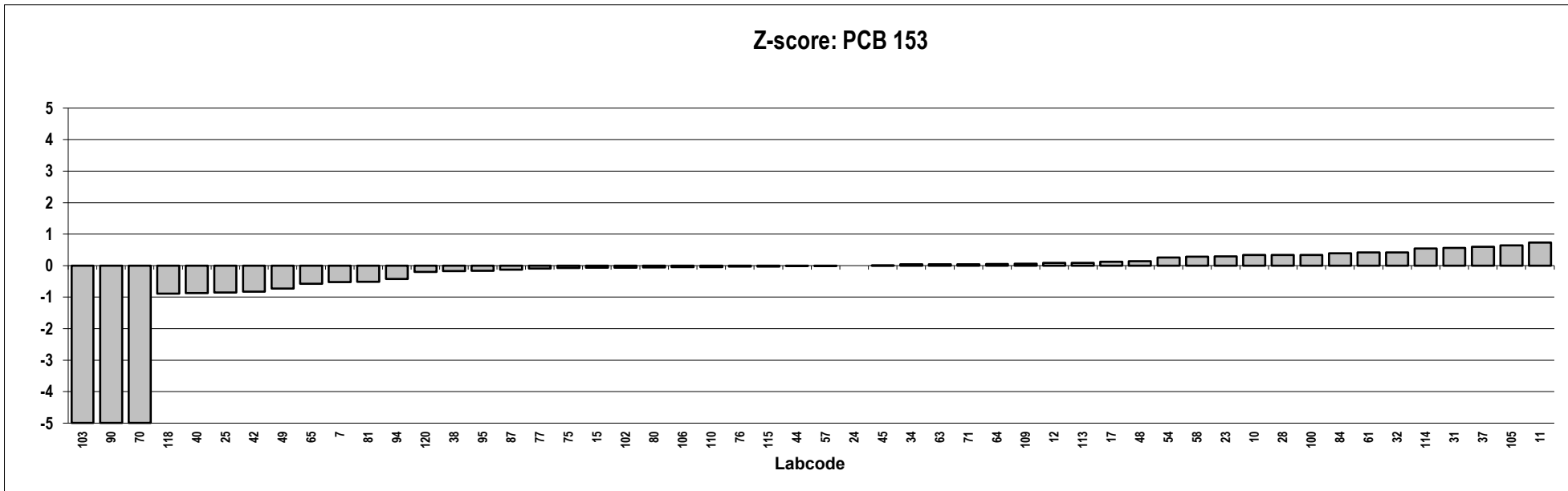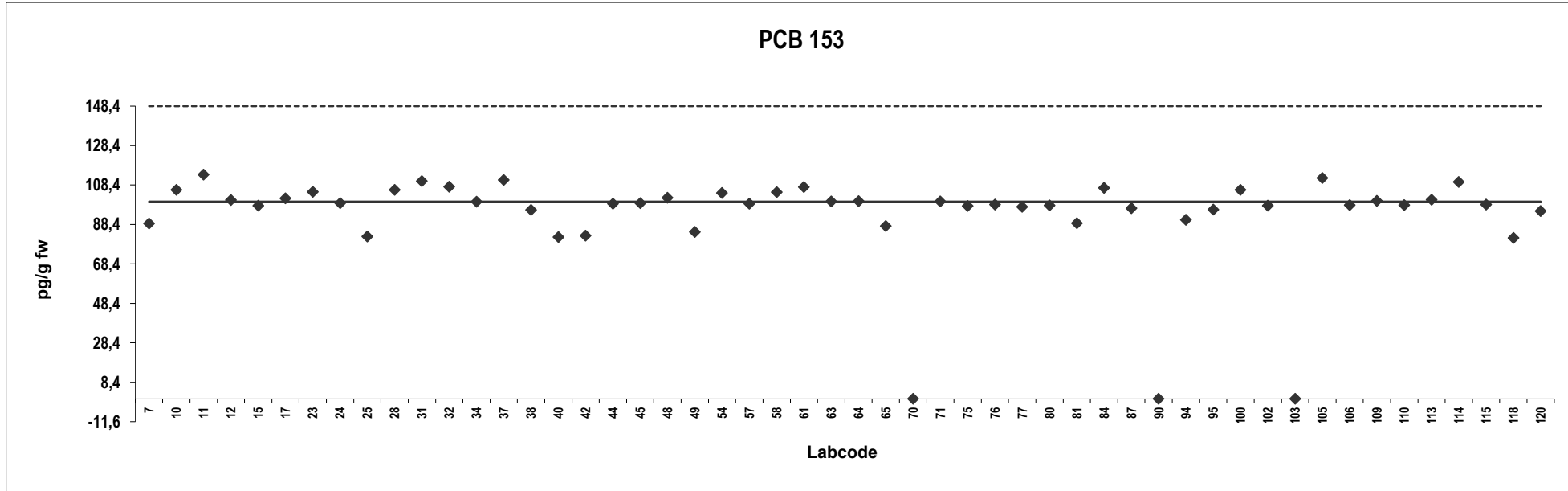
Analyte solution
Congener: PCB 180

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
7	88	-0,60		109	95	-0,26	
10	102	0,10		110	105	0,25	
11	117	0,85		113	96	-0,22	
12	101	0,051		114	110	0,50	
15	101	0,050		115	97	-0,15	
17	99	-0,031		118	86	-0,68	
23	100	0,00		120	98	-0,095	
24	102	0,079					
25	85	-0,74					
28	113	0,65					
31	105	0,24					
32	128	1,4					
34	100	0,0087					
37	106	0,30					
38	90	-0,49					
40	77	-1,2					
42	81	-0,96					
44	95	-0,26					
45	100	0,0061					
48	103	0,15					
49	91	-0,46					
54	110	0,51					
57	94	-0,28					
58	107	0,35					
61	108	0,41					
63	96	-0,18					
64	101	0,035					
65	87	-0,64					
70	0,092	-5,0	Outlier				
71	99	-0,027					
75	103	0,15					
76	106	0,28					
77	95	-0,23					
80	100	-0,020					
81	90	-0,50					
84	109	0,45					
87	92	-0,38					
90	0,10	-5,0	Outlier				
94	94	-0,32					
95	97	-0,18					
100	105	0,25					
102	101	0,050					
103	0,094	-5,0	Outlier				
105	100	0,00					
106	98	-0,12					

Consenus statistics

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	99
Standard deviation, pg/g	9,0
Relative standard deviation, %	9,1
No. of values reported	52
No. of values removed	3
No. of reported non-detects	0

PCB 180

Z-score: PCB 180
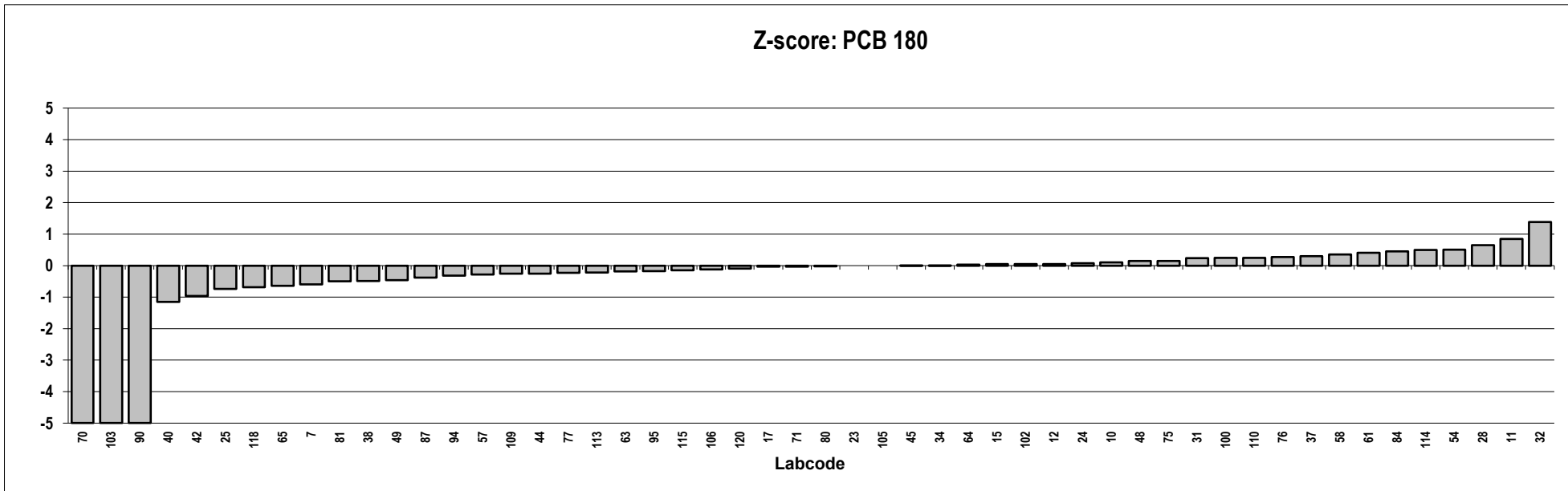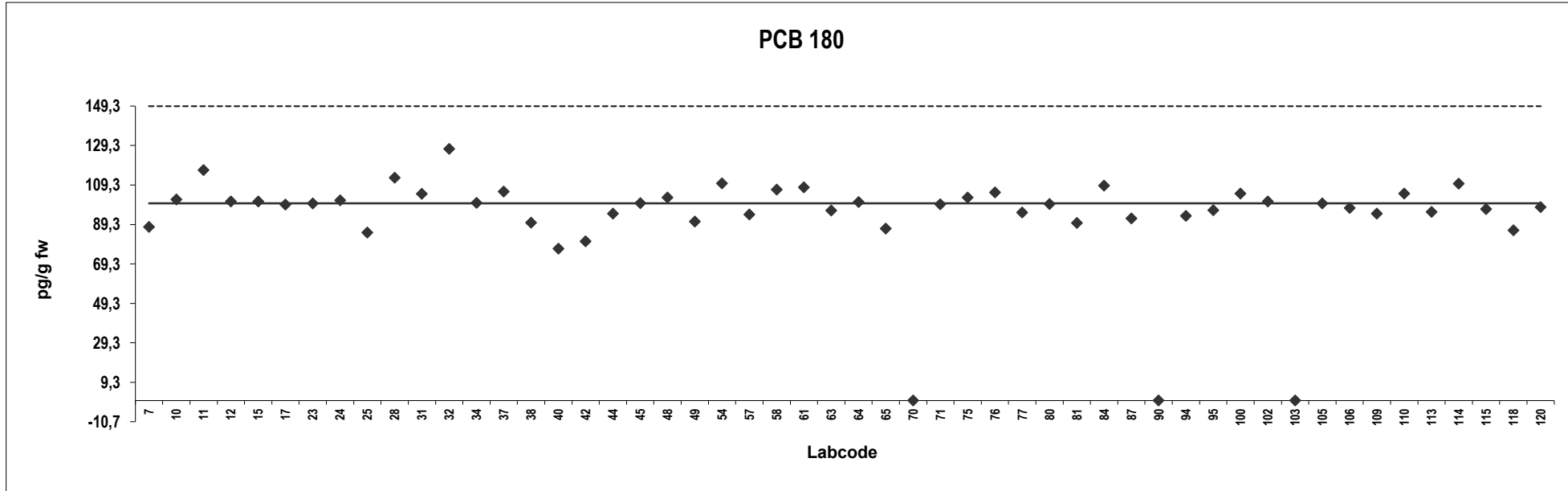
Analyte solution

Congener: PBDE 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	25	0,00					
23	26	0,30					
25	25	-0,036					
31	26	0,23					
36	25	0,081					
37	29	0,91					
40	24	-0,26					
42	22	-0,48					
49	19	-1,1					
54	23	-0,36					
57	23	-0,36					
63	25	0,046					
65	26	0,28					
77	25	0,12					
81	22	-0,53					
90	25	-0,038					
94	25	0,00					
95	24	-0,10					
100	25	0,10					
102	26	0,18					
113	26	0,14					
115	25	0,050					
116	23	-0,30					

Consenus 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, %	7,9
No. of values reported	23
No. of values removed	0
No. of reported non-detects	0

PBDE 28

Z-score: PBDE 28
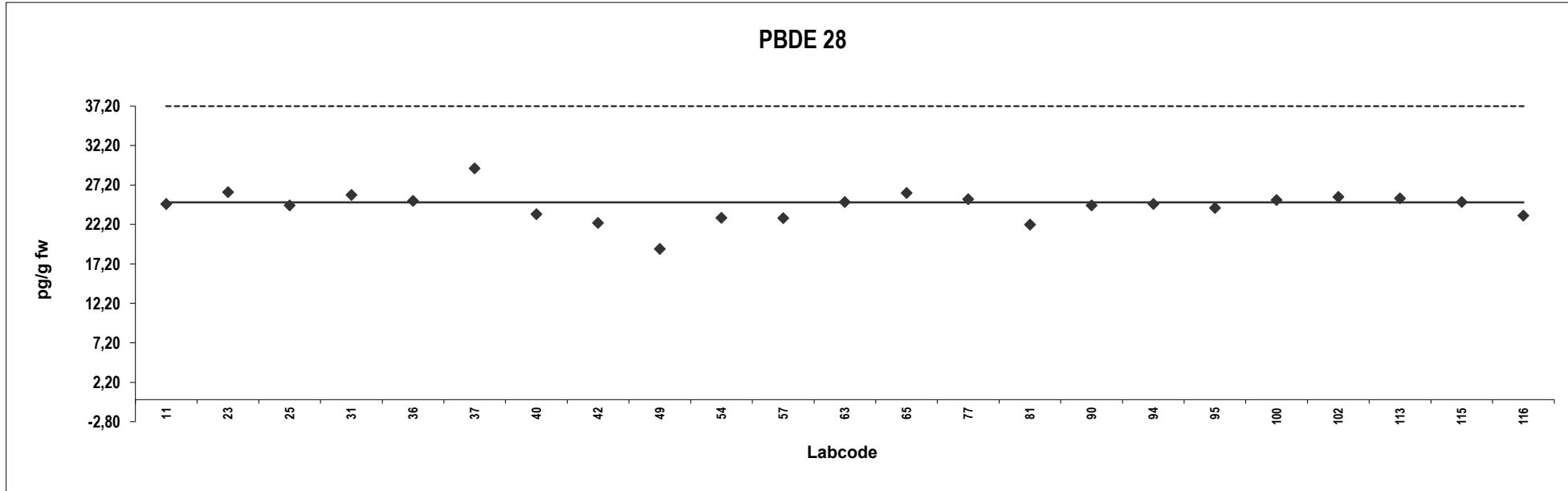
Analyte solution

Congener: PBDE 47

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	24	-0,13					
23	24	-0,17					
25	25	0,0020					
31	26	0,31					
36	26	0,25					
37	26	0,23					
40	25	0,051					
42	22	-0,56					
49	22	-0,62					
54	24	-0,17					
57	24	-0,14					
63	24	-0,11					
65	25	0,00					
77	24	-0,19					
81	22	-0,47					
90	24	-0,085					
94	24	-0,031					
95	25	0,071					
100	25	0,010					
102	25	0,17					
113	26	0,38					
115	25	0,0066					
116	25	0,018					

Consenus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	24
Standard deviation, pg/g	1,2
Relative standard deviation, %	5,1
No. of values reported	23
No. of values removed	0
No. of reported non-detects	0

PBDE 47

pg/g fw

Labcode: 11, 23, 25, 31, 36, 37, 40, 42, 49, 54, 57, 63, 65, 77, 81, 90, 94, 95, 100, 102, 113, 115, 116

Z-score: PBDE 47

Labcode: 49, 42, 81, 77, 23, 54, 57, 11, 63, 90, 94, 65, 25, 115, 100, 116, 40, 95, 102, 37, 36, 31, 113
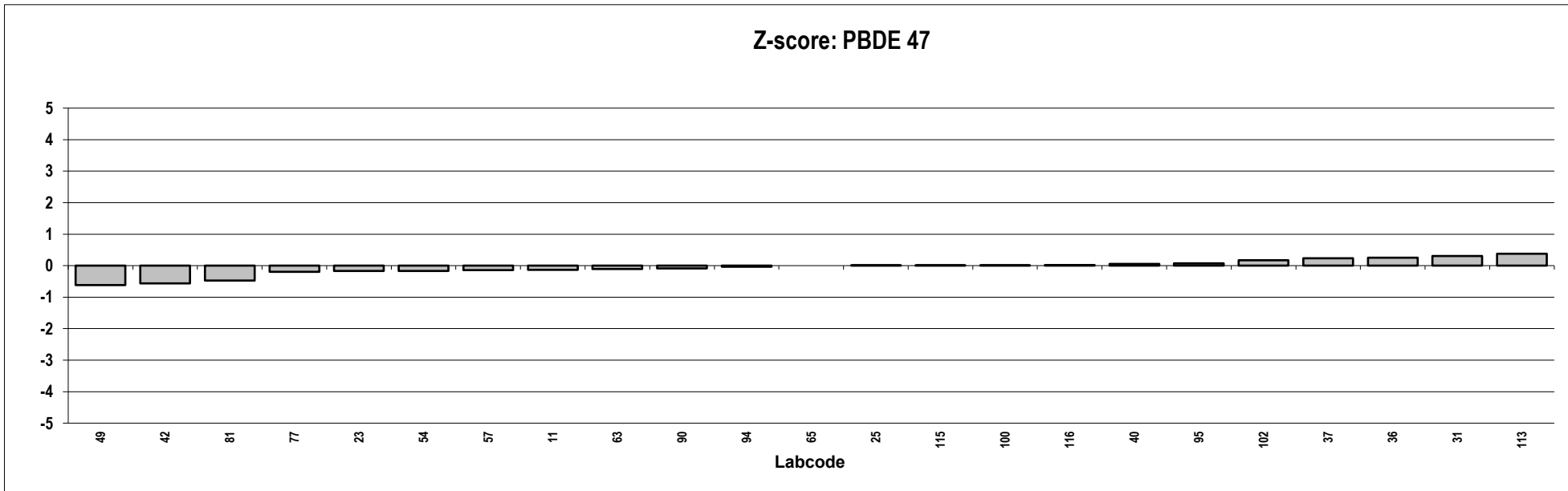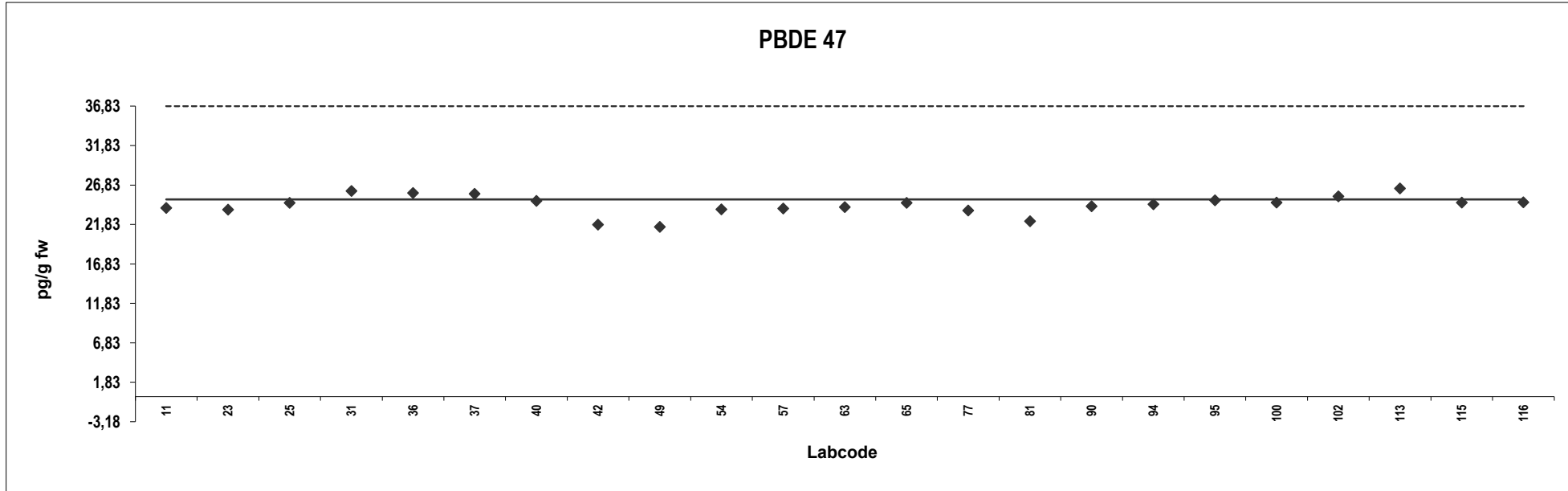
Analyte solution

Congener: PBDE 99

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	25	0,00					
23	25	0,080					
25	26	0,16					
31	26	0,21					
36	25	0,040					
37	24	-0,24					
40	26	0,12					
42	22	-0,64					
49	22	-0,70					
54	21	-0,70					
57	24	-0,29					
63	24	-0,16					
65	25	0,072					
77	25	-0,040					
81	21	-0,75					
90	26	0,15					
94	25	0,040					
95	25	-0,020					
100	24	-0,28					
102	26	0,12					
113	26	0,12					
115	25	0,075					
116	25	-0,032					

Consenus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	24
Standard deviation, pg/g	1,5
Relative standard deviation, %	6,3
No. of values reported	23
No. of values removed	0
No. of reported non-detects	0

PBDE 99

Z-score: PBDE 99
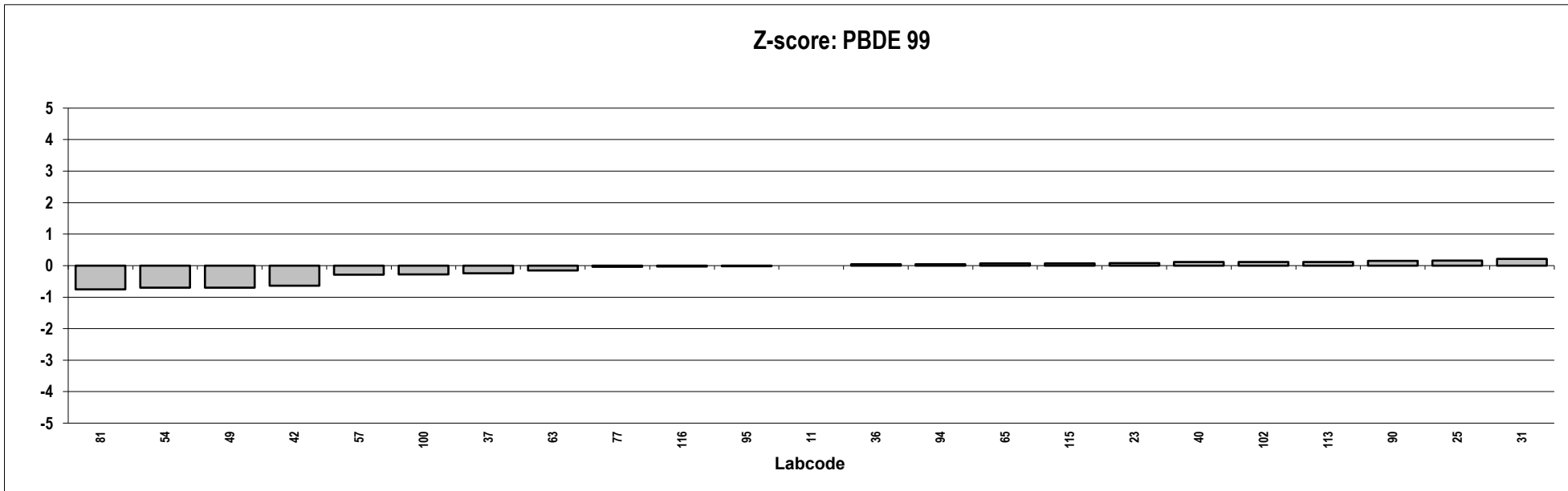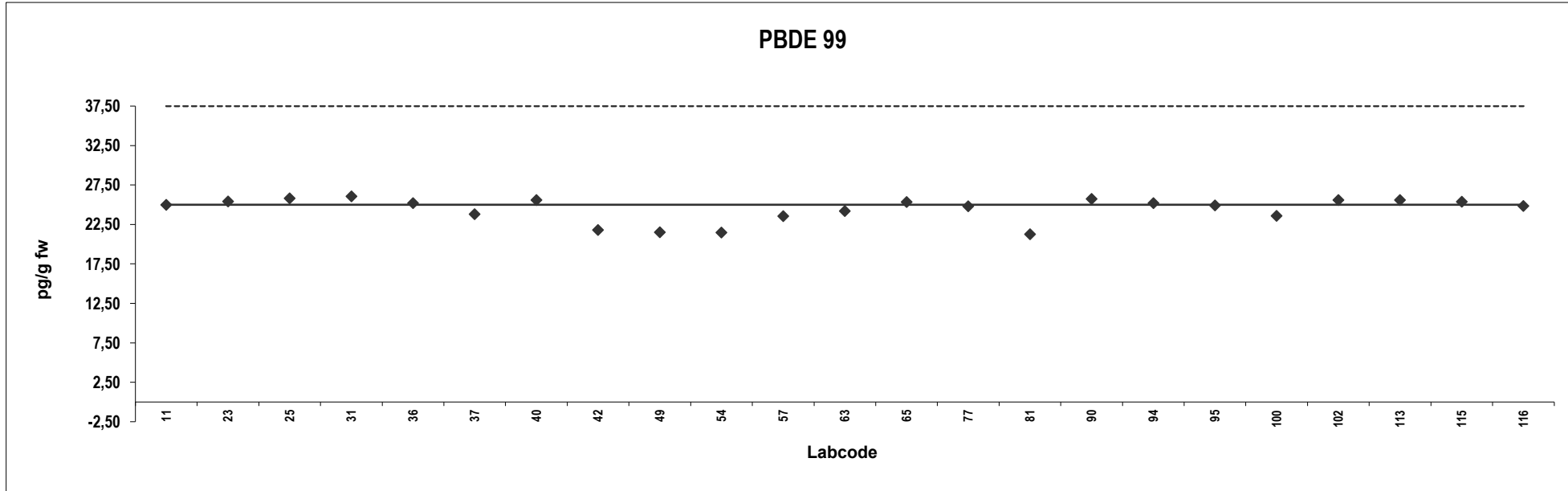
Analyte solution

Congener: PBDE 100

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	24	-0,12					
23	25	0,040					
25	27	0,30					
31	26	0,23					
36	26	0,18					
37	26	0,10					
40	25	-0,020					
42	20	-1,0					
49	22	-0,54					
54	22	-0,66					
57	24	-0,29					
63	25	0,076					
65	26	0,13					
77	26	0,24					
81	22	-0,70					
90	29	0,90					
94	25	0,00					
95	25	-0,020					
100	27	0,42					
102	25	0,00					
113	26	0,10					
115	24	-0,14					
116	25	-0,073					

Consenus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2,0
Relative standard deviation, %	8,1
No. of values reported	23
No. of values removed	0
No. of reported non-detects	0

PBDE 100

Z-score: PBDE 100
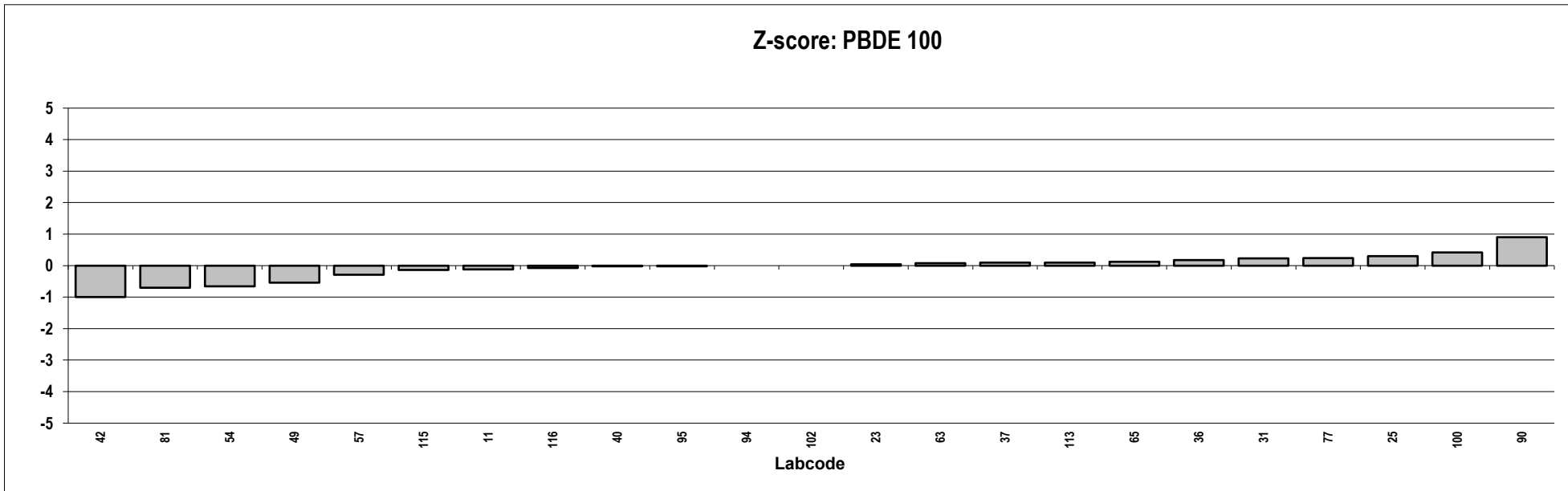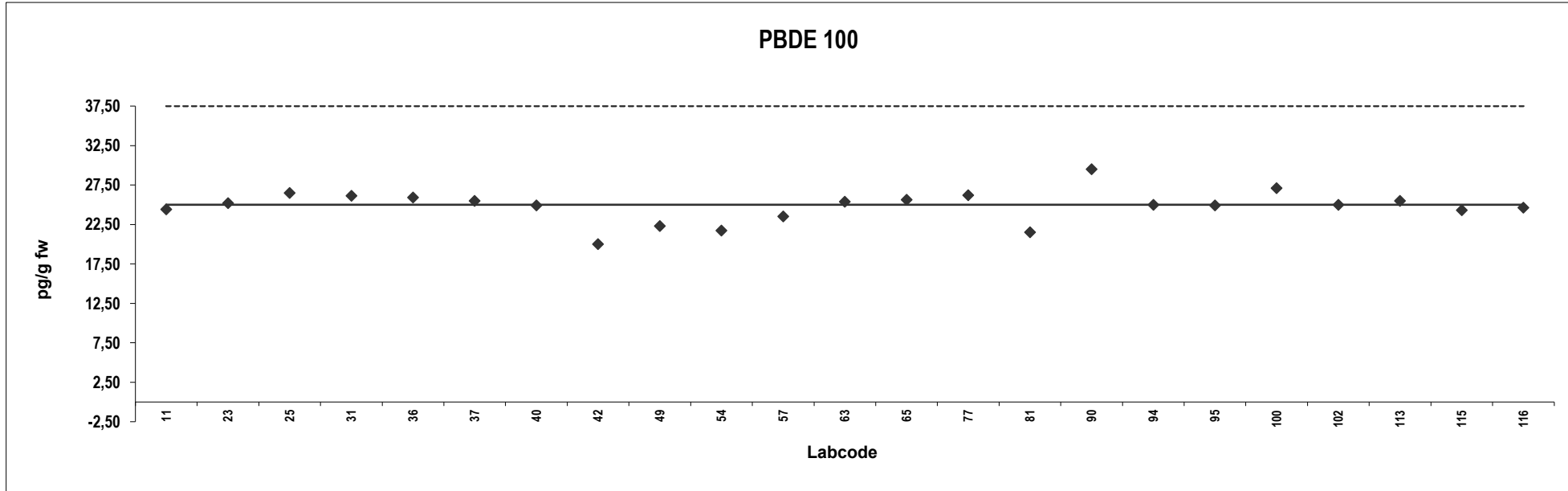
Analyte solution

Congener: PBDE 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	26	0,25					
23	25	0,14					
25	23	-0,28					
31	26	0,40					
36	24	-0,16					
37	24	-0,18					
40	24	0,00					
42	20	-0,88					
49	19	-1,1					
54	25	0,19					
57	23	-0,27					
63	25	0,10					
65	24	-0,031					
77	24	-0,041					
81	18	-1,3					
90	26	0,37					
94	24	-0,082					
95	22	-0,47					
100	25	0,061					
102	25	0,12					
113	27	0,49					
115	25	0,13					
116	27	0,49					

Consenus statistics	
Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2,3
Relative standard deviation, %	9,7
No. of values reported	23
No. of values removed	0
No. of reported non-detects	0

PBDE 153
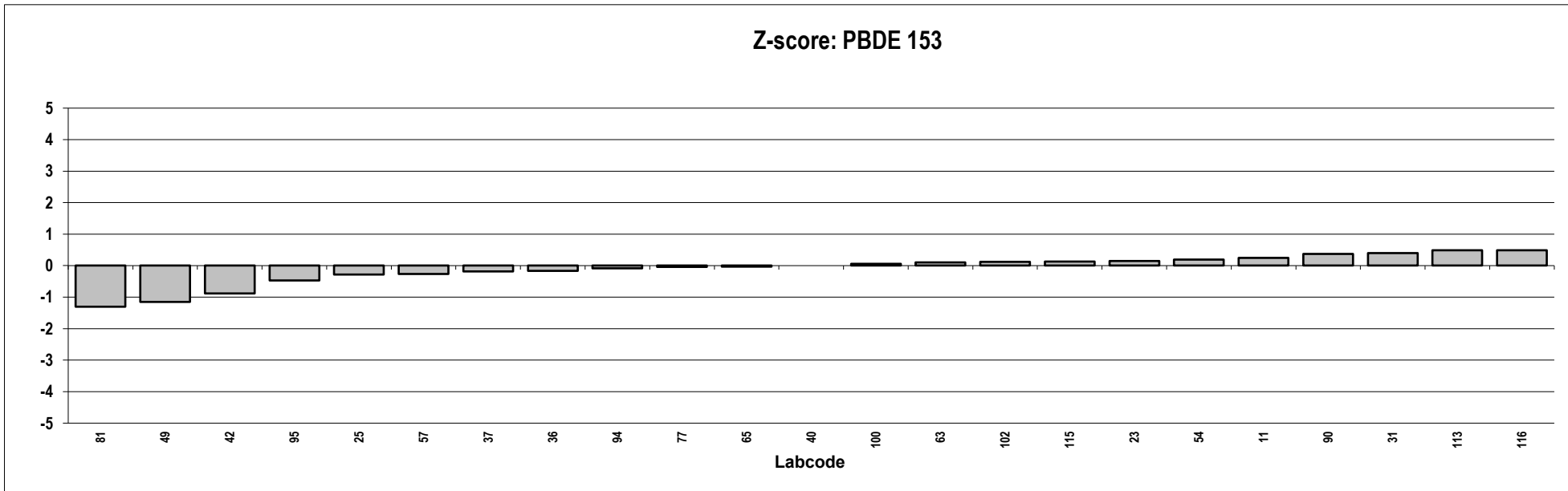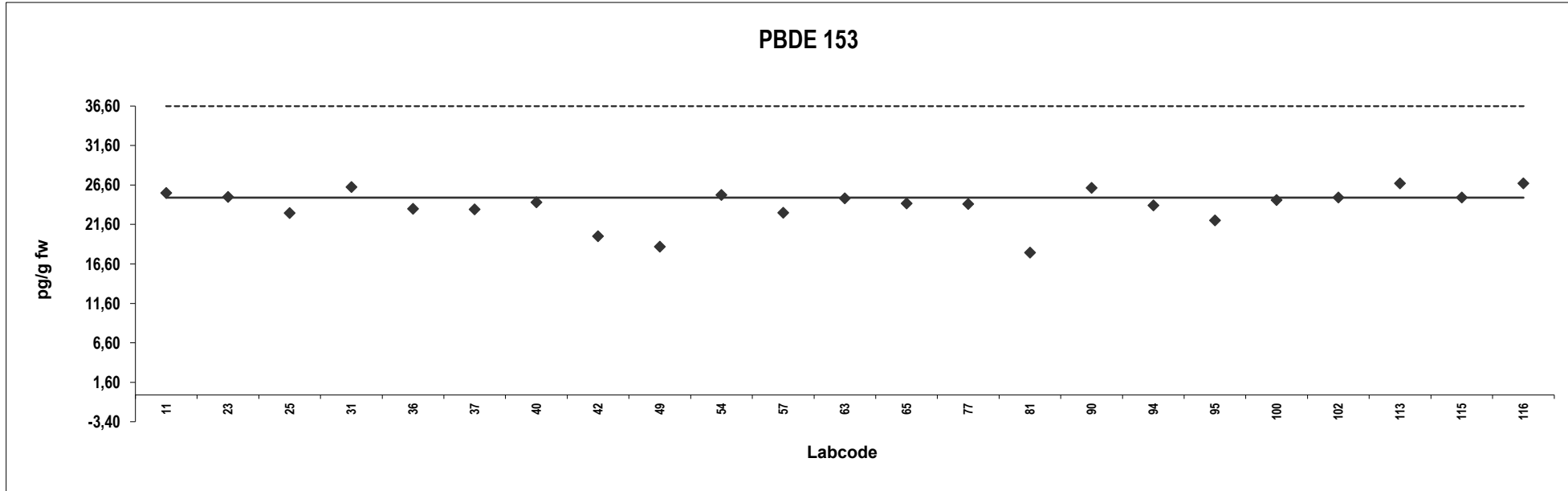
Z-score: PBDE 153

Analyte solution

Congener: PBDE 154

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	24	-0,091					
23	25	0,16					
25	26	0,35					
31	26	0,43					
36	25	0,14					
37	23	-0,15					
40	26	0,39					
42	19	-0,97					
49	19	-1,0					
54	26	0,53					
57	24	0,00					
63	25	0,29					
65	26	0,41					
77	24	-0,0071					
81	19	-0,97					
90	24	0,044					
94	23	-0,11					
95	22	-0,36					
100	23	-0,24					
102	23	-0,11					
113	26	0,35					
115	24	0,010					
116	23	-0,18					

Consenus 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, %	8,9
No. of values reported	23
No. of values removed	0
No. of reported non-detects	0

PBDE 154

pg/g fw
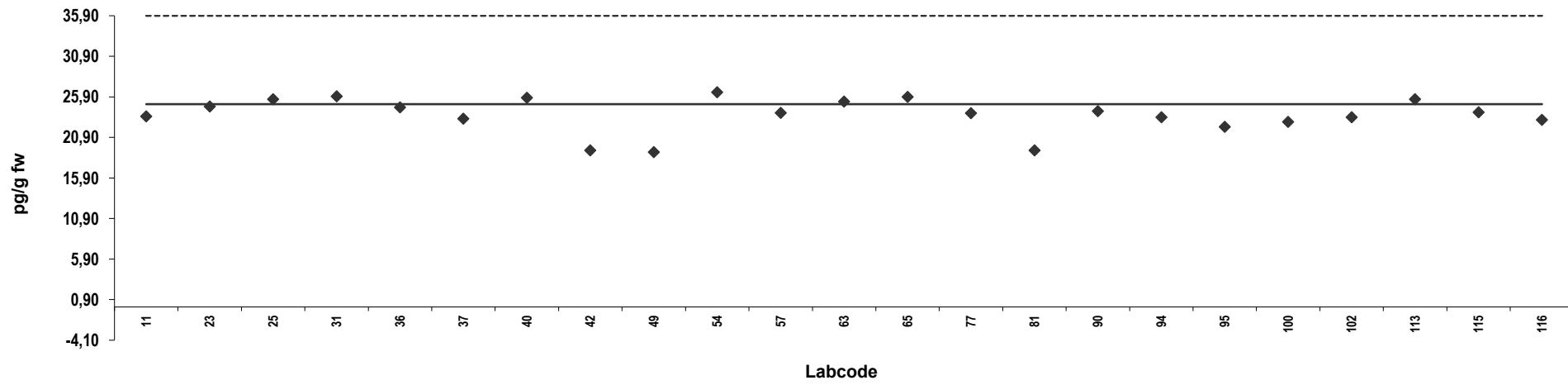
Labcode

Z-score: PBDE 154
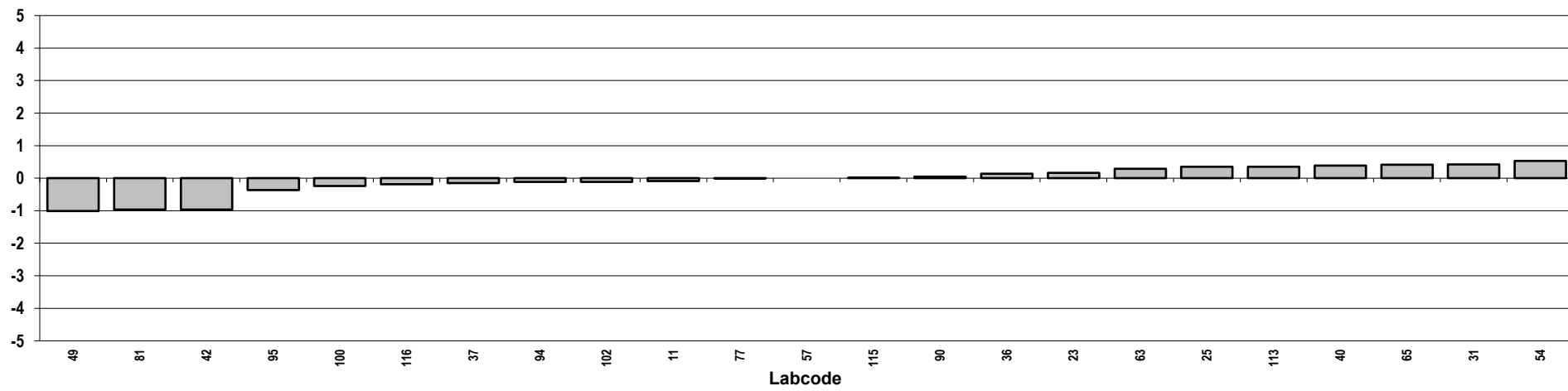
Labcode

Analyte solution

Congener: PBDE 183

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	25	0,00					
23	27	0,49					
25	25	0,13					
31	25	0,061					
36	26	0,26					
37	23	-0,38					
40	24	-0,12					
42	23	-0,38					
49	20	-0,91					
54	24	-0,18					
57	20	-0,97					
63	25	0,15					
65	24	-0,19					
77	25	0,12					
81	17	-1,5					
90	22	-0,49					
94	26	0,26					
95	24	-0,14					
100	21	-0,67					
102	25	0,10					
113	25	0,020					
115	27	0,37					
116	28	0,61					

Consenus statistics

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	24
Standard deviation, pg/g	2,5
Relative standard deviation, %	10
No. of values reported	23
No. of values removed	0
No. of reported non-detects	0

PBDE 183

Z-score: PBDE 183
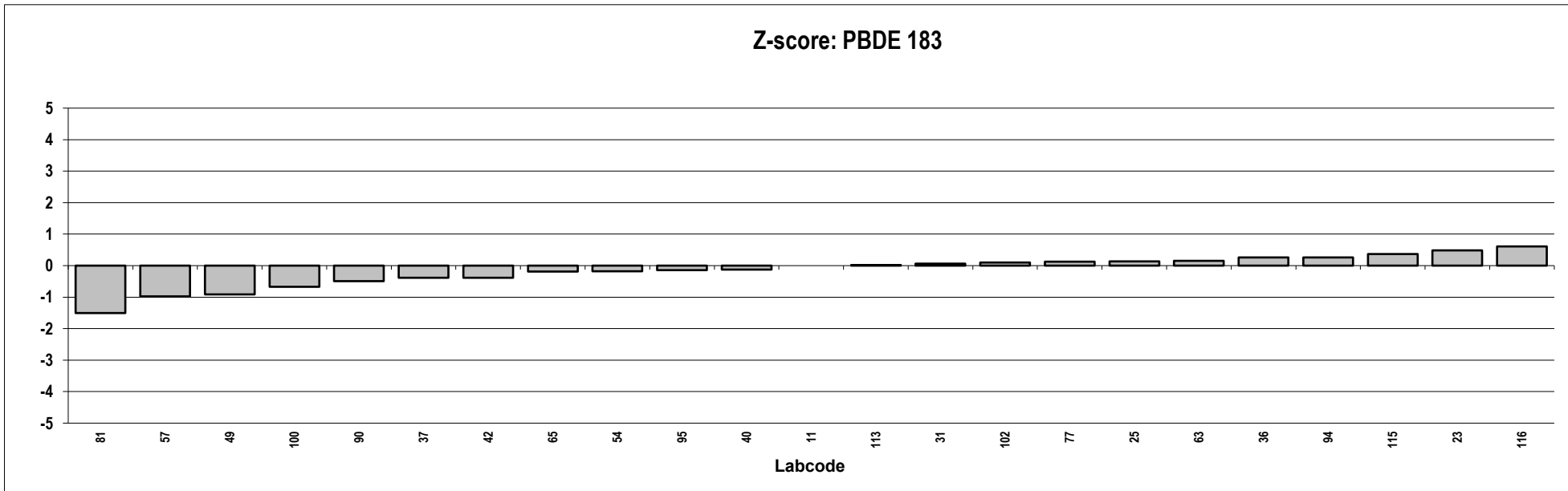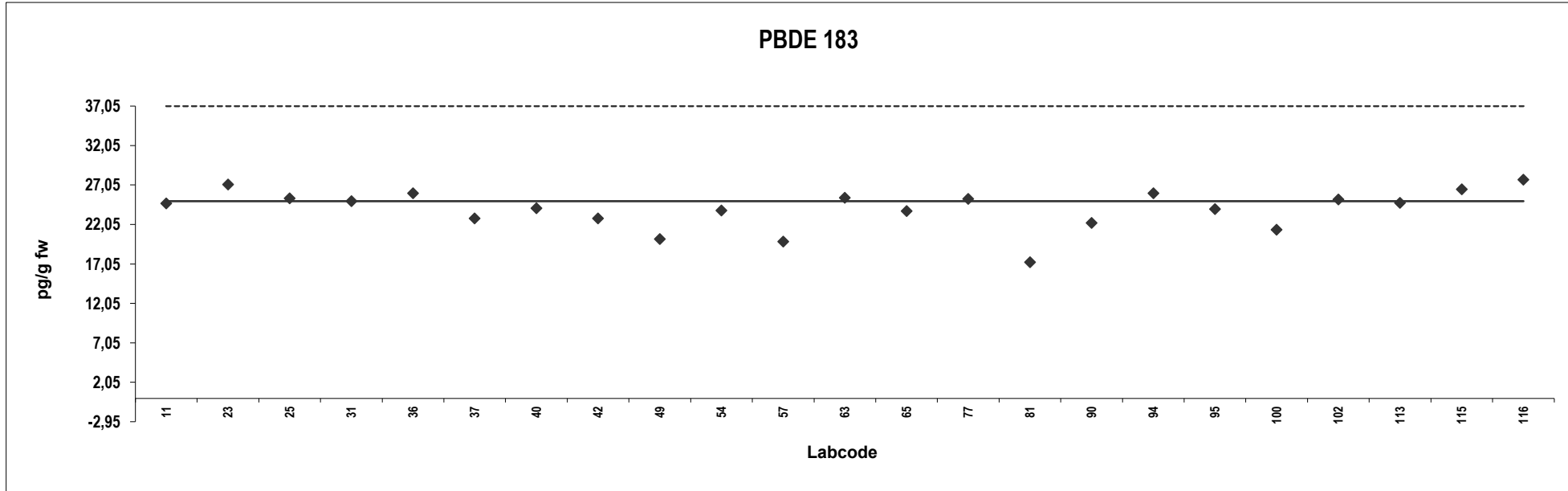
Analyte solution
Congener: PBDE 209

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	129	1,8					
23	96	0,032					
25	92	-0,17					
31	98	0,15					
36	98	0,11					
37	95	-0,0045					
57	87	-0,46					
63	0,0	-5,0	Outlier				
65	95	0,0045					
77	100	0,26					
81	80	-0,79					
90	98	0,13					
94	102	0,35					
95	92	-0,19					
100	95	-0,0045					
102	92	-0,18					
113	90	-0,26					
115	97	0,11					
116	82	-0,69					

Consensus statistics

Consensus median, pg/g	95
Median all values pg/g	95
Consensus mean, pg/g	96
Standard deviation, pg/g	10
Relative standard deviation, %	11
No. of values reported	19
No. of values removed	1
No. of reported non-detects	0
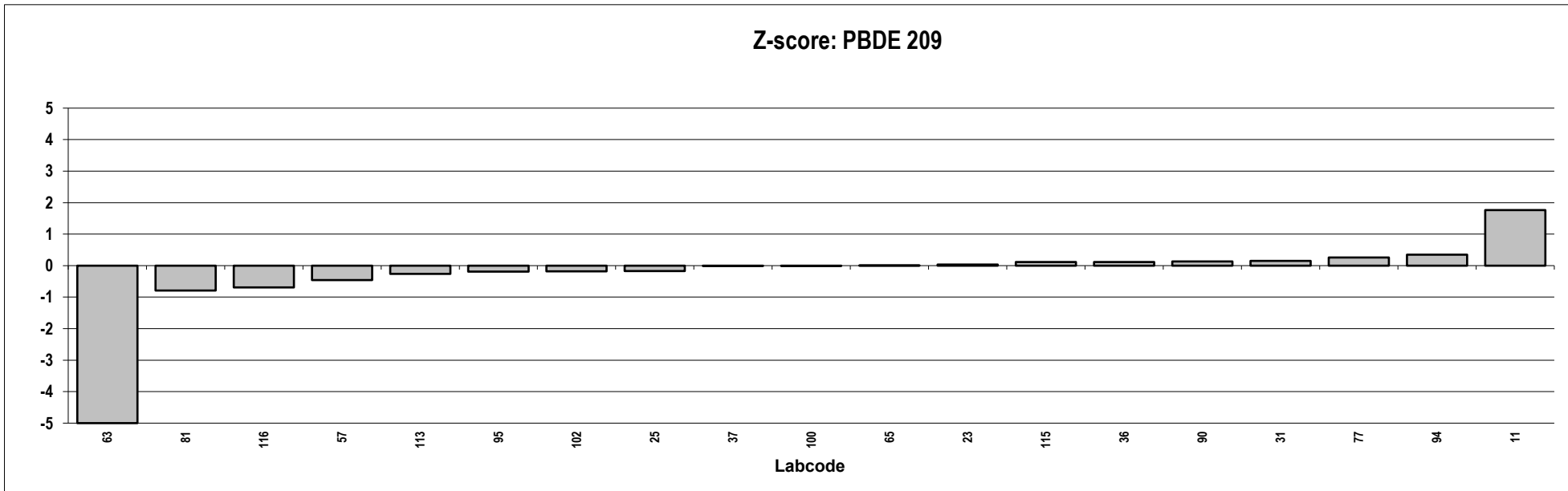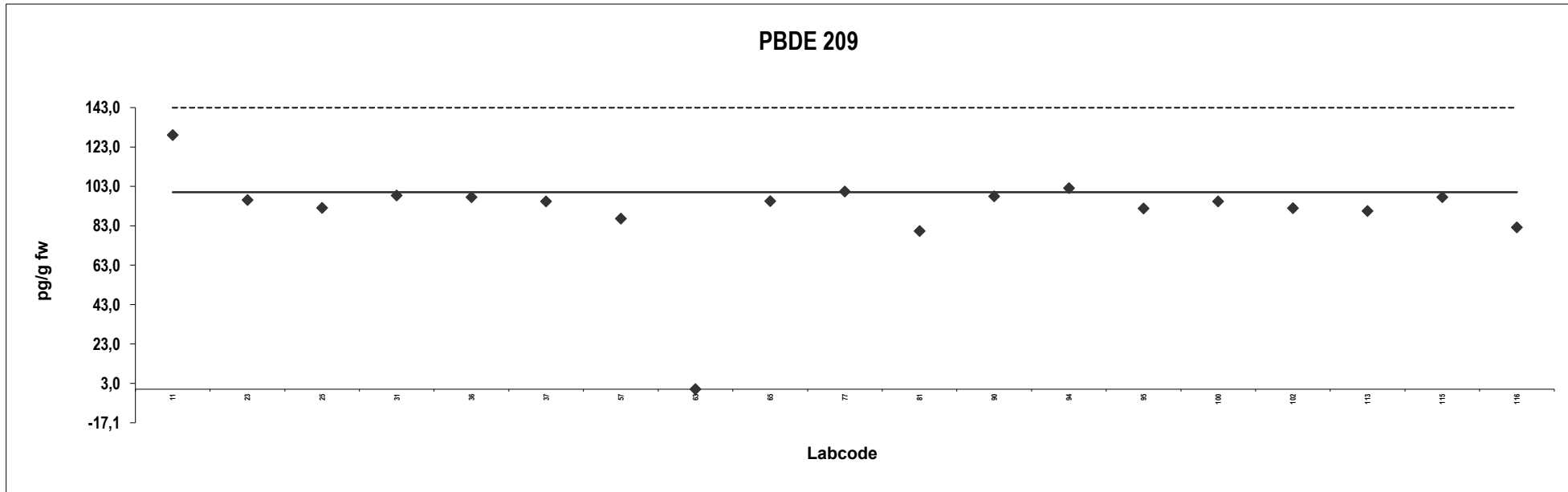
PBDE 209

Z-score: PBDE 209

Analyte solution

Congener: α-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	455	-0,24					
17	448	-0,31					
49	434	-0,46					
65	509	0,32					
81	570	0,97					
95	500	0,24					

Consenus statistics

Consensus median, pg/g	478
Median all values pg/g	478
Consensus mean, pg/g	486
Standard deviation, pg/g	51
Relative standard deviation, %	10
No. of values reported	6
No. of values removed	0
No. of reported non-detects	0

α-HBCD

Z-score: α-HBCD
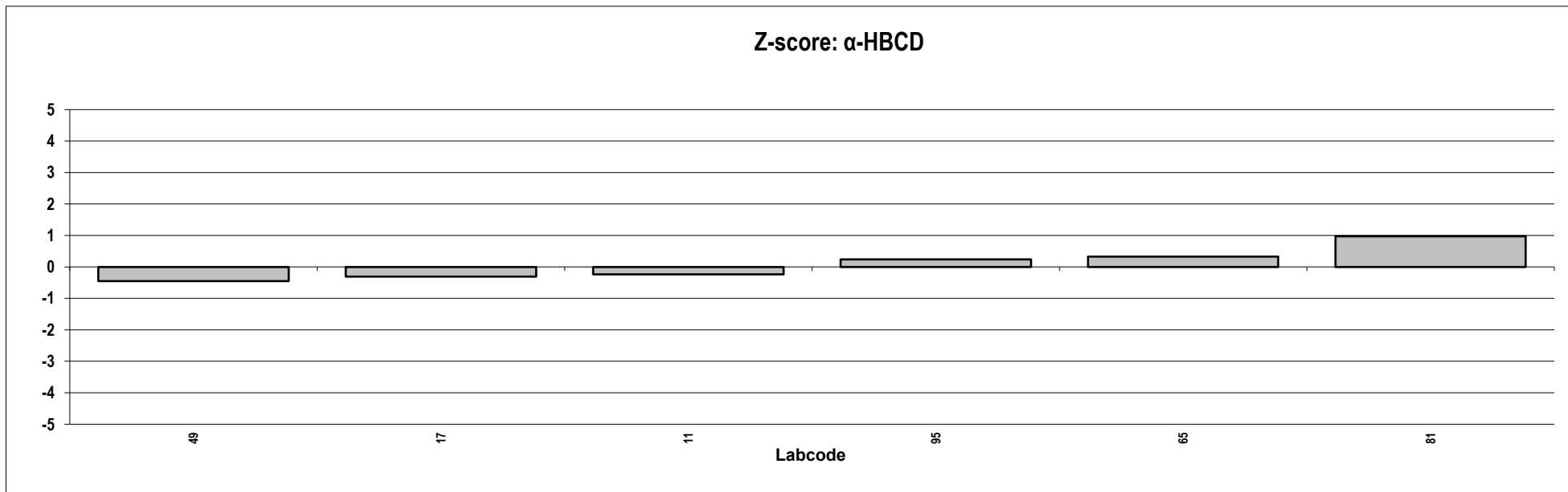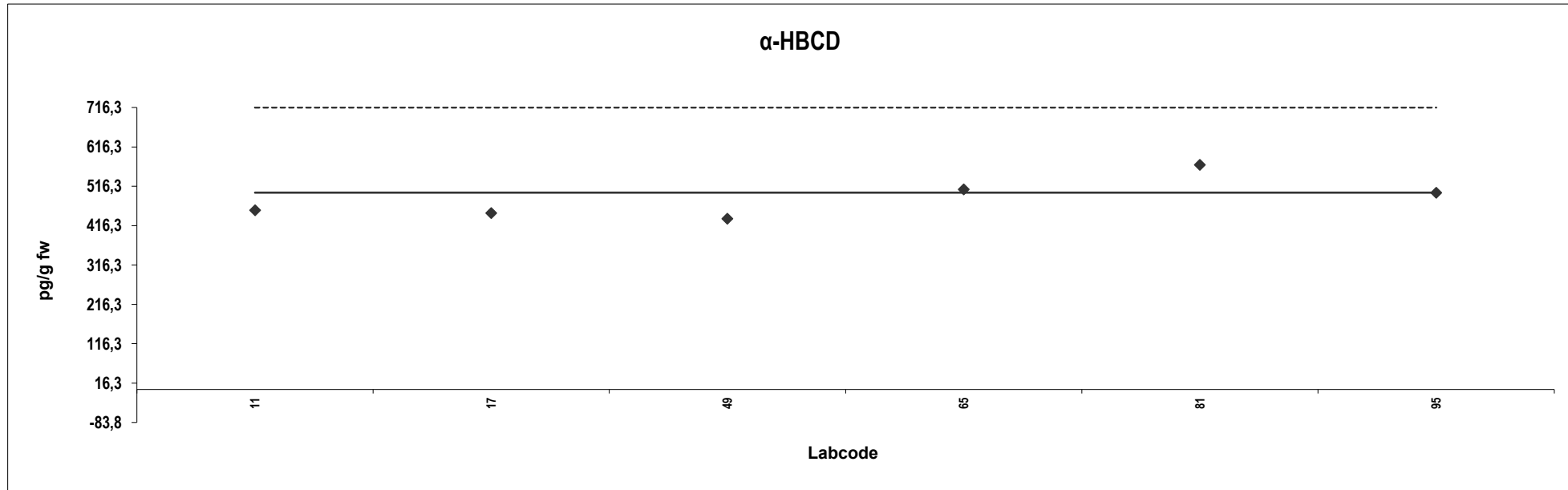
Appendix 2:

Presentation of results for
Veal-2019

Appendix 2: Presentation of results: Veal-2019

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 × 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 × 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 × 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 ± 20% from the consensus value.

Veal
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	83	Outlier,ND	114	0,0059	5,3	ND
5	0,00091	-3,4		115	0,00060	-3,9	
7	0,0020	-1,5	ND	116	0,0050	3,8	ND
10	0,0021	-1,4		118	0,0022	-1,2	ND
11	0,0018	-1,9	ND	120	0,0070	7,3	
15	0,0050	3,8	ND				
17	0,00098	-3,3					
20	0,0046	3,1	ND				
23	0,019	27	Outlier,ND				
24	0,0052	4,2					
27	0,0056	4,9	ND				
28	0,18	311	Outlier,ND				
31	0,0027	-0,26					
32	0,0041	2,3	ND				
33	0,0013	-2,7	ND				
34	0,0024	-0,79	ND				
36	0,0030	0,26	ND				
37	0,0020	-1,5	ND				
40	0,011	14	Outlier,ND				
43	0,010	13	Outlier,ND				
44	0,00091	-3,4	ND				
45	0,0062	5,8	ND				
49	0,0020	-1,5					
54	0,00071	-3,8					
57	0,0019	-1,7					
58	0,050	83	Outlier,ND				
61	0,0095	12	ND				
63	0,0060	5,5	ND				
64	0,0090	11					
65	0,00091	-3,4					
70	0,079	134	Outlier,ND				
73	0,0069	7,1					
75	0,0050	3,8	ND				
76	0,0032	0,61	ND				
80	0,013	17	Outlier,ND				
87	0,0030	0,26					
88	0,0010	-3,2	ND				
89	0,0012	-2,9					
95	0,0060	5,5	ND				
100	0,0085	9,8	ND				
103	0,0050	3,8	ND				
106	0,0019	-1,7	ND				
108	0,010	13	Outlier,ND				
109	0,010	13	Outlier,ND				
113	0,0013	-2,7	ND				

Consenus statistics

Consensus median, pg/g	0,0029
Median all values pg/g	0,0048
Consensus mean, pg/g	0,0036
Standard deviation, pg/g	0,0025
Relative standard deviation, %	69
No. of values reported	50
No. of values removed	10
No. of reported non-detects	35

2,3,7,8 TCDD
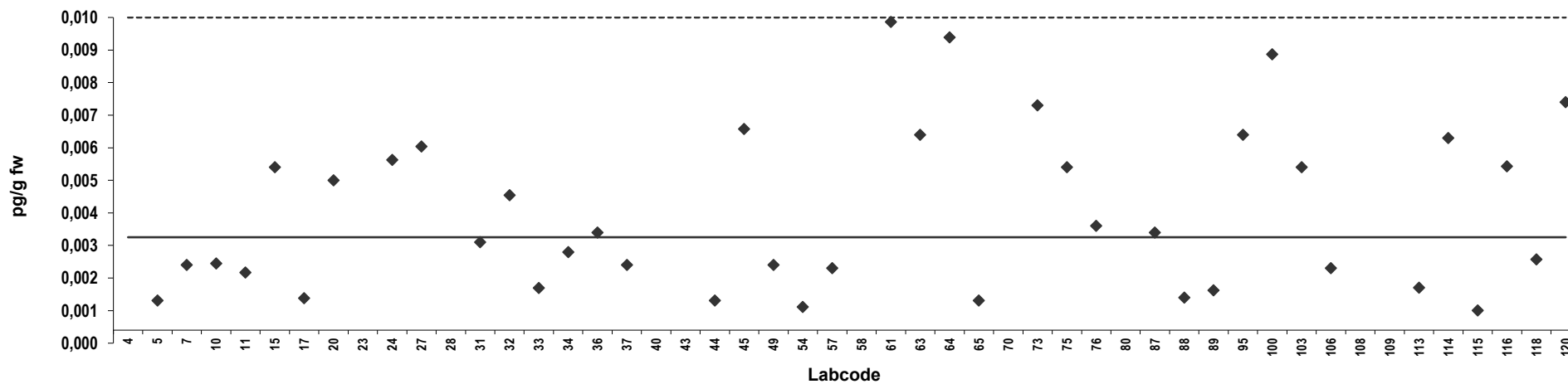
Z-score: 2,3,7,8 TCDD
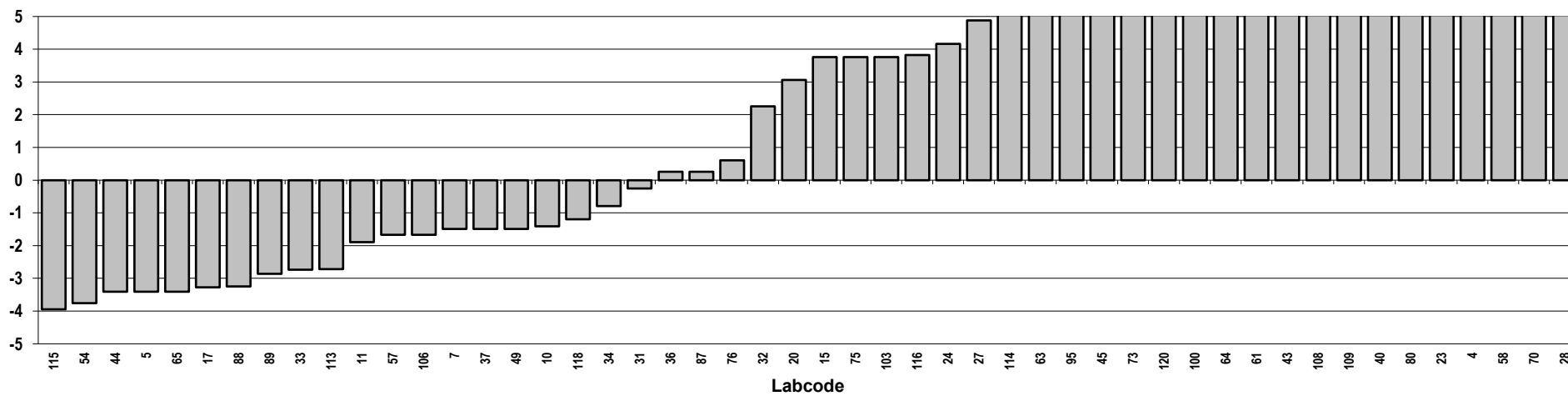
Veal
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	31	Outlier,ND	114	0,0084	1,0	ND
5	0,0039	-2,2		115	0,0012	-4,1	
7	0,0050	-1,4		116	0,0057	-0,96	ND
10	0,0053	-1,2		118	0,0045	-1,8	
11	0,0065	-0,35	ND	120	0,011	2,9	
15	0,0080	0,71					
17	0,0018	-3,7					
20	0,0090	1,4					
23	0,022	11	Outlier,ND				
24	0,0080	0,73					
27	0,015	5,5	ND				
28	0,14	97	Outlier				
31	0,0050	-1,5					
32	0,0046	-1,7					
33	0,0060	-0,71					
34	0,0076	0,43					
36	0,0082	0,86					
37	0,0022	-3,5					
40	0,0090	1,4	ND				
43	0,010	2,1	ND				
44	0,0089	1,4					
45	0,0086	1,1	ND				
49	0,0070	0,00					
54	0,0089	1,4					
57	0,0056	-1,0					
58	0,050	31	Outlier,ND				
61	0,016	6,5	Outlier				
63	0,0070	0,00	ND				
64	0,027	14	Outlier				
65	0,0049	-1,5					
70	0,087	57	Outlier,ND				
73	0,014	5,2					
75	0,0080	0,71					
76	0,0042	-2,0					
80	0,013	3,9	ND				
87	0,010	2,1					
88	0,0065	-0,38					
89	0,0052	-1,3					
95	0,0070	0,00	ND				
100	0,0087	1,2	ND				
103	0,016	6,4	ND				
106	0,0052	-1,3					
108	0,010	2,1	ND				
109	0,010	2,1	ND				
113	0,0065	-0,36					

Consenus statistics

Consensus median, pg/g	0,0070
Median all values pg/g	0,0080
Consensus mean, pg/g	0,0075
Standard deviation, pg/g	0,0032
Relative standard deviation, %	43
No. of values reported	50
No. of values removed	7
No. of reported non-detects	18

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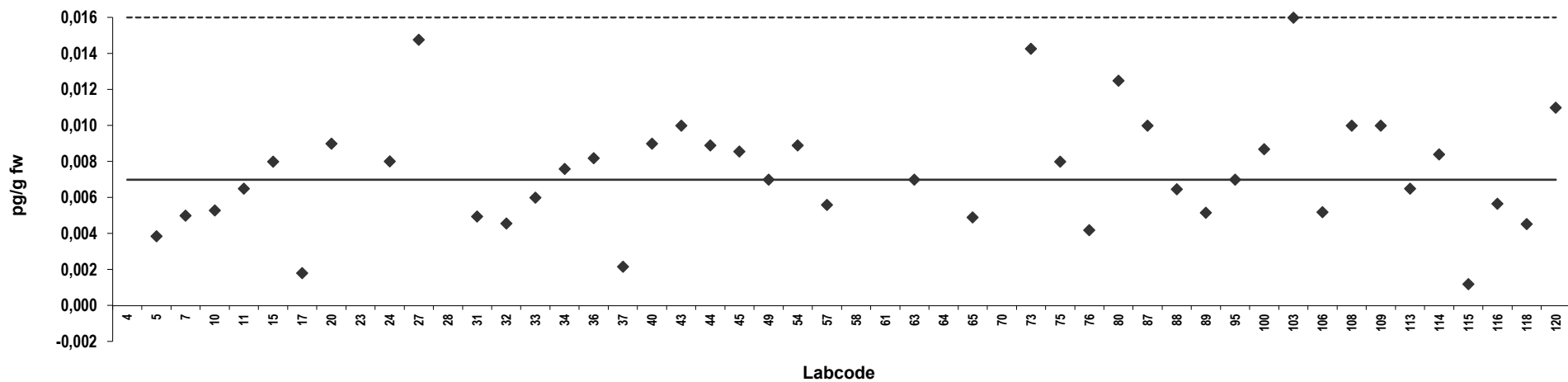
Z-score: 1,2,3,7,8 PeCDD
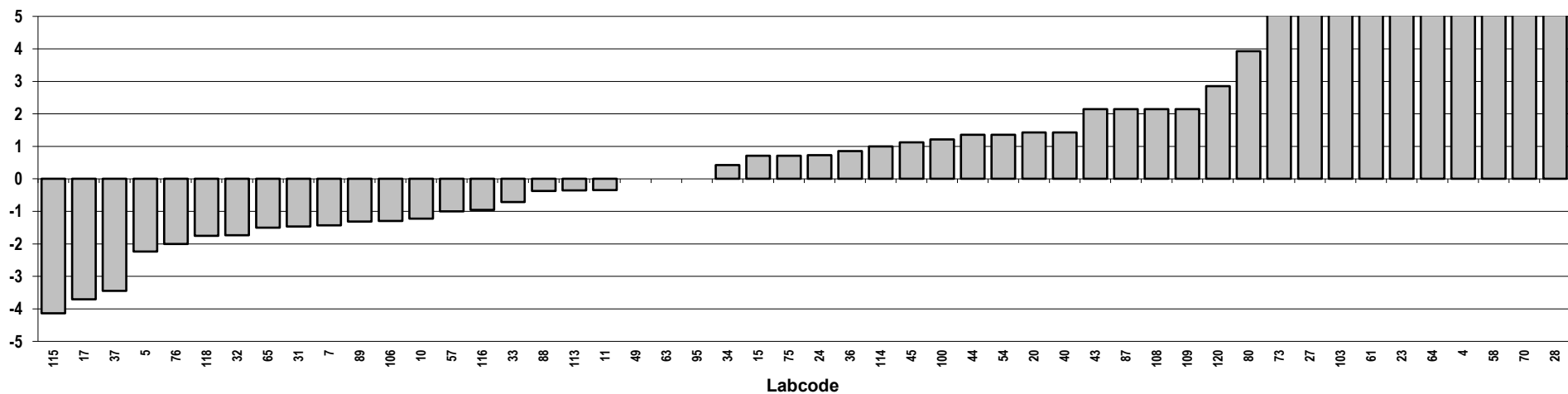
Veal
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	58	Outlier,ND	114	0,0053	1,6	ND
5	0,0039	-0,17		115	0,0036	-0,48	
7	0,0080	5,0		116	0,0061	2,6	ND
10	0,0025	-1,9		118	0,0016	-3,0	
11	0,0011	-3,6	ND	120	0,010	7,5	
15	0,0050	1,3	ND				
17	0,0016	-2,9					
20	0,0038	-0,25	ND				
23	0,019	19	Outlier,ND				
24	0,0031	-1,1					
27	0,027	28	Outlier,ND				
28	0,12	145	Outlier,ND				
31	0,0038	-0,20	ND				
32	0,0041	0,17	ND				
33	0,0027	-1,6					
34	0,0031	-1,1					
36	0,0040	0,00	ND				
37	0,0050	1,3	ND				
40	0,0050	1,3					
43	0,030	33	Outlier,ND				
44	0,0039	-0,13					
45	0,015	14	Outlier,ND				
49	0,0040	0,00					
54	0,0099	7,4					
57	0,0025	-1,9					
58	0,050	58	Outlier,ND				
61	0,019	19	Outlier				
63	0,0050	1,3	ND				
64	0,017	16	Outlier				
65	0,0039	-0,13					
70	0,097	117	Outlier,ND				
73	0,0062	2,8					
75	0,0050	1,3	ND				
76	0,0032	-1,0	ND				
80	0,025	26	Outlier,ND				
87	0,0080	5,0					
88	0,0050	1,3					
89	0,0018	-2,8					
95	0,010	7,5	ND				
100	0,0079	4,9	ND				
103	0,0060	2,5	ND				
106	0,0020	-2,5	ND				
108	0,010	7,5	ND				
109	0,0040	0,00					
113	0,0027	-1,6					

Consensus statistics

Consensus median, pg/g	0,0040
Median all values pg/g	0,0050
Consensus mean, pg/g	0,0047
Standard deviation, pg/g	0,0025
Relative standard deviation, %	52
No. of values reported	50
No. of values removed	11
No. of reported non-detects	26

1,2,3,4,7,8 HxCDD
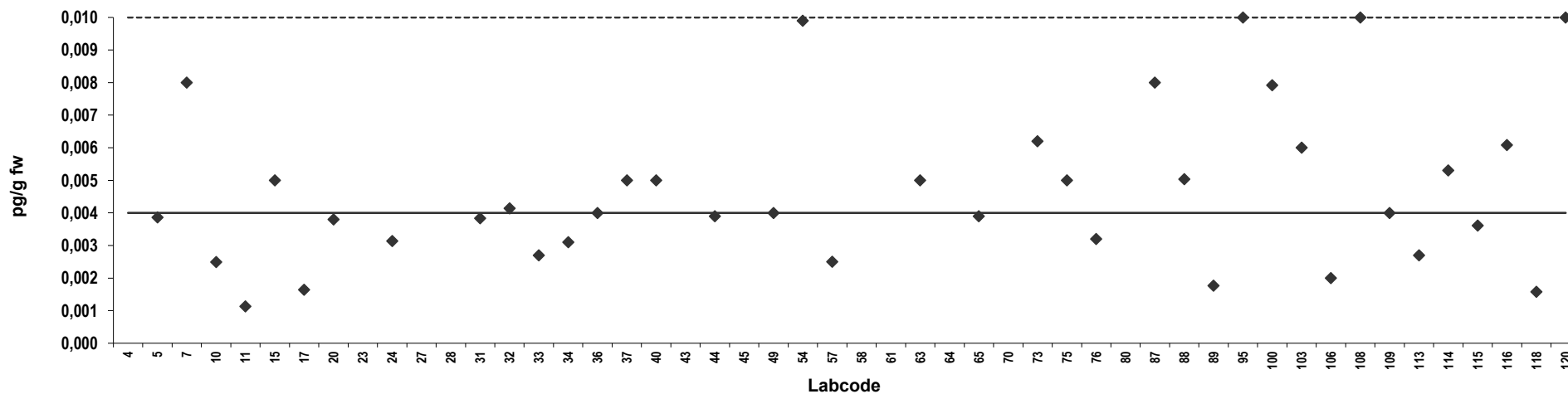
Z-score: 1,2,3,4,7,8 HxCDD
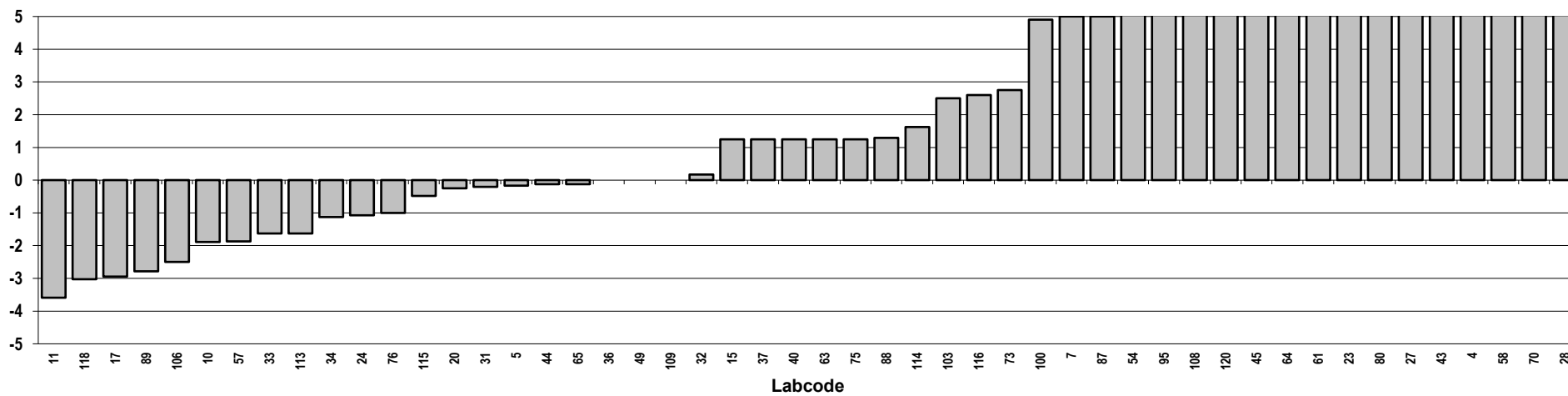
Veal
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	23	Outlier,ND	114	0,0070	-1,1	ND
5	0,0075	-0,83		115	0,0066	-1,3	
7	0,0080	-0,56		116	0,0059	-1,7	ND
10	0,0095	0,29		118	0,0057	-1,8	
11	0,0091	0,04	ND	120	0,016	3,9	
15	0,011	1,1					
17	0,0095	0,29					
20	0,0039	-2,8	ND				
23	0,020	6,1	Outlier,ND				
24	0,0087	-0,16					
27	0,029	11	Outlier,ND				
28	0,12	62	Outlier,ND				
31	0,0088	-0,13					
32	0,0078	-0,69					
33	0,010	0,56					
34	0,0061	-1,6					
36	0,010	0,67					
37	0,011	1,4					
40	0,0056	-1,9					
43	0,030	12	Outlier,ND				
44	0,0060	-1,7					
45	0,015	3,6	ND				
49	0,013	2,2					
54	0,013	2,2					
57	0,0086	-0,22					
58	0,050	23	Outlier,ND				
61	0,017	4,5					
63	0,0080	-0,56					
64	0,025	9,0	Outlier				
65	0,0081	-0,50					
70	0,093	47	Outlier,ND				
73	0,012	1,4					
75	0,010	0,56					
76	0,0082	-0,44					
80	0,025	8,9	Outlier,ND				
87	0,015	3,3					
88	0,0090	-0,0050					
89	0,011	0,83					
95	0,0090	0,00	ND				
100	0,0076	-0,77	ND				
103	0,016	3,9					
106	0,0077	-0,73					
108	0,010	0,56	ND				
109	0,012	1,4					
113	0,0097	0,39					

Consenus statistics

Consensus median, pg/g	0,0090
Median all values pg/g	0,0099
Consensus mean, pg/g	0,0096
Standard deviation, pg/g	0,0031
Relative standard deviation, %	32
No. of values reported	50
No. of values removed	9
No. of reported non-detects	16
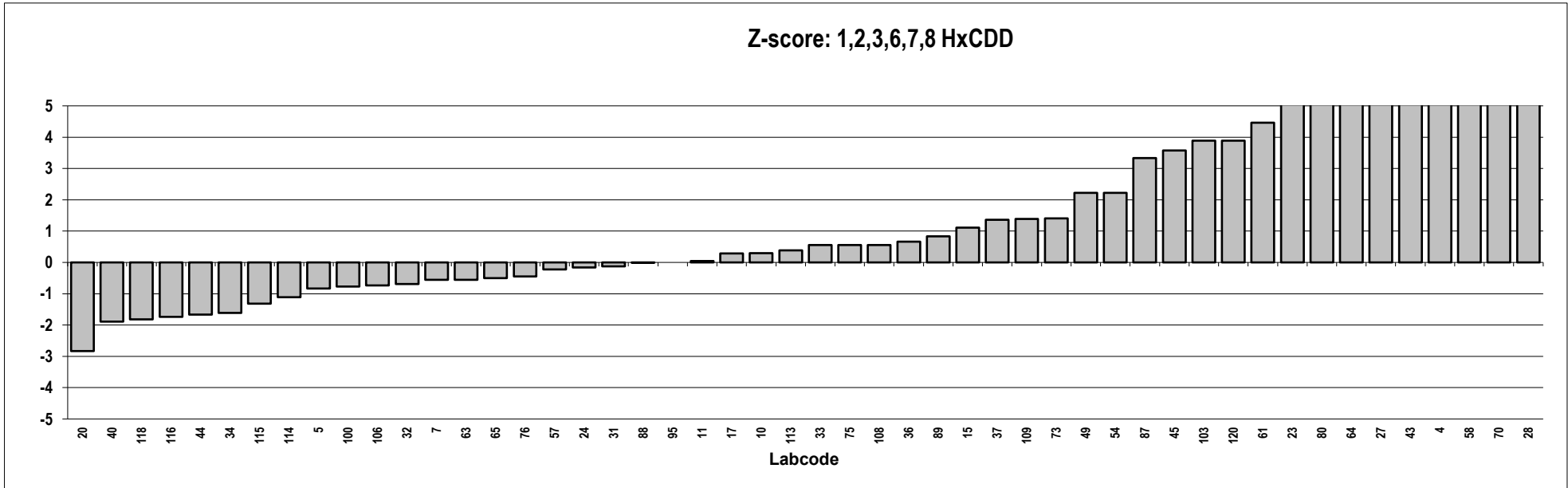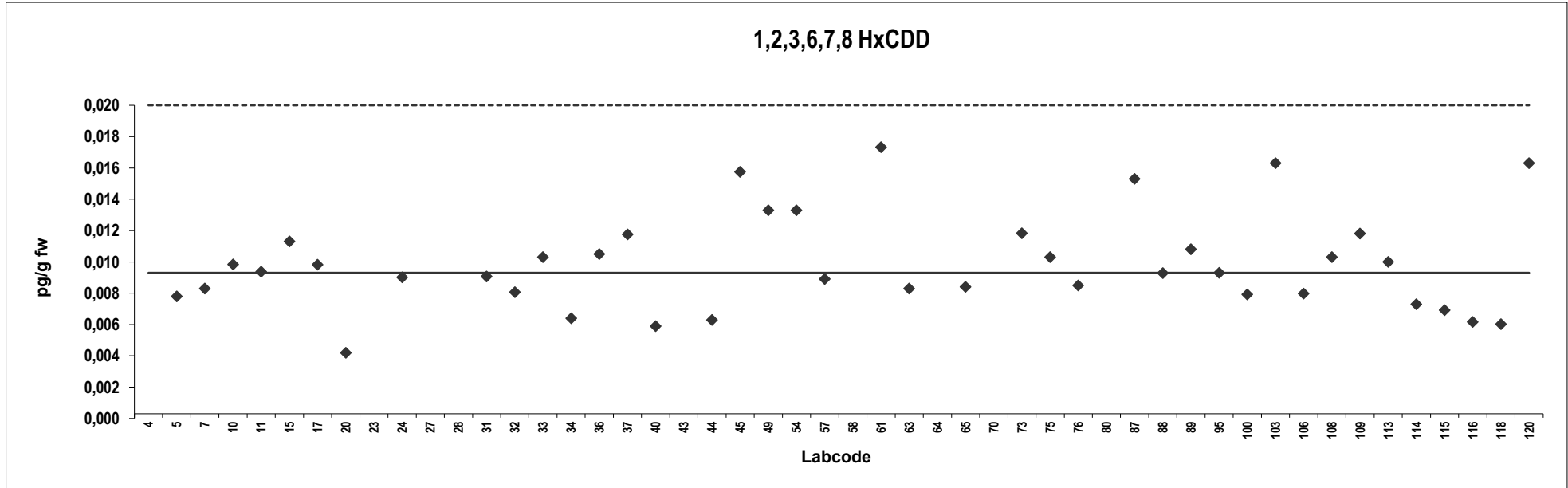
1,2,3,6,7,8 HxCDD

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

Veal

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	61	Outlier,ND	114	0,0055	2,2	ND
5	0,0027	-1,4		115	0,0024	-1,8	
7	0,0020	-2,4	ND	116	0,0061	3,0	ND
10	0,0026	-1,6		118	0,0016	-2,9	
11	0,0011	-3,6	ND	120	0,012	11	Outlier
15	0,0050	1,6	ND				
17	0,0016	-2,8					
20	0,0038	0,00	ND				
23	0,019	20	Outlier,ND				
24	0,0024	-1,8					
27	0,026	30	Outlier,ND				
28	0,26	331	Outlier				
31	0,0038	0,048	ND				
32	0,0041	0,45	ND				
33	0,0030	-1,1					
34	0,0040	0,26					
36	0,0050	1,6	ND				
37	0,0050	1,6	ND				
40	0,0035	-0,39					
43	0,030	34	Outlier,ND				
44	0,0010	-3,7	ND				
45	0,013	12	Outlier,ND				
49	0,0040	0,26					
54	0,0086	6,3					
57	0,0024	-1,8					
58	0,050	61	Outlier,ND				
61	0,016	16	Outlier				
63	0,0050	1,6	ND				
64	0,0089	6,7					
65	0,0031	-0,92					
70	0,091	115	Outlier,ND				
73	0,0015	-3,1					
75	0,0050	1,6	ND				
76	0,0036	-0,26					
80	0,025	28	Outlier,ND				
87	0,0070	4,2					
88	0,0018	-2,6					
89	0,0032	-0,74					
95	0,011	9,5	Outlier,ND				
100	0,022	24	Outlier				
103	0,0060	2,9	ND				
106	0,0042	0,55					
108	0,010	8,2	ND				
109	0,010	8,2	ND				
113	0,0022	-2,1	ND				

Consenus statistics

Consensus median, pg/g	0,0038
Median all values pg/g	0,0050
Consensus mean, pg/g	0,0041
Standard deviation, pg/g	0,0024
Relative standard deviation, %	57
No. of values reported	50
No. of values removed	13
No. of reported non-detects	26

1,2,3,7,8,9 HxCDD
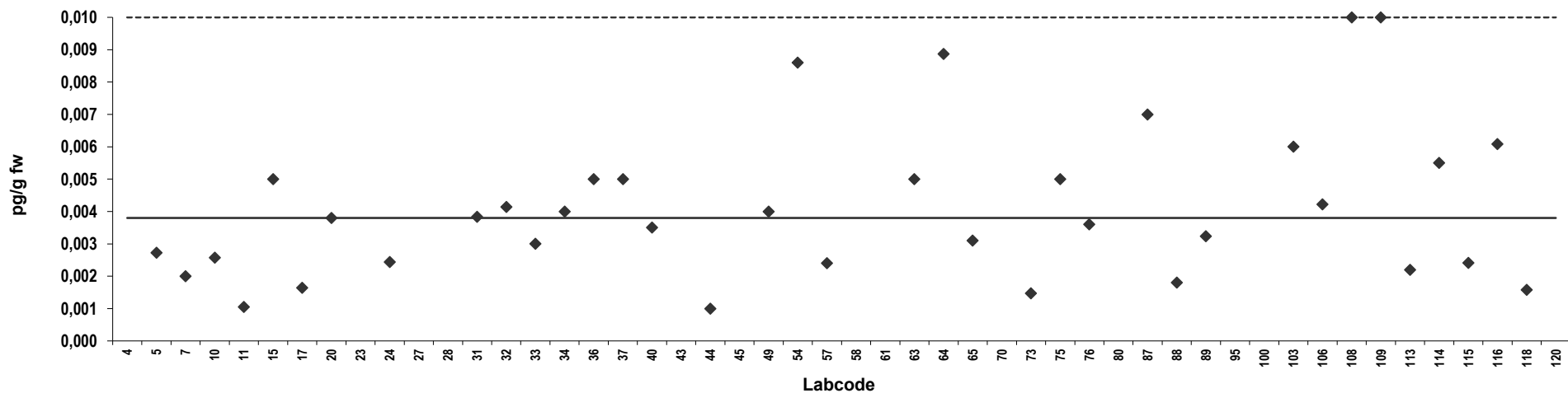
Z-score: 1,2,3,7,8,9 HxCDD
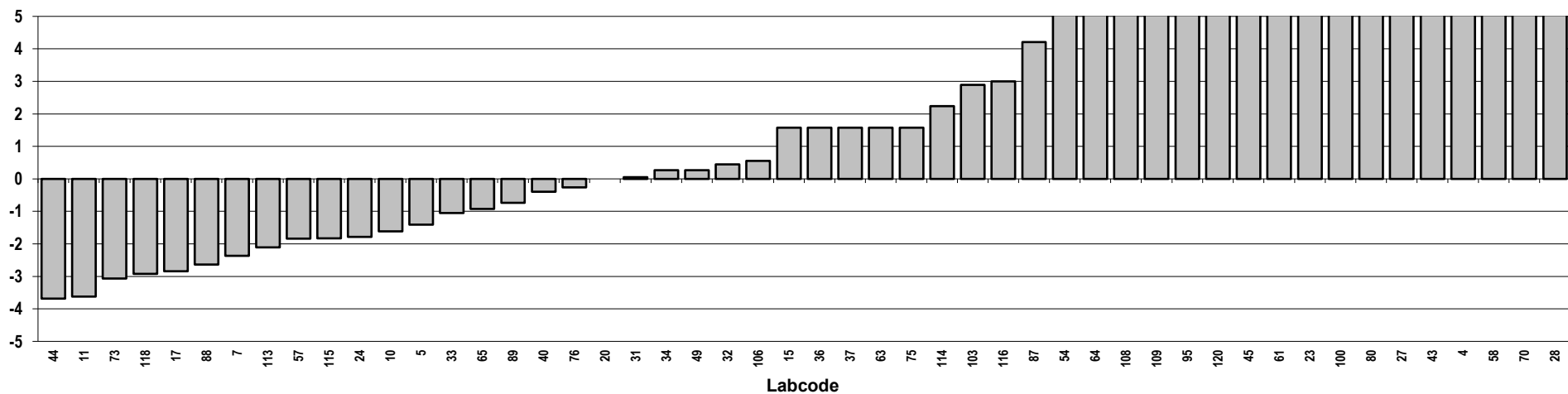
Veal
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	8,2	Outlier,ND	114	0,016	-0,79	
5	0,0096	-2,5		115	0,026	1,8	
7	0,017	-0,52		116	0,011	-2,1	ND
10	0,017	-0,60		118	0,011	-2,1	
11	0,023	1,1		120	0,063	12	Outlier
15	0,024	1,3					
17	0,019	0,10					
20	0,019	-0,10					
23	0,025	1,6	ND				
24	0,015	-0,96					
27	0,028	2,3					
28	0,085	17	Outlier,ND				
31	0,031	3,1	ND				
32	0,017	-0,60					
33	0,012	-1,7					
34	0,020	0,29					
36	0,020	0,27	ND				
37	0,020	0,35					
40	0,0090	-2,6					
43	0,030	2,9	ND				
44	0,017	-0,47					
45	0,015	-0,99					
49	0,020	0,27					
54	0,031	3,2					
57	0,015	-1,0					
58	0,050	8,2	Outlier,ND				
61	0,0095	-2,5	ND				
63	0,015	-1,0					
64	0,044	6,6	Outlier				
65	0,018	-0,26					
70	0,073	14	Outlier,ND				
73	0,021	0,60					
75	0,024	1,3					
76	0,012	-1,9					
80	0,050	8,2	Outlier,ND				
87	0,024	1,3					
88	0,027	2,0					
89	0,018	-0,29					
95	0,021	0,53					
100	0,014	-1,2					
103	0,052	8,7	Outlier				
106	0,029	2,7					
108	0,027	2,1					
109	0,015	-1,2					
113	0,022	0,79					

Consensus statistics

Consensus median, pg/g	0,019
Median all values pg/g	0,020
Consensus mean, pg/g	0,019
Standard deviation, pg/g	0,0061
Relative standard deviation, %	32
No. of values reported	50
No. of values removed	8
No. of reported non-detects	11

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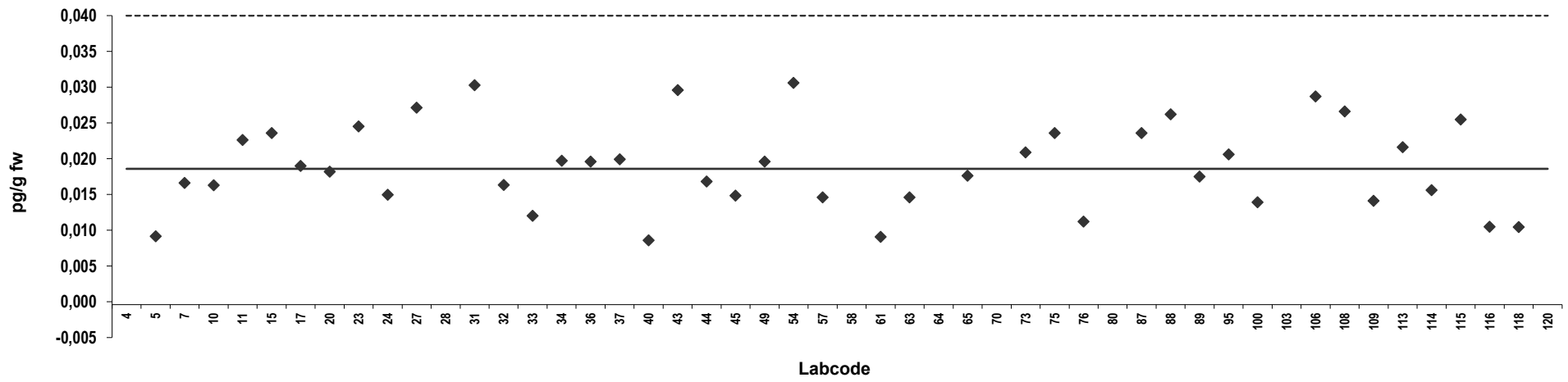
Z-score: 1,2,3,4,6,7,8 HpCDD
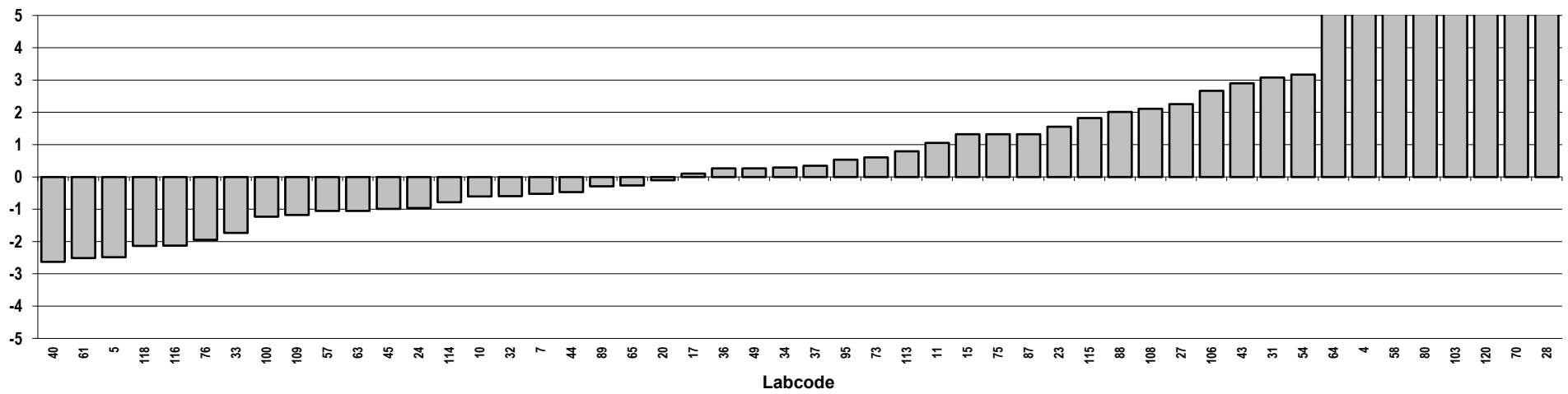
Veal

Congener: OCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	0,94	ND	114	0,033	-1,1	
5	0,021	-2,5		115	0,12	8,7	Outlier
7	0,026	-1,9		116	0,037	-0,61	ND
10	0,033	-1,1		118	0,020	-2,6	
11	0,080	4,4		120	0,55	60	Outlier
15	0,087	5,3					
17	0,025	-2,0					
20	0,041	-0,12					
23	0,056	1,7					
24	0,024	-2,1					
27	0,075	3,9					
28	0,13	10	Outlier,ND				
31	0,061	2,3	ND				
32	0,043	0,12					
33	0,033	-1,1					
34	0,036	-0,70					
36	0,024	-2,1					
37	0,055	1,5					
40	0,020	-2,6	ND				
43	0,050	0,94	ND				
44	0,062	2,4					
45	0,041	-0,15					
49	0,044	0,23					
54	0,081	4,6					
57	0,028	-1,7					
58	0,064	2,6					
61	0,075	3,9					
63	0,048	0,70					
64	0,079	4,4					
65	0,039	-0,37					
70	0,14	12	Outlier				
73	0,030	-1,5					
75	0,084	5,0					
76	0,032	-1,2					
80	0,10	6,9	Outlier,ND				
87	0,046	0,47					
88	0,036	-0,73					
89	0,032	-1,2					
95	0,080	4,5	ND				
100	0,046	0,45					
103	0,090	5,7					
106	0,13	10	Outlier				
108	0,080	4,5	ND				
109	0,028	-1,7					
113	0,040	-0,247					

Consenus statistics

Consensus median, pg/g	0,042
Median all values pg/g	0,046
Consensus mean, pg/g	0,048
Standard deviation, pg/g	0,021
Relative standard deviation, %	44
No. of values reported	50
No. of values removed	6
No. of reported non-detects	9
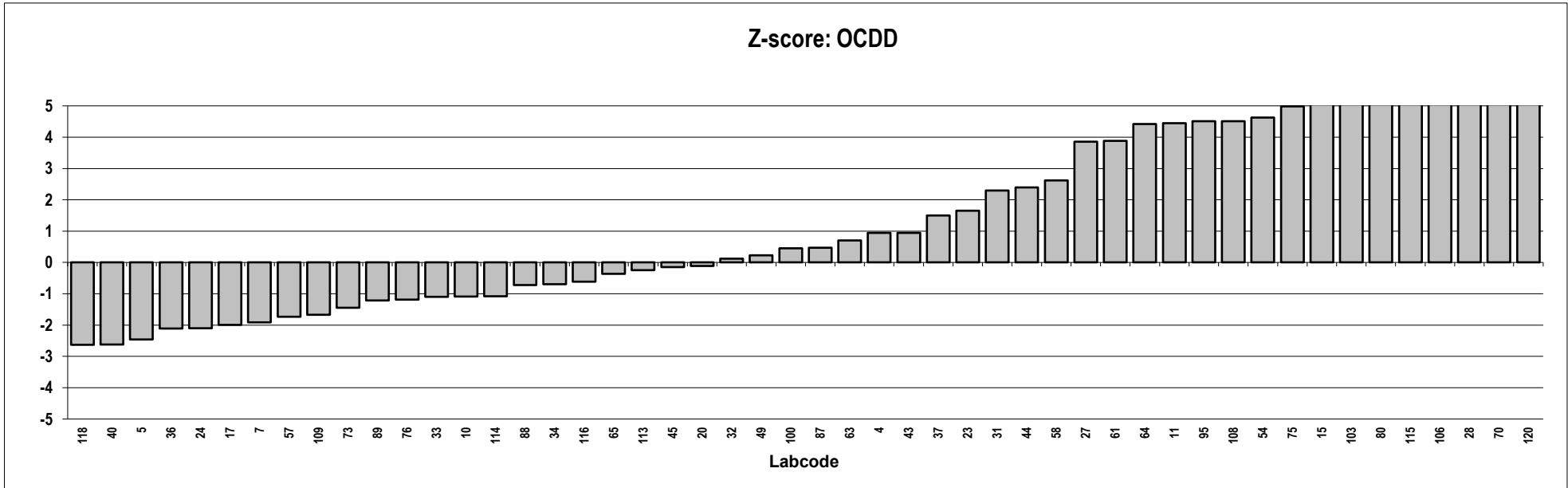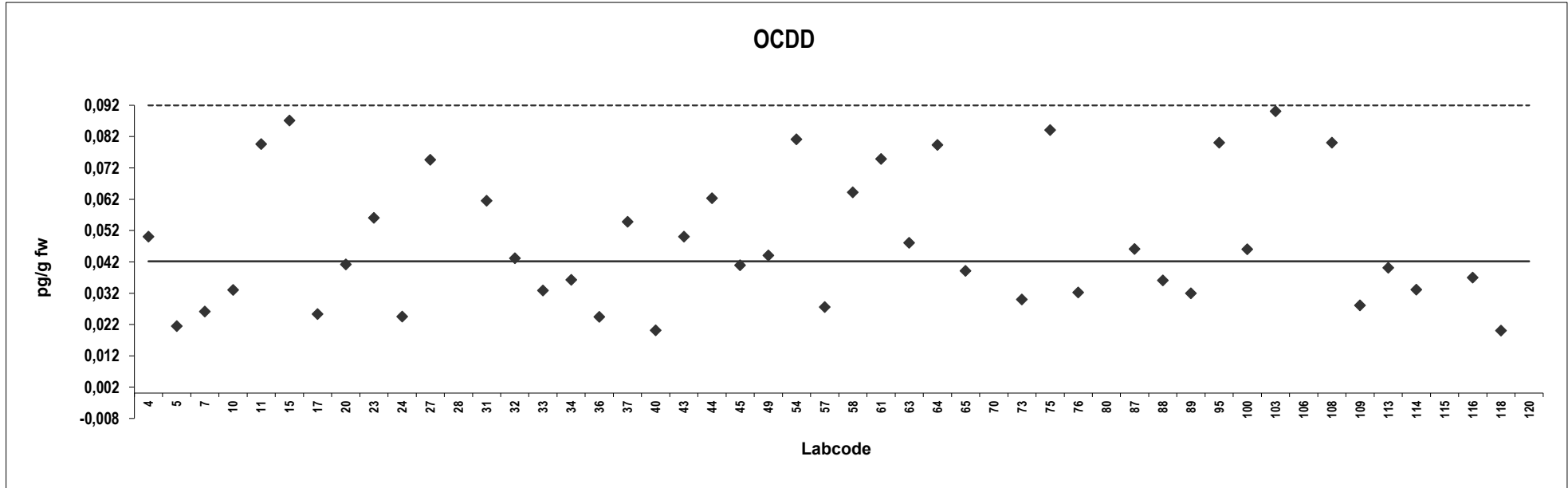
OCDD

Z-score: OCDD

Veal
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,20	208	Outlier,ND	114	0,033	30	Outlier
5	0,0027	-2,1		115	0,018	14	Outlier
7	0,0040	-0,75		116	0,0040	-0,77	ND
10	0,0024	-2,5		118	0,0024	-2,5	
11	0,0053	0,66	ND	120	0,025	22	Outlier
15	0,0050	0,31	ND				
17	0,0034	-1,3					
20	0,0074	2,9	ND				
23	0,024	20	Outlier				
24	0,0035	-1,3					
27	0,014	10	ND				
28	0,12	123	Outlier,ND				
31	0,0061	1,5	ND				
32	0,0044	-0,36					
33	0,0073	2,8					
34	0,0017	-3,2	ND				
36	0,0060	1,4	ND				
37	0,0044	-0,31					
40	0,0070	2,4	ND				
43	0,010	5,6	ND				
44	0,0017	-3,2					
45	0,0031	-1,7	ND				
49	0,0030	-1,8					
54	0,0022	-2,7					
57	0,0015	-3,4	ND				
58	0,050	48	Outlier,ND				
61	0,0095	5,1	ND				
63	0,0080	3,5	ND				
64	0,038	35	Outlier				
65	0,0024	-2,4					
70	0,086	87	Outlier,ND				
73	0,025	21	Outlier				
75	0,0050	0,31	ND				
76	0,0034	-1,4					
80	0,034	31	Outlier				
87	0,029	26	Outlier				
88	0,058	56	Outlier				
89	0,0028	-2,1					
95	0,018	14	Outlier				
100	0,0073	2,8	ND				
103	0,0080	3,5					
106	0,011	6,5					
108	0,010	5,6	ND				
109	0,010	5,6	ND				
113	0,0097	5,3					

Consensus statistics

Consensus median, pg/g	0,0047
Median all values pg/g	0,0073
Consensus mean, pg/g	0,0055
Standard deviation, pg/g	0,0032
Relative standard deviation, %	57
No. of values reported	50
No. of values removed	14
No. of reported non-detects	22

2,3,7,8 TCDF
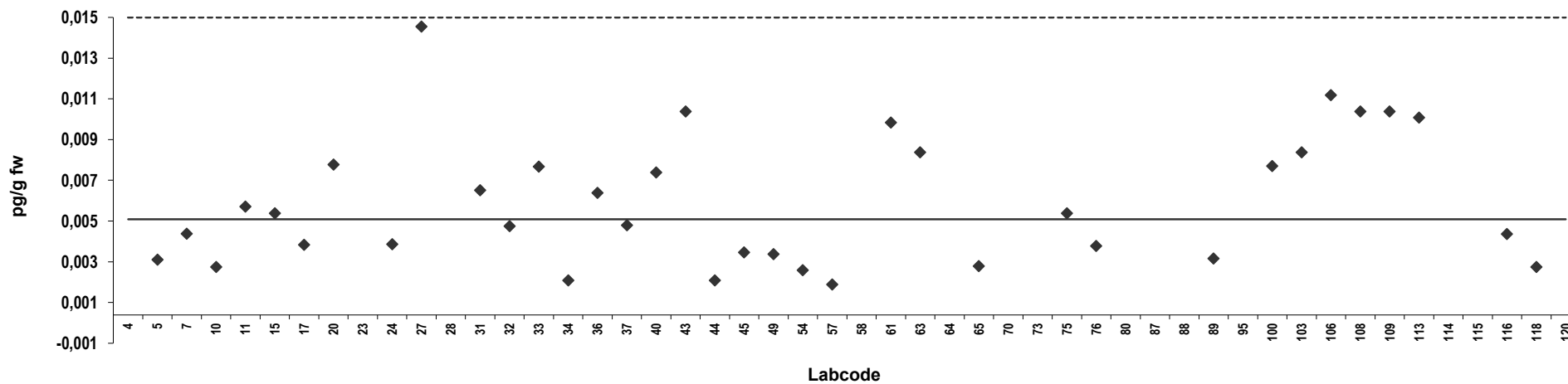
Z-score: 2,3,7,8 TCDF
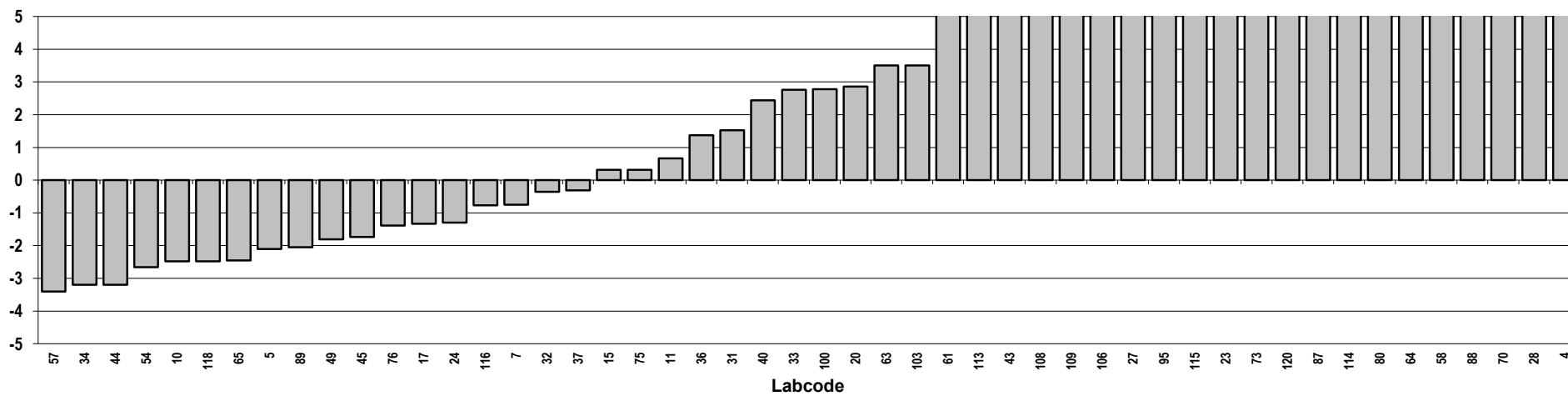
Veal
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	55	Outlier,ND	114	0,0060	2,2	ND
5	0,0027	-1,7		115	0,0066	3,0	
7	0,0010	-3,8	ND	116	0,0031	-1,2	ND
10	0,0020	-2,6	ND	118	0,0016	-3,1	
11	0,0029	-1,5	ND	120	0,010	7,1	
15	0,0050	1,0	ND				
17	0,0016	-3,0					
20	0,011	8,3	ND				
23	0,022	22	Outlier,ND				
24	0,0024	-2,1					
27	0,017	15	Outlier,ND				
28	0,11	128	Outlier,ND				
31	0,0038	-0,37	ND				
32	0,0041	0,00	ND				
33	0,0026	-1,9					
34	0,0037	-0,53	ND				
36	0,0060	2,2	ND				
37	0,0050	1,0	ND				
40	0,011	8,3					
43	0,010	7,1	ND				
44	0,0013	-3,5	ND				
45	0,0077	4,3	ND				
49	0,0010	-3,8	ND				
54	0,0019	-2,7					
57	0,0014	-3,3					
58	0,050	55	Outlier,ND				
61	0,0095	6,4	ND				
63	0,0070	3,5	ND				
64	0,010	7,1					
65	0,0024	-2,1					
70	0,10	115	Outlier,ND				
73	0,011	8,0					
75	0,0050	1,0	ND				
76	0,0032	-1,1	ND				
80	0,013	10	Outlier,ND				
87	0,0060	2,2					
88	0,034	36	Outlier				
89	0,0022	-2,3					
95	0,014	12	Outlier				
100	0,0065	2,8	ND				
103	0,0060	2,2	ND				
106	0,0030	-1,4	ND				
108	0,010	7,1	ND				
109	0,010	7,1	ND				
113	0,0037	-0,53					

Consenus statistics

Consensus median, pg/g	0,0041
Median all values pg/g	0,0060
Consensus mean, pg/g	0,0051
Standard deviation, pg/g	0,0033
Relative standard deviation, %	63
No. of values reported	50
No. of values removed	9
No. of reported non-detects	32

1,2,3,7,8 PeCDF

Z-score: 1,2,3,7,8 PeCDF
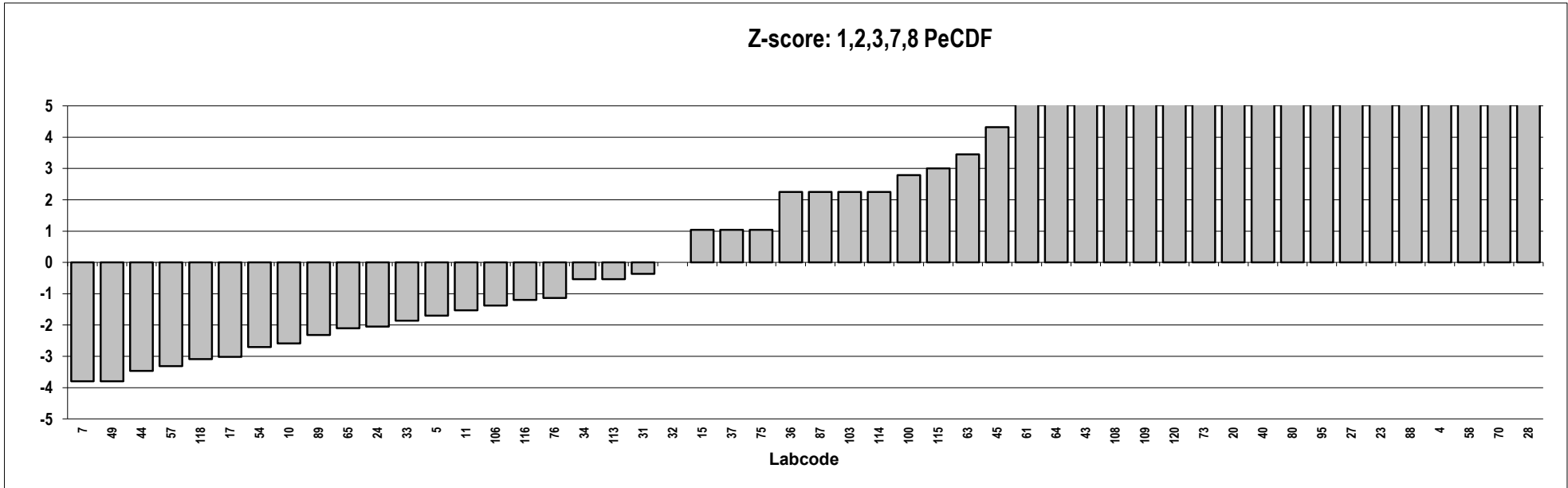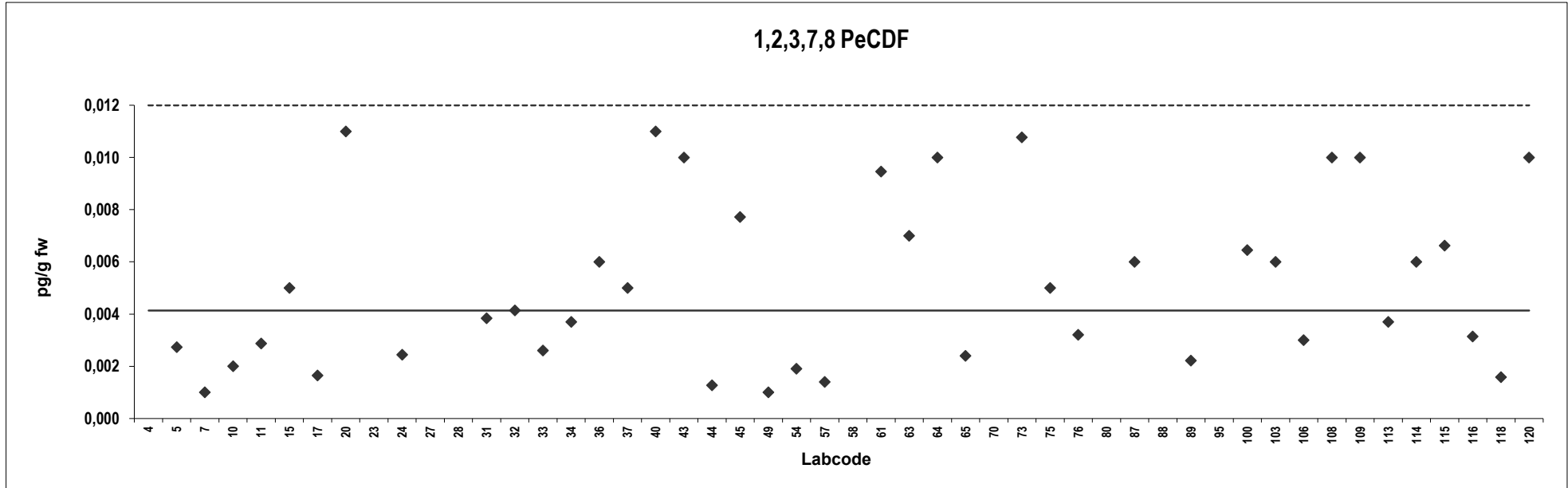
Veal
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	7,2	Outlier,ND	114	0,011	-2,3	
5	0,018	-0,66		115	0,022	0,30	
7	0,022	0,38		116	0,023	0,69	
10	0,020	-0,21		118	0,010	-2,4	
11	0,021	0,23		120	0,026	1,4	
15	0,022	0,38					
17	0,0079	-3,1					
20	0,013	-1,9					
23	0,022	0,43	ND				
24	0,020	-0,22					
27	0,023	0,69					
28	0,087	16	Outlier,ND				
31	0,019	-0,31					
32	0,017	-0,80					
33	0,021	0,038					
34	0,011	-2,3					
36	0,022	0,45					
37	0,017	-0,79					
40	0,0089	-2,8					
43	0,020	-0,11					
44	0,012	-2,1					
45	0,020	-0,038					
49	0,023	0,62					
54	0,027	1,6					
57	0,019	-0,30					
58	0,050	7,2	Outlier,ND				
61	0,0095	-2,7	ND				
63	0,025	1,1					
64	0,090	17	Outlier				
65	0,021	0,14					
70	0,093	18	Outlier,ND				
73	0,038	4,4					
75	0,021	0,14					
76	0,015	-1,3					
80	0,036	3,8					
87	0,024	0,87					
88	0,045	6,0	Outlier				
89	0,019	-0,26					
95	0,023	0,62					
100	0,016	-1,0					
103	0,032	2,8					
106	0,018	-0,57					
108	0,027	1,6					
109	0,022	0,38					
113	0,014	-1,6					

Consensus statistics	
Consensus median, pg/g	0,020
Median all values pg/g	0,021
Consensus mean, pg/g	0,020
Standard deviation, pg/g	0,0065
Relative standard deviation, %	33
No. of values reported	50
No. of values removed	6
No. of reported non-detects	6

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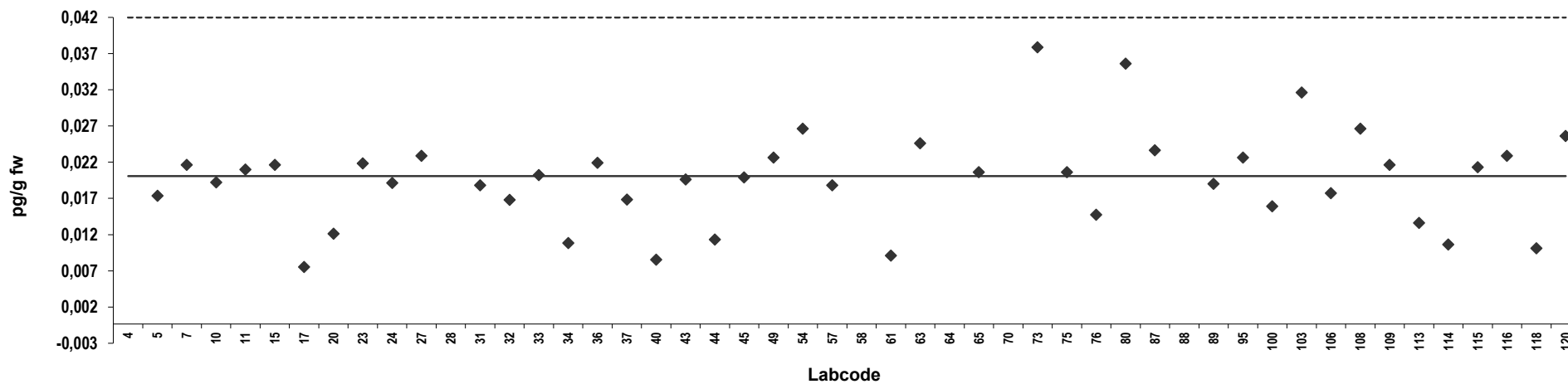
Z-score: 2,3,4,7,8 PeCDF
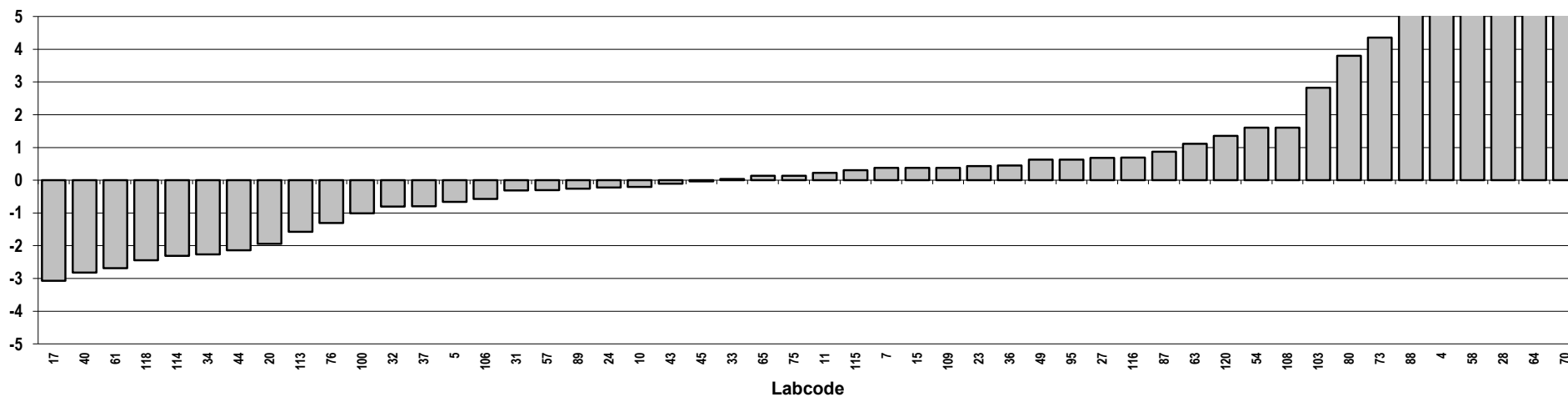
Veal
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	18	Outlier,ND	114	0,0055	-2,5	
5	0,0066	-2,0		115	0,0084	-1,2	
7	0,0060	-2,3		116	0,0031	-3,6	
10	0,0093	-0,79		118	0,0067	-1,9	
11	0,015	1,8		120	0,020	4,1	
15	0,011	0,00					
17	0,0089	-0,97					
20	0,012	0,27					
23	0,031	9,2	Outlier,ND				
24	0,0087	-1,0					
27	0,025	6,5	Outlier,ND				
28	0,18	79	Outlier				
31	0,0088	-0,98					
32	0,0087	-1,1					
33	0,012	0,64					
34	0,0052	-2,6					
36	0,011	0,045					
37	0,012	0,36					
40	0,013	0,91					
43	0,030	8,6	Outlier,ND				
44	0,014	1,2					
45	0,015	2,0	ND				
49	0,011	0,00					
54	0,017	2,7					
57	0,0082	-1,3					
58	0,050	18	Outlier,ND				
61	0,018	3,2					
63	0,0080	-1,4					
64	0,17	74	Outlier				
65	0,011	0,00					
70	0,068	26	Outlier,ND				
73	0,024	5,8	Outlier				
75	0,011	0,00					
76	0,010	-0,32					
80	0,025	6,4	Outlier,ND				
87	0,015	1,8					
88	0,021	4,3					
89	0,0087	-1,0					
95	0,018	3,2					
100	0,0055	-2,5	ND				
103	0,018	3,2					
106	0,0068	-1,9					
108	0,013	0,91					
109	0,011	0,00					
113	0,0075	-1,6					

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	50
No. of values removed	10
No. of reported non-detects	9

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

pg/g fw

Labcode

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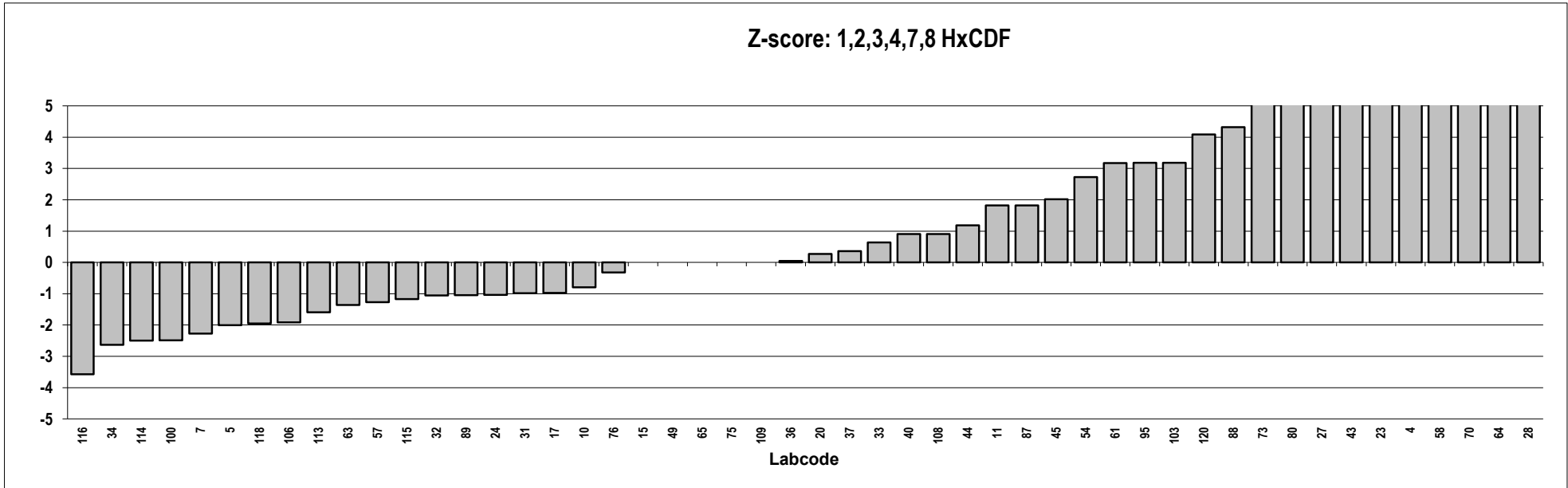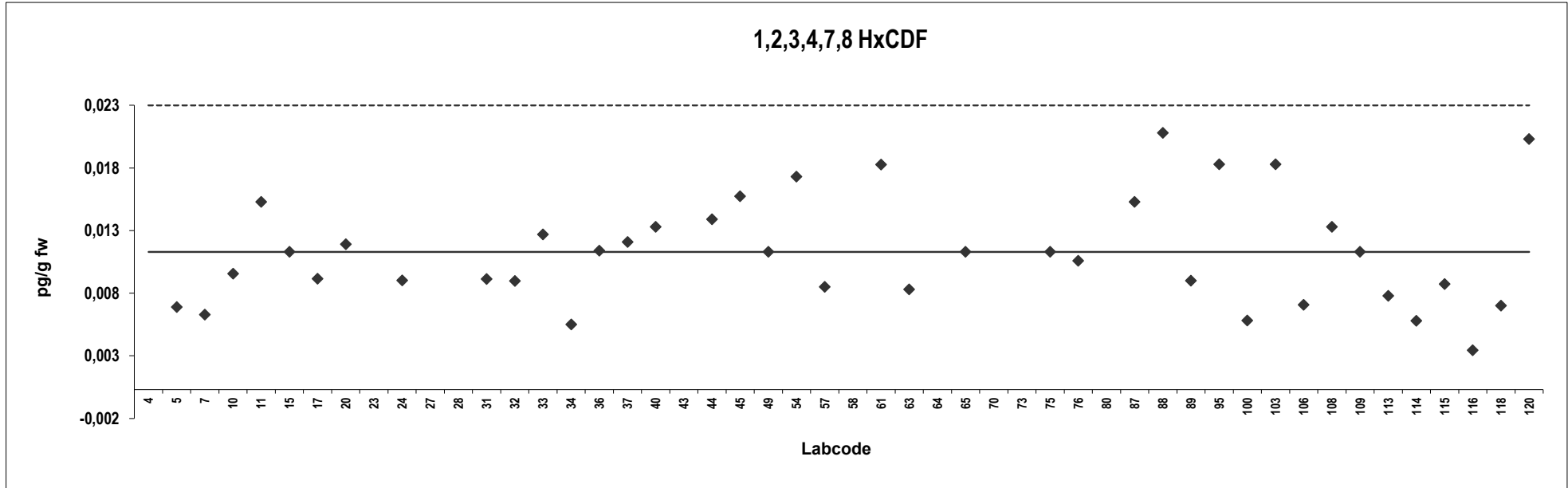
Labcode

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	26	Outlier,ND	114	0,0038	-2,6	ND
5	0,0055	-1,6		115	0,0090	0,65	
7	0,0080	0,00		116	0,0031	-3,0	ND
10	0,0078	-0,15		118	0,0040	-2,5	
11	0,0090	0,62		120	0,018	6,3	
15	0,0090	0,62					
17	0,0089	0,54					
20	0,0055	-1,6					
23	0,017	5,8	ND				
24	0,0066	-0,86					
27	0,014	4,0	ND				
28	0,068	38	Outlier,ND				
31	0,0070	-0,60					
32	0,0083	0,17					
33	0,012	2,5					
34	0,0055	-1,6					
36	0,0090	0,62					
37	0,0093	0,84					
40	0,024	10	Outlier				
43	0,030	14	Outlier,ND				
44	0,0078	-0,13					
45	0,015	4,7	ND				
49	0,0080	0,00					
54	0,0067	-0,81					
57	0,0062	-1,1					
58	0,050	26	Outlier,ND				
61	0,041	20	Outlier				
63	0,0070	-0,63					
64	0,082	46	Outlier				
65	0,0071	-0,56					
70	0,066	36	Outlier,ND				
73	0,018	6,5	Outlier				
75	0,0090	0,62					
76	0,0087	0,44					
80	0,025	11	Outlier,ND				
87	0,012	2,5					
88	0,017	5,8					
89	0,0081	0,079					
95	0,012	2,5					
100	0,0056	-1,5	ND				
103	0,019	6,9	Outlier				
106	0,0061	-1,2					
108	0,0080	0,00					
109	0,0080	0,00					
113	0,011	1,9					

Consenus statistics	
Consensus median, pg/g	0,0080
Median all values pg/g	0,0090
Consensus mean, pg/g	0,0088
Standard deviation, pg/g	0,0036
Relative standard deviation, %	41
No. of values reported	50
No. of values removed	11
No. of reported non-detects	12

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

Z-score: 1,2,3,6,7,8 HxCDF
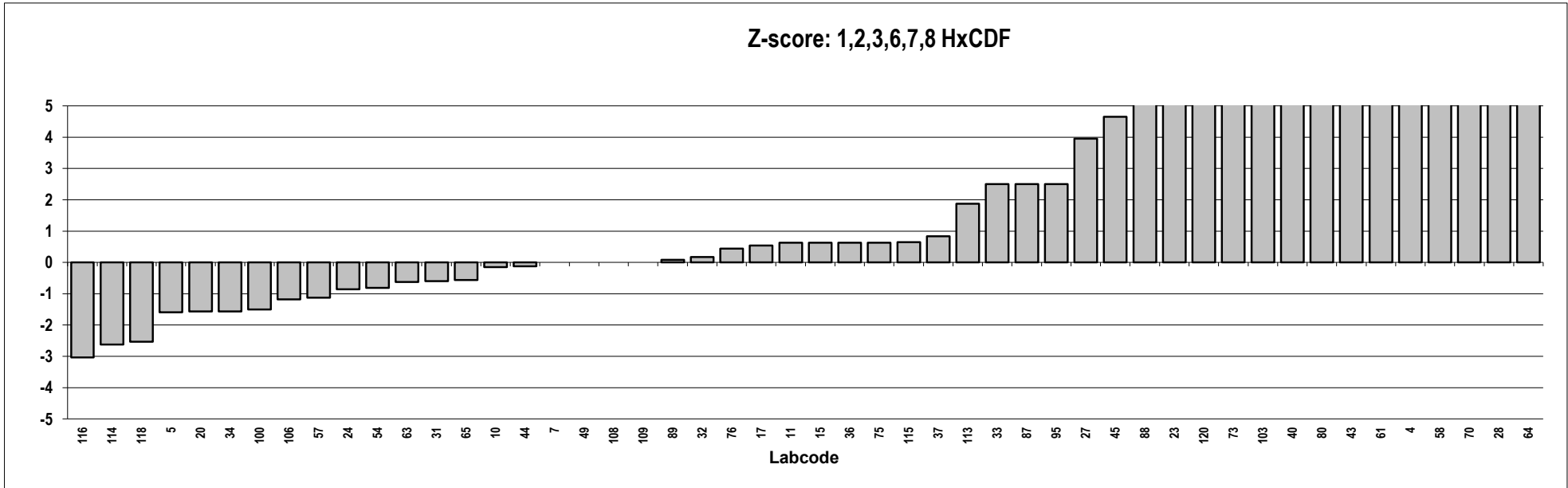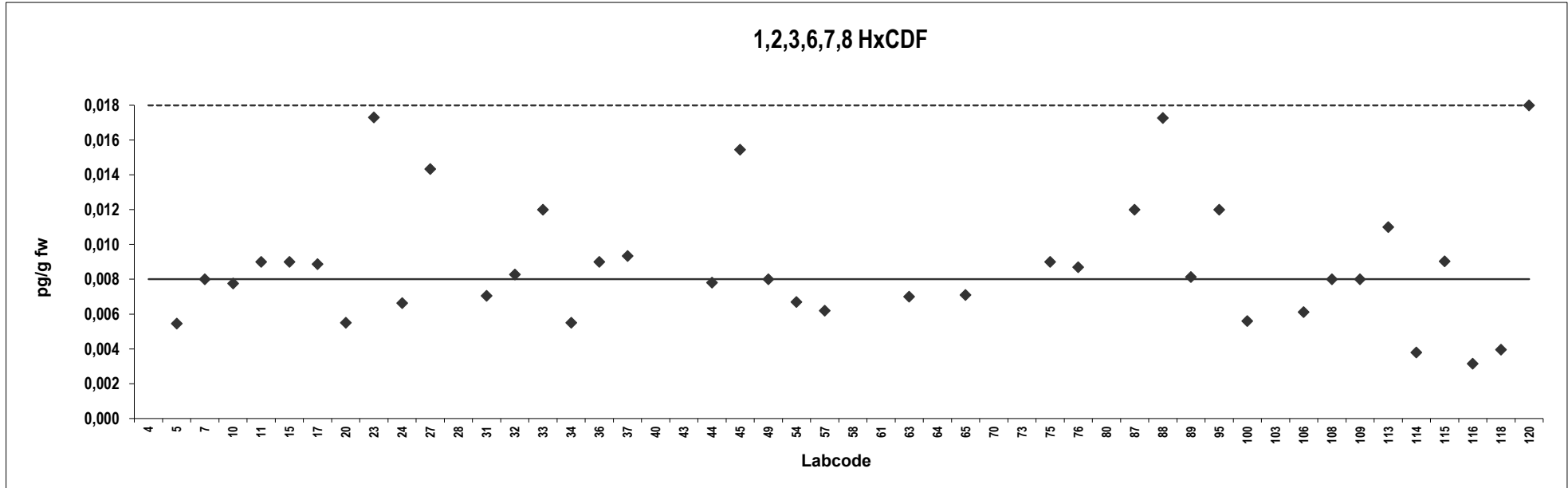
Veal
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	27	Outlier,ND	114	0,0055	-1,5	
5	0,0070	-0,49		115	0,0075	-0,19	
7	0,010	1,4		116	0,0031	-3,0	ND
10	0,0078	0,00		118	0,0051	-1,7	
11	0,010	1,5	ND	120	0,012	2,7	
15	0,010	1,4					
17	0,0056	-1,4					
20	0,0066	-0,78					
23	0,037	19	Outlier,ND				
24	0,0066	-0,76					
27	0,013	3,1	ND				
28	0,070	40	Outlier,ND				
31	0,0052	-1,7					
32	0,0071	-0,45					
33	0,0090	0,75					
34	0,0062	-1,0					
36	0,0081	0,18					
37	0,0051	-1,8					
40	0,0070	-0,52					
43	0,030	14	Outlier,ND				
44	0,0092	0,88					
45	0,015	4,9	ND				
49	0,010	1,4					
54	0,018	6,5					
57	0,0081	0,18					
58	0,050	27	Outlier,ND				
61	0,043	22	Outlier				
63	0,0050	-1,8					
64	0,029	14	Outlier				
65	0,0083	0,31					
70	0,064	36	Outlier,ND				
73	0,020	7,7	Outlier				
75	0,0090	0,75					
76	0,0061	-1,1					
80	0,025	11	Outlier,ND				
87	0,013	3,3					
88	0,019	7,0	Outlier				
89	0,0077	-0,062					
95	0,011	2,0					
100	0,028	13	Outlier				
103	0,026	12	Outlier				
106	0,0041	-2,4					
108	0,0090	0,75					
109	0,0085	0,43					
113	0,0066	-0,78					

Consensus statistics

Consensus median, pg/g	0,0078
Median all values pg/g	0,0090
Consensus mean, pg/g	0,0083
Standard deviation, pg/g	0,0031
Relative standard deviation, %	37
No. of values reported	50
No. of values removed	13
No. of reported non-detects	11

2,3,4,6,7,8 HxCDF
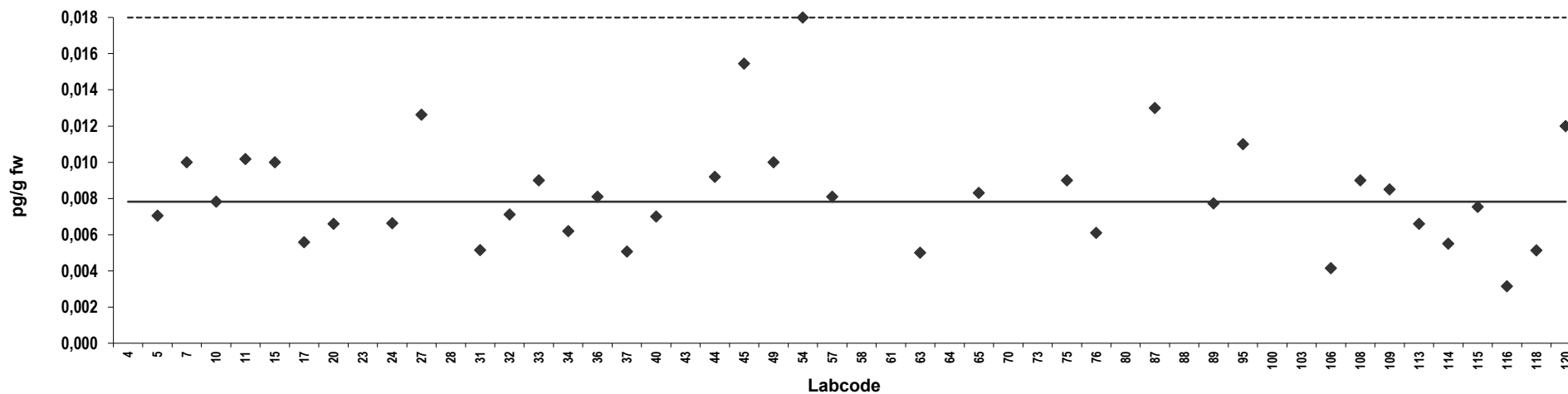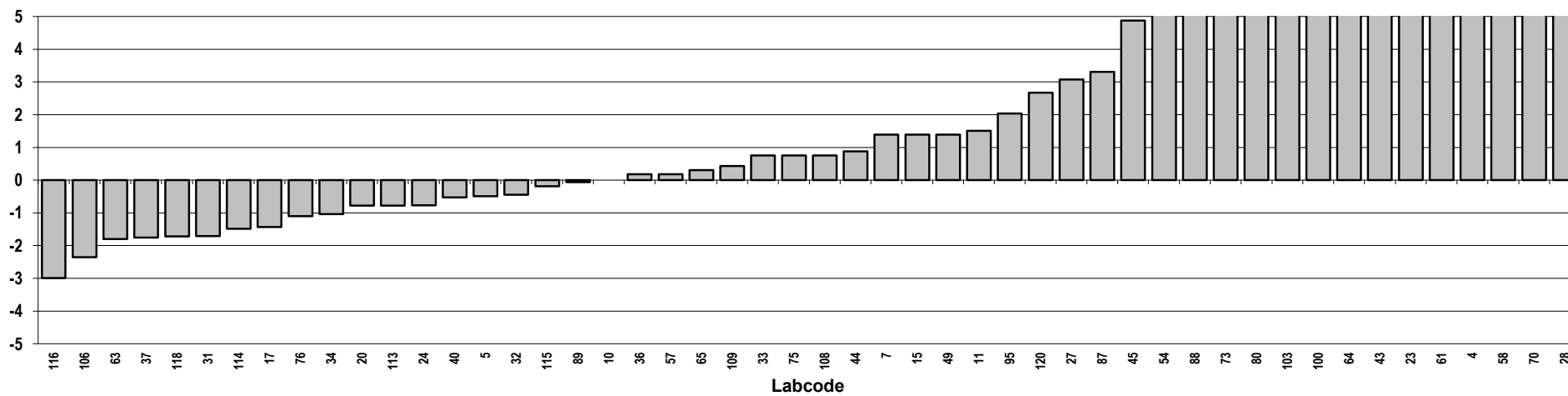
pg/g fw

Labcode

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

Labcode

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	63	Outlier,ND	114	0,0059	3,0	
5	0,0055	2,4		115	0,0033	-0,52	
7	0,0010	-3,6	ND	116	0,0036	-0,18	ND
10	0,0020	-2,3	ND	118	0,00079	-3,9	ND
11	0,0035	-0,26	ND	120	0,0040	0,41	
15	0,0050	1,8	ND				
17	0,00098	-3,7					
20	0,0023	-1,9					
23	0,024	27	Outlier,ND				
24	0,0025	-1,6	ND				
27	0,017	17	Outlier,ND				
28	0,32	430	Outlier				
31	0,0038	0,18	ND				
32	0,0041	0,59	ND				
33	0,0031	-0,81					
34	0,0010	-3,6	ND				
36	0,0040	0,41	ND				
37	0,0050	1,8	ND				
40	0,0060	3,1	ND				
43	0,030	36	Outlier,ND				
44	0,0014	-3,1					
45	0,015	16	Outlier,ND				
49	0,0010	-3,6	ND				
54	0,0045	1,1					
57	0,0024	-1,8	ND				
58	0,050	63	Outlier,ND				
61	0,025	28	Outlier				
63	0,0040	0,41	ND				
64	0,0091	7,4					
65	0,0014	-3,1					
70	0,067	85	Outlier,ND				
73	0,012	11	Outlier				
75	0,0050	1,8	ND				
76	0,0032	-0,68	ND				
80	0,025	29	Outlier,ND				
87	0,0050	1,8					
88	0,018	20	Outlier				
89	0,0011	-3,5					
95	0,0080	5,8	ND				
100	0,013	13	Outlier				
103	0,0070	4,5	ND				
106	0,0019	-2,4	ND				
108	0,010	8,5	ND				
109	0,010	8,5	ND				
113	0,011	9,9	Outlier				

Consenus statistics

Consensus median, pg/g	0,0037
Median all values pg/g	0,0050
Consensus mean, pg/g	0,0040
Standard deviation, pg/g	0,0025
Relative standard deviation, %	64
No. of values reported	50
No. of values removed	14
No. of reported non-detects	31

1,2,3,7,8,9 HxCDF
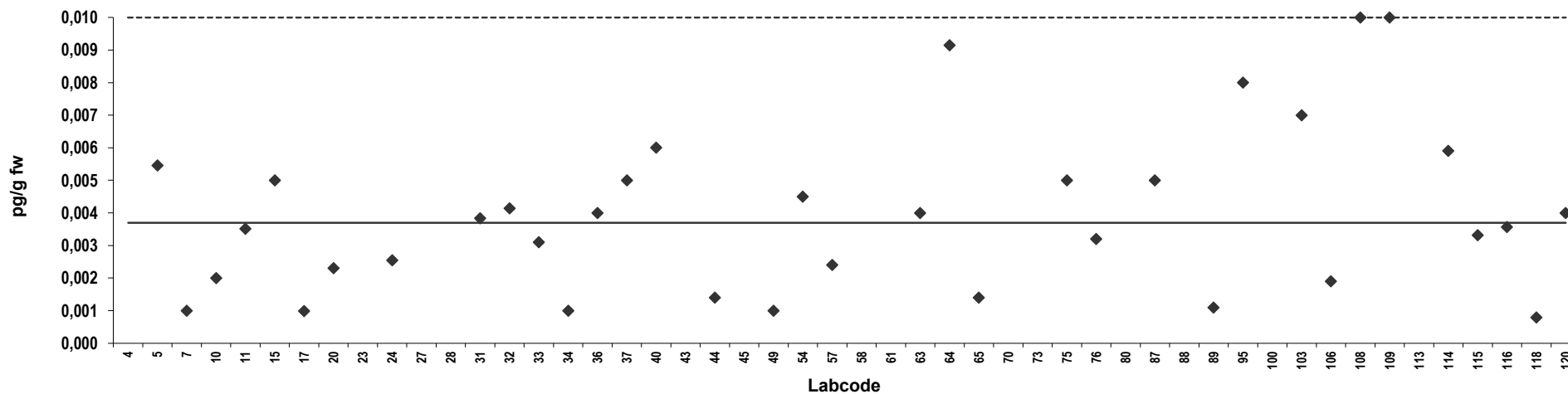
Z-score: 1,2,3,7,8,9 HxCDF
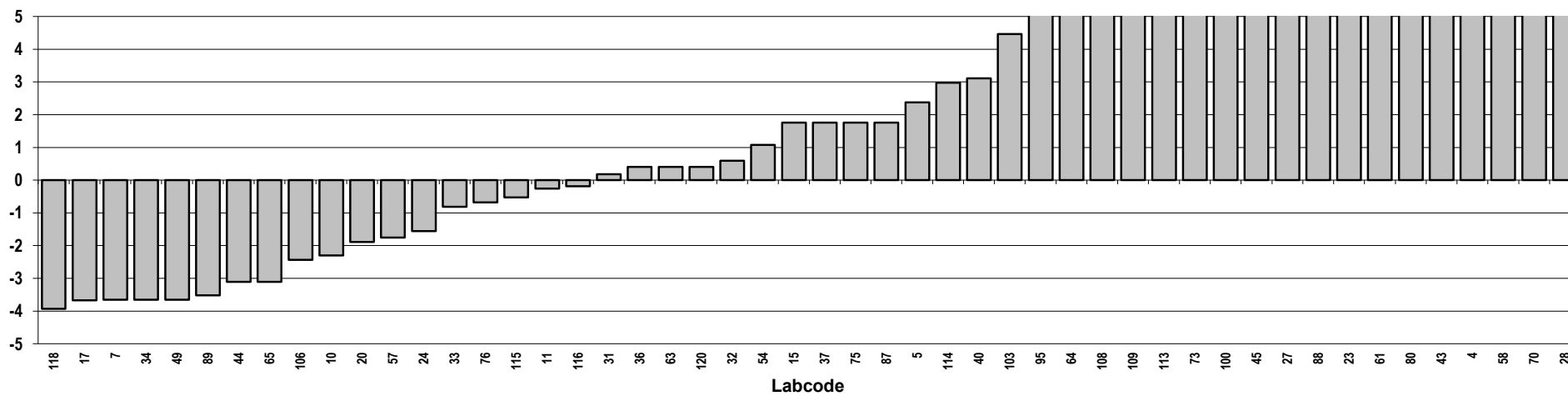
Veal
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	25	Outlier,ND	114	0,012	2,2	ND
5	0,0050	-2,0		115	0,0078	-0,28	
7	0,0050	-2,0		116	0,0040	-2,6	ND
10	0,0053	-1,8		118	0,0045	-2,3	
11	0,0083	0,00		120	0,022	8,3	Outlier
15	0,010	1,0					
17	0,011	1,5					
20	0,0039	-2,7					
23	0,019	6,1	ND				
24	0,0066	-1,0					
27	0,015	3,8	ND				
28	0,32	185	Outlier				
31	0,0077	-0,38	ND				
32	0,0063	-1,2					
33	0,0063	-1,2					
34	0,0049	-2,0					
36	0,0093	0,60					
37	0,0054	-1,7					
40	0,015	4,0					
43	0,030	13	Outlier,ND				
44	0,0059	-1,4					
45	0,015	4,3	ND				
49	0,0050	-2,0					
54	0,011	1,6					
57	0,0053	-1,8					
58	0,050	25	Outlier,ND				
61	0,0095	0,70	ND				
63	0,0070	-0,78					
64	0,023	8,7	Outlier				
65	0,0085	0,12					
70	0,062	33	Outlier,ND				
73	0,029	12	Outlier				
75	0,0090	0,42					
76	0,0039	-2,7					
80	0,050	25	Outlier,ND				
87	0,013	2,8					
88	0,052	26	Outlier				
89	0,010	1,2					
95	0,016	4,6					
100	0,011	1,7					
103	0,053	27	Outlier				
106	0,011	1,6					
108	0,0090	0,42					
109	0,010	1,0					
113	0,0056	-1,6					

Consenus statistics

Consensus median, pg/g	0,0083
Median all values pg/g	0,0097
Consensus mean, pg/g	0,0087
Standard deviation, pg/g	0,0038
Relative standard deviation, %	43
No. of values reported	50
No. of values removed	11
No. of reported non-detects	12

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

Z-score: 1,2,3,4,6,7,8 HpCDF
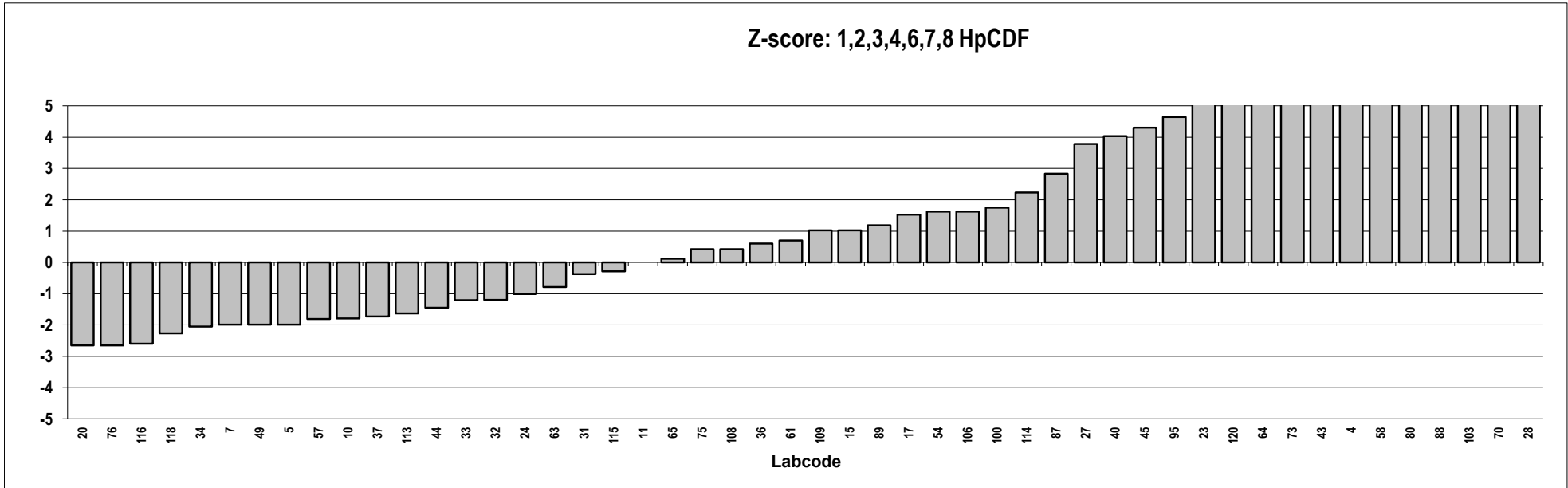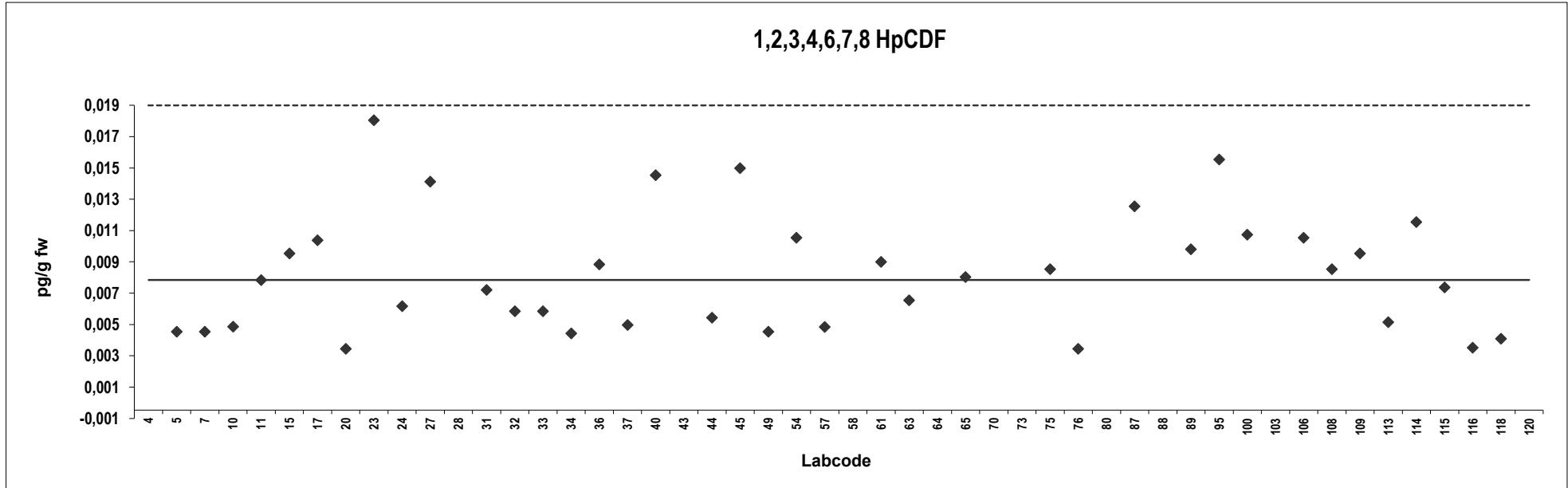
Veal
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	73	Outlier,ND	114	0,017	22	Outlier,ND
5	0,0011	-3,2		115	0,00060	-4,1	
7	0,0010	-3,4	ND	116	0,0078	7,1	ND
10	0,0050	2,8	ND	118	0,0012	-3,1	ND
11	0,0037	0,73	ND	120	0,0060	4,4	
15	0,0050	2,8	ND				
17	0,00082	-3,7					
20	0,0020	-1,9	ND				
23	0,026	35	Outlier,ND				
24	0,0010	-3,4					
27	0,017	21	Outlier,ND				
28	0,097	147	Outlier,ND				
31	0,0077	7,0	ND				
32	0,0041	1,5	ND				
33	0,0014	-2,8					
34	0,00090	-3,6	ND				
36	0,0020	-1,9	ND				
37	0,0050	2,8	ND				
40	0,0080	7,5	ND				
43	0,030	42	Outlier,ND				
44	0,00033	-4,5	ND				
45	0,015	19	Outlier,ND				
49	0,0020	-1,9					
54	0,011	12	Outlier				
57	0,0021	-1,7					
58	0,050	73	Outlier,ND				
61	0,013	16	Outlier				
63	0,0050	2,8	ND				
64	0,0080	7,5	ND				
65	0,0026	-0,94					
70	0,061	90	Outlier,ND				
73	0,0065	5,1					
75	0,0050	2,8	ND				
76	0,0032	0,00	ND				
80	0,050	73	Outlier,ND				
87	0,0080	7,5					
88	0,016	20	Outlier				
89	0,0027	-0,72					
95	0,011	12	Outlier,ND				
100	0,013	15	Outlier				
103	0,0080	7,5	ND				
106	0,0033	0,16	ND				
108	0,010	11	ND				
109	0,0020	-1,9					
113	0,0016	-2,5	ND				

Consenus statistics	
Consensus median, pg/g	0,0032
Median all values pg/g	0,0050
Consensus mean, pg/g	0,0038
Standard deviation, pg/g	0,0028
Relative standard deviation, %	71
No. of values reported	50
No. of values removed	15
No. of reported non-detects	33

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

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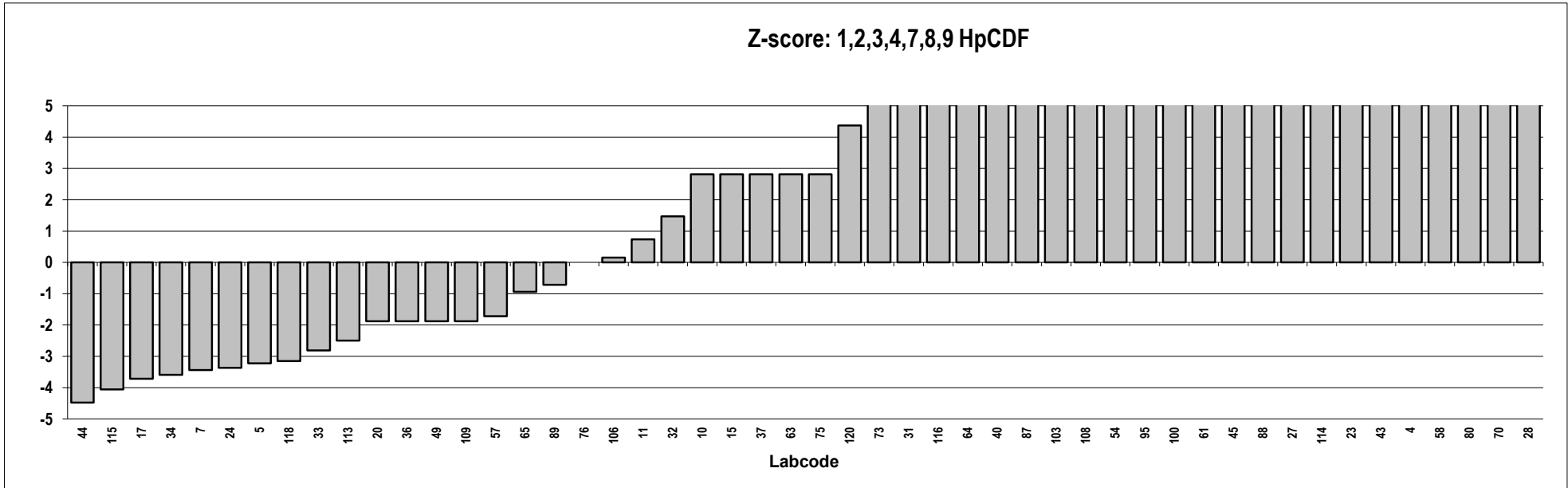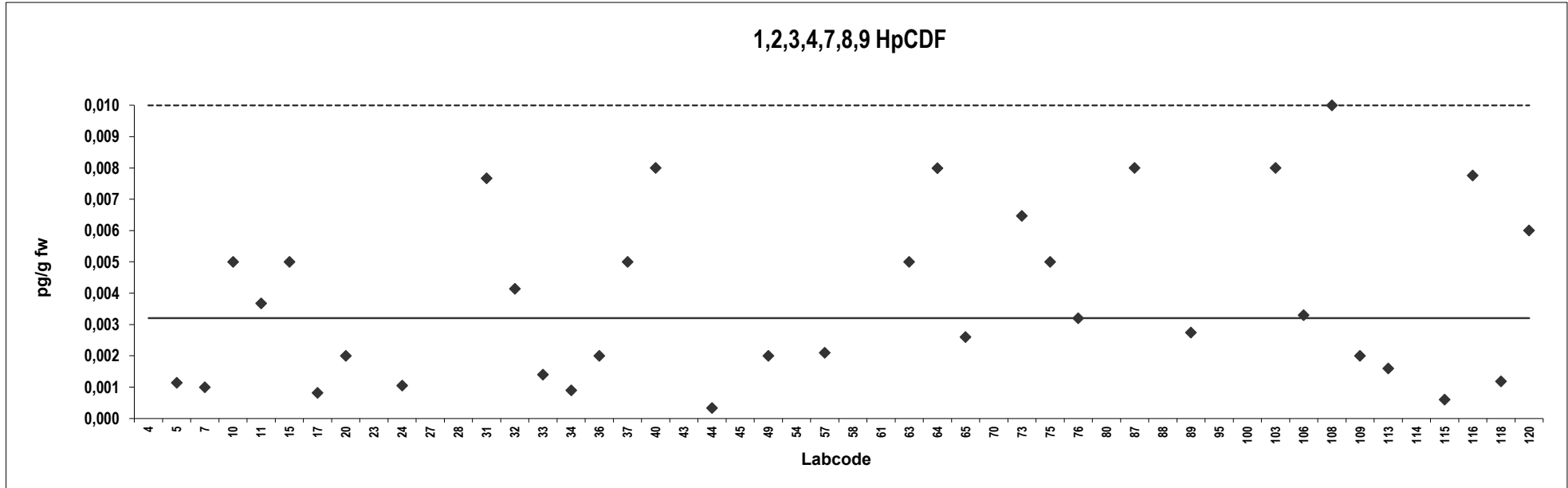
Veal

Congener: OCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,20	95	Outlier,ND	114	0,0077	-1,2	ND
5	0,00068	-4,7		115	0,024	7,2	
7	0,0080	-1,0		116	0,010	0,24	ND
10	0,010	0,00	ND	118	0,00059	-4,7	ND
11	0,0045	-2,7	ND	120	0,023	6,5	
15	0,010	0,00	ND				
17	0,0030	-3,5					
20	0,012	1,2	ND				
23	0,030	9,8	Outlier,ND				
24	0,0045	-2,7					
27	0,26	127	Outlier,ND				
28	0,64	314	Outlier				
31	0,015	2,7	ND				
32	0,0083	-0,86	ND				
33	0,0071	-1,4	ND				
34	0,0035	-3,3					
36	0,0030	-3,5	ND				
37	0,010	0,00	ND				
40	0,046	18	Outlier,ND				
43	0,050	20	Outlier,ND				
44	0,00091	-4,5	ND				
45	0,039	14	Outlier,ND				
49	0,0050	-2,5					
54	0,038	14	Outlier				
57	0,0060	-2,0					
58	0,050	20	Outlier,ND				
61	0,050	20	Outlier				
63	0,0080	-1,0	ND				
64	0,018	4,2					
65	0,0093	-0,35					
70	0,062	26	Outlier,ND				
73	0,013	1,7					
75	0,020	5,0	ND				
76	0,0064	-1,8	ND				
80	0,10	45	Outlier,ND				
87	0,012	1,0					
88	0,026	7,9	Outlier				
89	0,012	1,0					
95	0,025	7,5	ND				
100	0,018	4,1	ND				
103	0,019	4,5					
106	0,017	3,7					
108	0,020	5,0	ND				
109	0,024	7,0					
113	0,0071	-1,5	ND				

Consenus statistics

Consensus median, pg/g	0,010
Median all values pg/g	0,013
Consensus mean, pg/g	0,011
Standard deviation, pg/g	0,0071
Relative standard deviation, %	65
No. of values reported	50
No. of values removed	13
No. of reported non-detects	29

OCDF

Z-score: OCDF
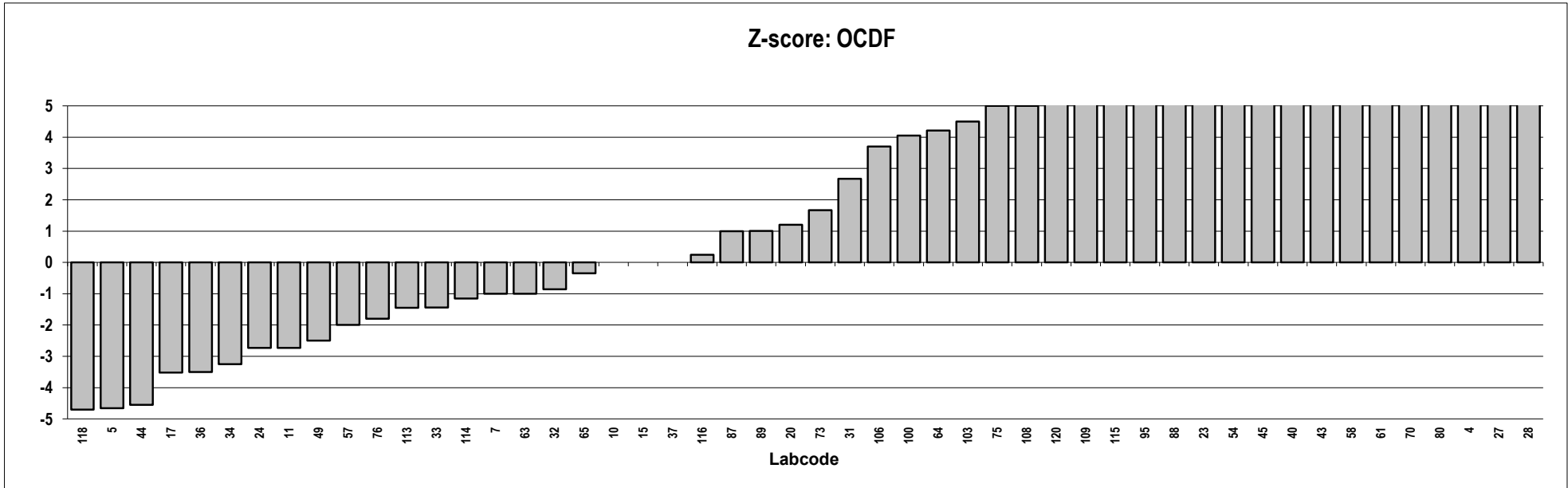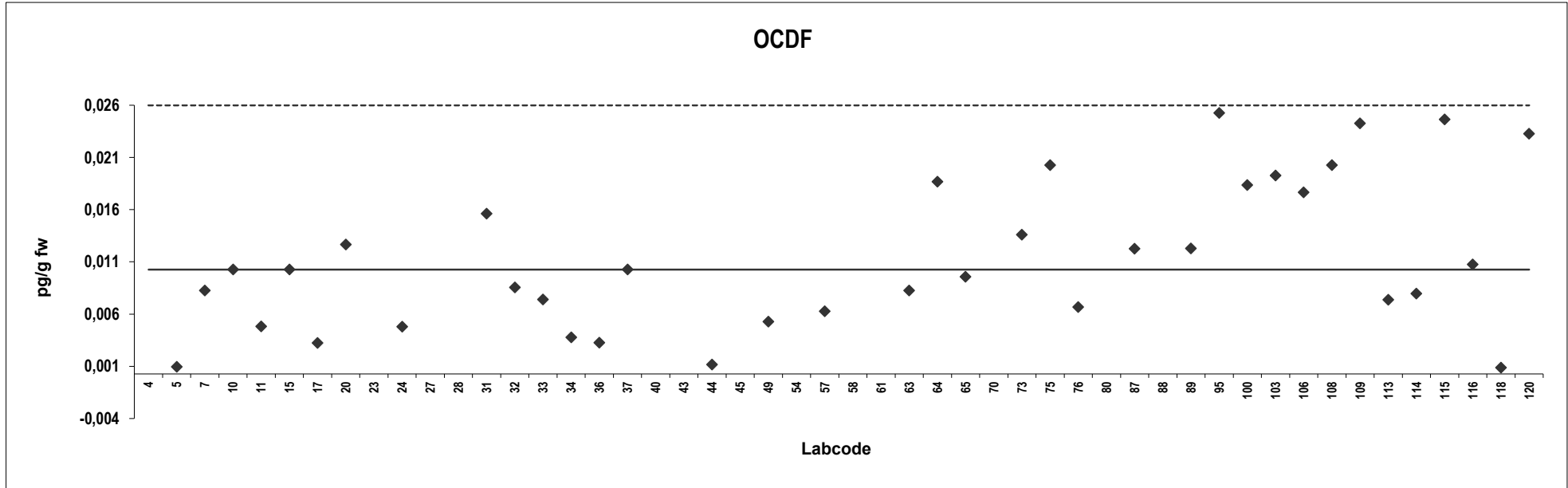
Veal
Congener: PCB 77

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	2,0	8,8	Outlier,ND	115	0,96	1,6	
5	0,63	-0,68		116	0,59	-0,96	
7	0,76	0,24		117	0,50	-1,6	
10	0,66	-0,46		118	0,86	0,93	
11	1,1	2,9		120	1,5	5,5	Outlier
15	0,98	1,8					
17	0,75	0,14					
20	0,75	0,17					
23	0,78	0,34					
24	0,86	0,94					
27	0,56	-1,1					
28	0,45	-1,9	ND				
31	0,65	-0,53					
32	0,60	-0,84					
33	0,33	-2,7					
34	0,59	-0,92					
36	0,57	-1,0					
37	0,63	-0,66					
40	0,71	-0,10					
43	0,36	-2,5					
44	0,75	0,17					
45	0,71	-0,12					
49	0,76	0,21					
54	0,76	0,24					
57	0,82	0,66					
58	0,73	0,030					
61	0,67	-0,35					
63	0,79	0,44					
64	1,4	5,0					
65	0,67	-0,35					
70	8,9	56	Outlier,ND				
73	0,95	1,5					
75	0,96	1,6					
80	0,93	1,4					
87	0,93	1,4					
88	0,57	-1,1					
89	0,53	-1,3					
95	0,78	0,38					
100	0,50	-1,6					
103	0,73	0,00					
106	0,64	-0,55					
108	0,91	1,3					
109	0,62	-0,70					
113	0,60	-0,84					
114	0,80	0,52					

Consensus statistics

Consensus median, pg/g	0,73
Median all values pg/g	0,74
Consensus mean, pg/g	0,73
Standard deviation, pg/g	0,20
Relative standard deviation, %	27
No. of values reported	50
No. of values removed	3
No. of reported non-detects	3

PCB 77

Z-score: PCB 77
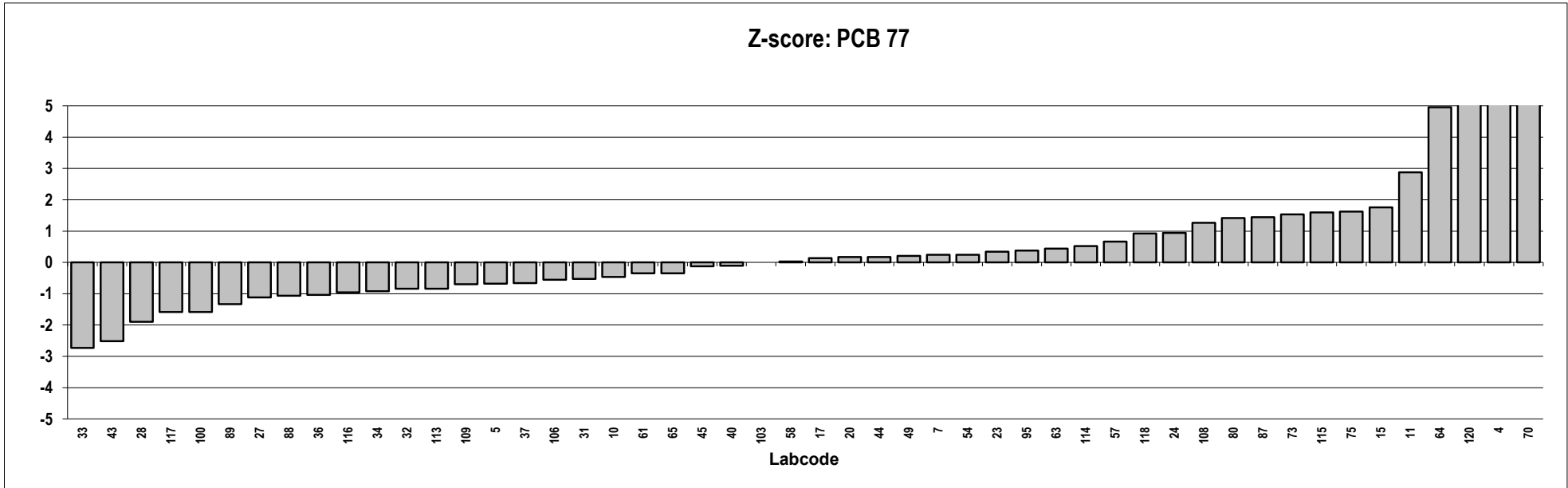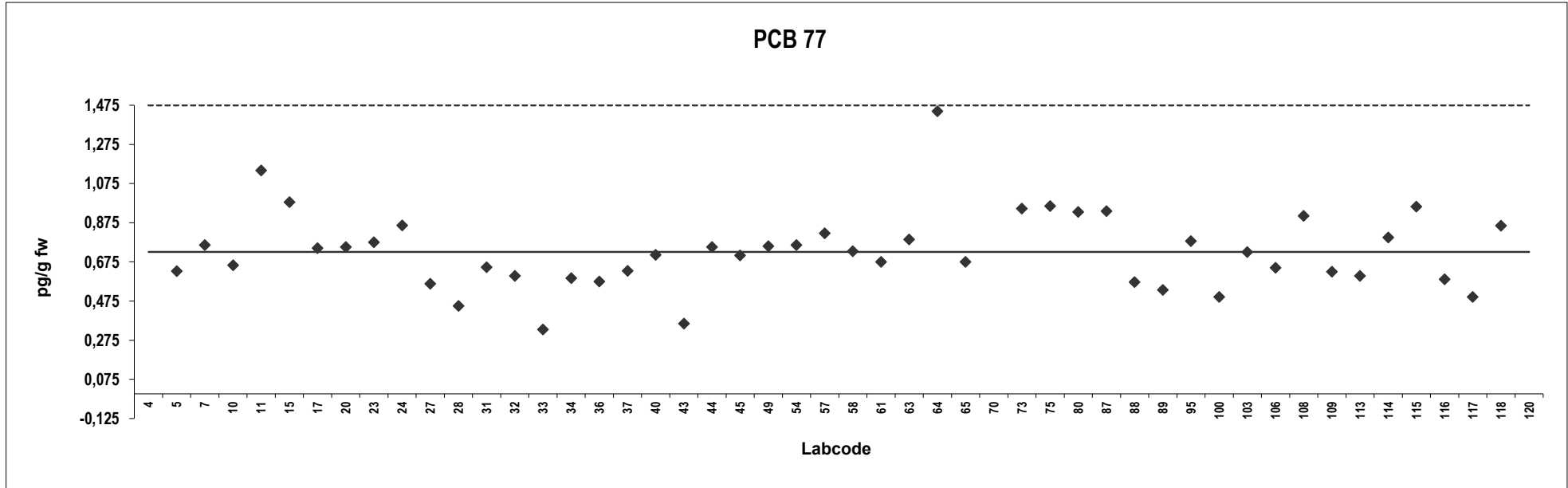
Veal

Congener: PCB 126

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,69	1,3		115	0,54	-0,10	
5	0,64	0,78		116	0,76	1,9	
7	0,68	1,2		117	0,42	-1,2	
10	0,55	0,00		118	0,57	0,13	
11	0,62	0,65		120	0,85	2,7	
15	0,59	0,35					
17	0,59	0,31					
20	0,58	0,26					
23	0,60	0,42					
24	0,55	0,0023					
27	0,50	-0,44					
28	0,59	0,35	ND				
31	0,52	-0,25					
32	0,49	-0,59					
33	0,63	0,73					
34	0,49	-0,55					
36	0,47	-0,71					
37	0,48	-0,69					
40	0,24	-2,8					
43	0,41	-1,3					
44	0,67	1,1					
45	0,59	0,37					
49	0,53	-0,20					
54	0,55	-0,0091					
57	0,54	-0,060					
58	0,62	0,62					
61	0,34	-1,9					
63	0,58	0,22					
64	0,64	0,79					
65	0,55	-0,023					
70	4,3	34	Outlier,ND				
73	0,73	1,6					
75	0,58	0,26					
80	0,54	-0,10					
87	0,59	0,38					
88	0,47	-0,74					
89	0,46	-0,83					
95	0,47	-0,74					
100	0,44	-1,0					
103	0,58	0,25					
106	0,45	-0,90					
108	0,51	-0,38					
109	0,55	0,0045					
113	0,49	-0,55					
114	0,20	-3,2					

Consenus statistics

Consensus median, pg/g	0,55
Median all values pg/g	0,55
Consensus mean, pg/g	0,54
Standard deviation, pg/g	0,11
Relative standard deviation, %	21
No. of values reported	50
No. of values removed	1
No. of reported non-detects	2

PCB 126

Z-score: PCB 126
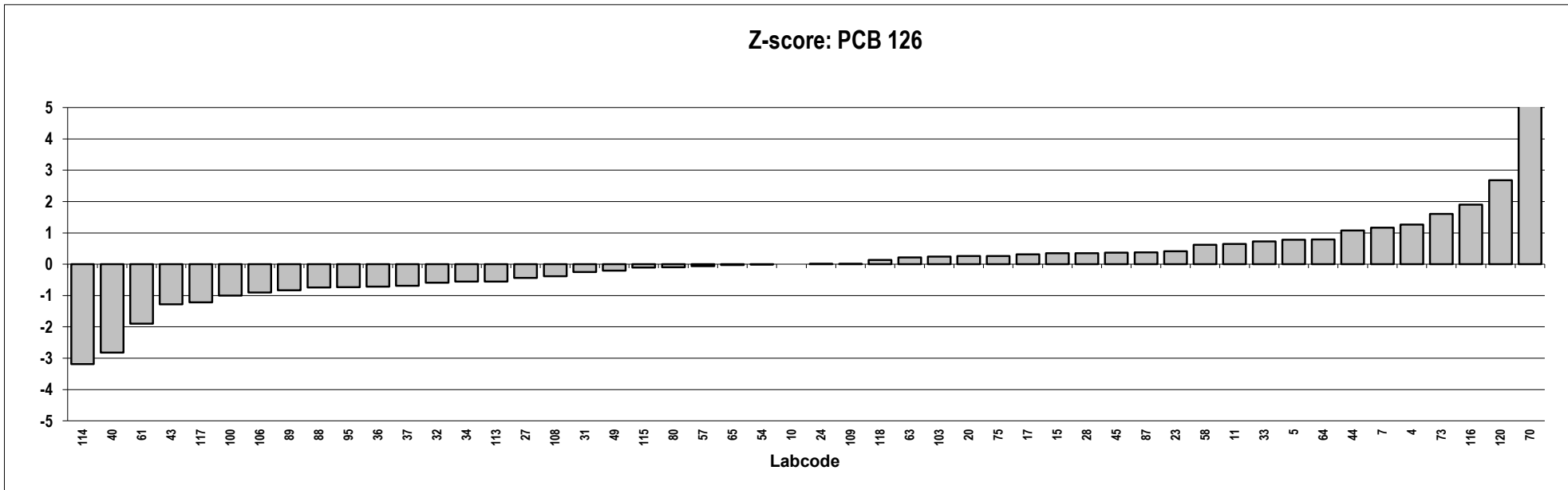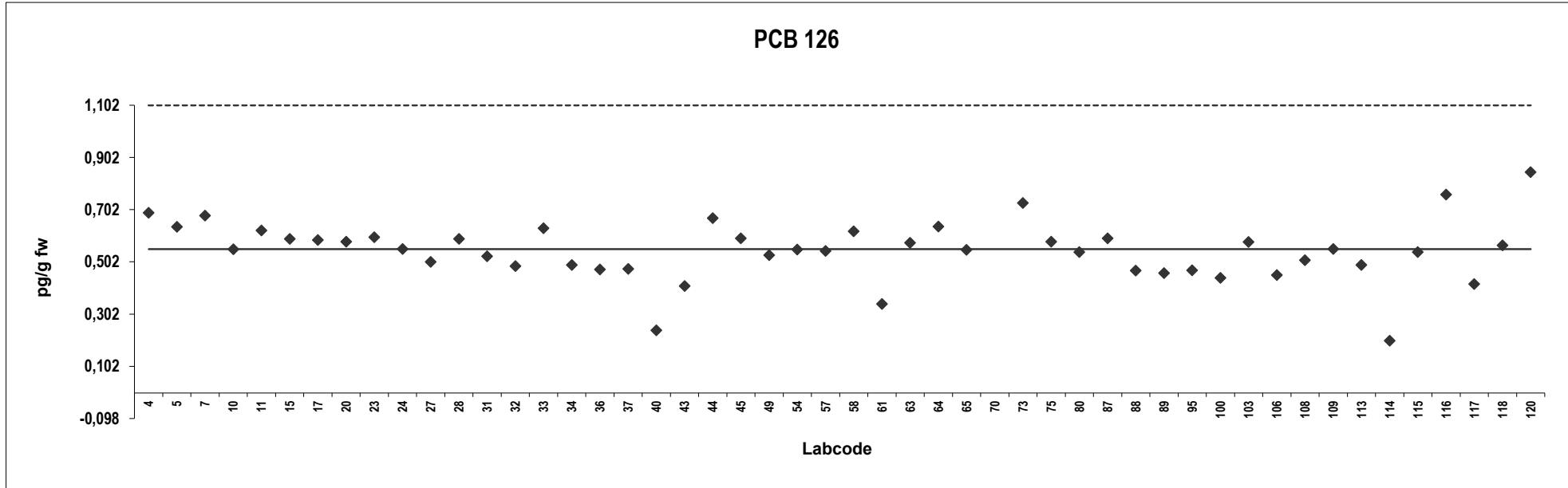
Veal

Congener: PCB 169

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	2,0	129	Outlier,ND	115	0,082	0,51	
5	0,084	0,67		116	0,087	0,87	
7	0,11	2,4		117	0,054	-1,4	
10	0,081	0,47		118	0,076	0,14	
11	0,074	-0,025		120	0,18	6,8	Outlier
15	0,080	0,37					
17	0,084	0,65					
20	0,060	-0,97					
23	0,076	0,11					
24	0,069	-0,39					
27	1,7	112	Outlier,ND				
28	0,38	21	Outlier,ND				
31	0,064	-0,68					
32	0,073	-0,11					
33	0,087	0,82					
34	0,063	-0,77					
36	0,065	-0,62					
37	0,059	-1,0					
40	0,082	0,51					
43	0,050	-1,6	ND				
44	0,10	1,7					
45	0,074	0,00					
49	0,15	5,1					
54	0,071	-0,23					
57	0,072	-0,14					
58	0,066	-0,57					
61	0,056	-1,3					
63	0,10	1,8					
64	0,12	3,3					
65	0,11	2,3					
70	6,7	445	Outlier,ND				
73	0,078	0,24					
75	0,080	0,37					
80	0,070	-0,30					
87	0,11	2,4					
88	0,075	0,025					
89	0,062	-0,84					
95	0,073	-0,096					
100	0,063	-0,74					
103	0,095	1,4	ND				
106	0,056	-1,3					
108	0,070	-0,30					
109	0,077	0,14					
113	0,0020	-4,9	ND				
114	0,042	-2,2					

Consensus statistics

Consensus median, pg/g	0,074
Median all values pg/g	0,076
Consensus mean, pg/g	0,076
Standard deviation, pg/g	0,023
Relative standard deviation, %	30
No. of values reported	50
No. of values removed	5
No. of reported non-detects	7

PCB 169

Labcode

Z-score: PCB 169
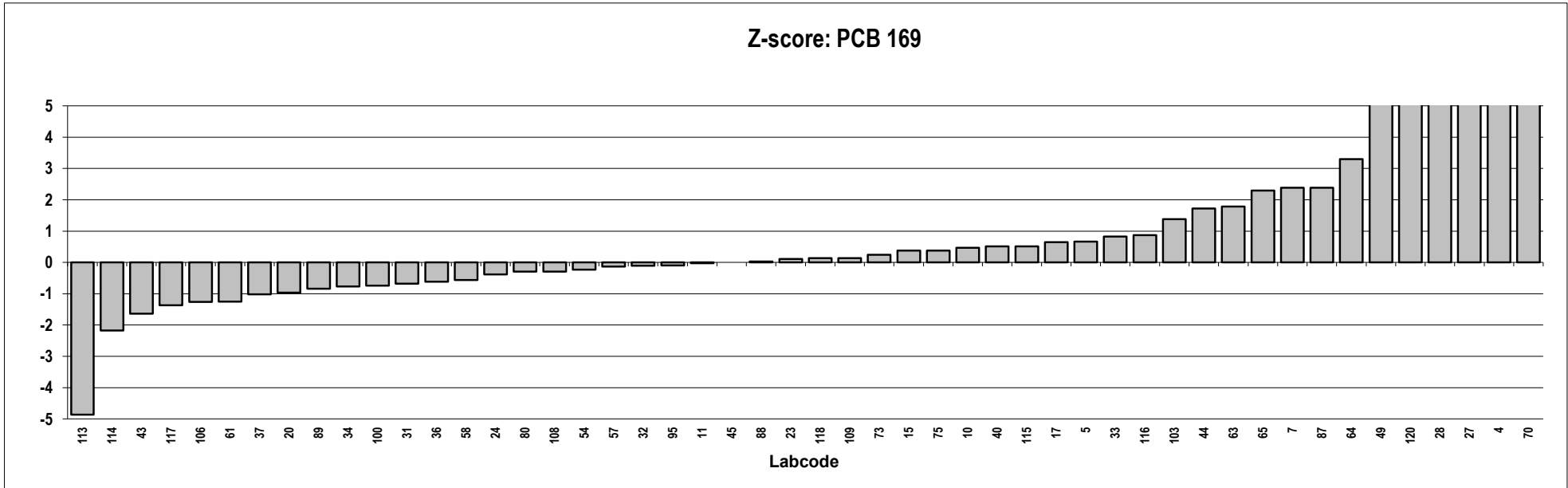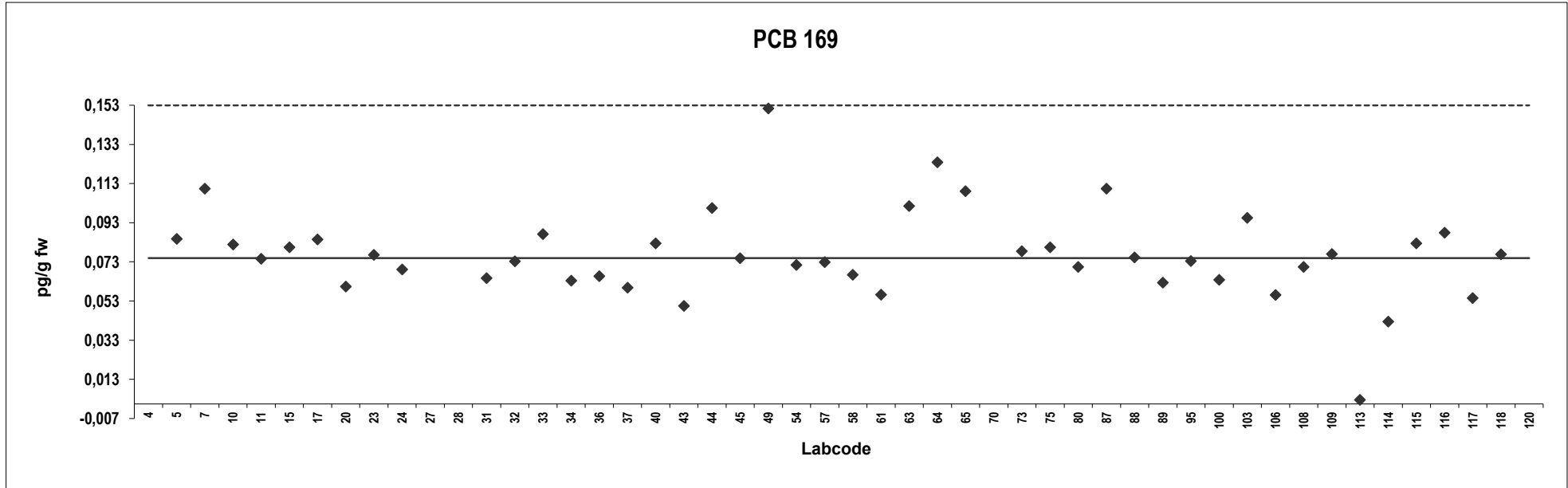
Labcode

Veal
Congener: PCB 81

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	2,0	183	Outlier,ND	115	0,011	-4,0	
5	0,027	-2,5		116	0,088	3,3	
7	0,054	0,066		117	0,040	-1,2	
10	0,050	-0,31	ND	118	0,059	0,52	
11	0,054	0,053		120	0,12	6,4	Outlier
15	0,080	2,5					
17	0,038	-1,4					
20	0,060	0,63					
23	0,064	1,0					
24	0,052	-0,13					
27	0,32	25	Outlier,ND				
28	0,42	34	Outlier,ND				
31	0,052	-0,14					
32	0,052	-0,15	ND				
33	0,026	-2,6					
34	0,043	-0,97					
36	0,050	-0,35					
37	0,023	-2,8					
40	0,080	2,5	ND				
43	0,50	42	Outlier,ND				
44	0,080	2,5					
45	0,055	0,20					
49	0,076	2,1					
54	0,043	-0,97					
57	0,016	-3,5	ND				
58	0,060	0,61					
61	0,052	-0,12					
63	0,059	0,54					
64	0,21	15	Outlier				
65	0,053	0,00					
70	8,8	821	Outlier,ND				
73	0,87	77	Outlier				
75	0,080	2,5					
80	0,070	1,6					
87	0,080	2,5					
88	0,056	0,30					
89	0,047	-0,54					
95	0,045	-0,78					
100	0,022	-2,9					
103	0,20	14	Outlier				
106	0,050	-0,33					
108	0,077	2,2					
109	0,069	1,4					
113	0,017	-3,4					
114	0,10	4,4					

Consensus statistics	
Consensus median, pg/g	0,053
Median all values pg/g	0,058
Consensus mean, pg/g	0,054
Standard deviation, pg/g	0,021
Relative standard deviation, %	39
No. of values reported	50
No. of values removed	9
No. of reported non-detects	9

PCB 81

Z-score: PCB 81
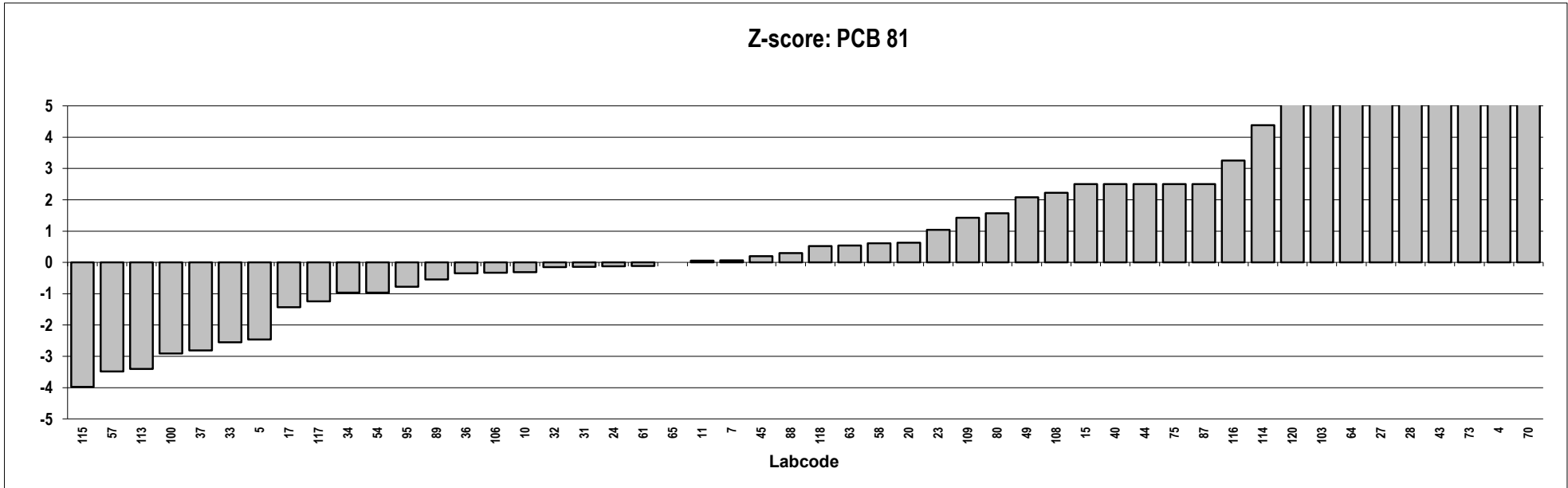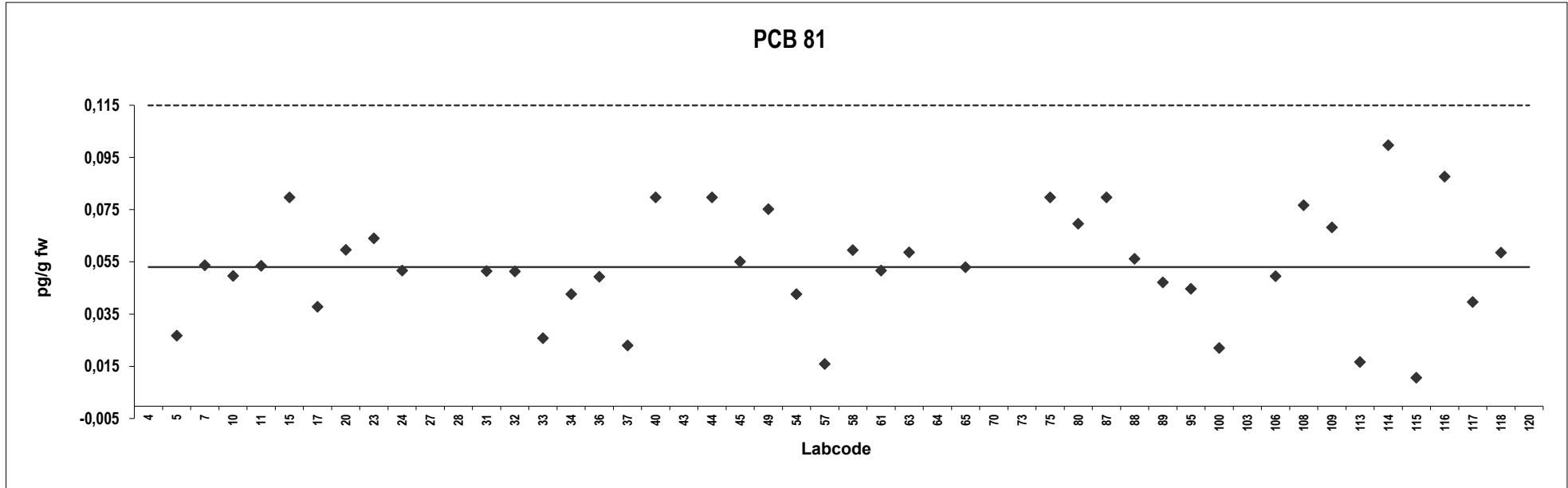
Veal
Congener: PCB 105

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	13	1,0		115	11	-0,028	
5	11	0,0019		116	10	-0,29	
7	11	0,28		117	8,1	-1,2	
10	9,8	-0,45		118	12	0,73	
11	12	0,48		120	18	3,2	
15	11	0,046					
17	11	0,21					
20	9,1	-0,79					
23	11	0,28					
24	11	0,075					
27	9,6	-0,55					
28	9,7	-0,50					
31	10	-0,35					
32	9,8	-0,45					
33	13	1,1					
34	9,3	-0,68					
36	9,7	-0,50					
37	9,1	-0,79					
40	9,9	-0,41					
43	10	-0,14					
44	9,2	-0,75					
45	8,7	-0,98					
49	11	-0,11					
54	20	4,2					
57	11	0,12					
58	11	0,13					
61	11	-0,071					
63	11	0,28					
64	15	1,8					
65	11	0,031					
70	10	-0,32					
73	16	2,3					
75	11	0,00					
80	11	0,27					
87	11	0,28					
88	8,1	-1,3					
89	9,5	-0,58					
95	11	-0,046					
100	9,0	-0,85					
103	11	0,21					
106	9,0	-0,86					
108	11	0,19					
109	11	0,015					
113	12	0,69					
114	37	12	Outlier				

Consensus statistics

Consensus median, pg/g	11
Median all values pg/g	11
Consensus mean, pg/g	11
Standard deviation, pg/g	2,2
Relative standard deviation, %	20
No. of values reported	50
No. of values removed	1
No. of reported non-detects	0

PCB 105

Z-score: PCB 105
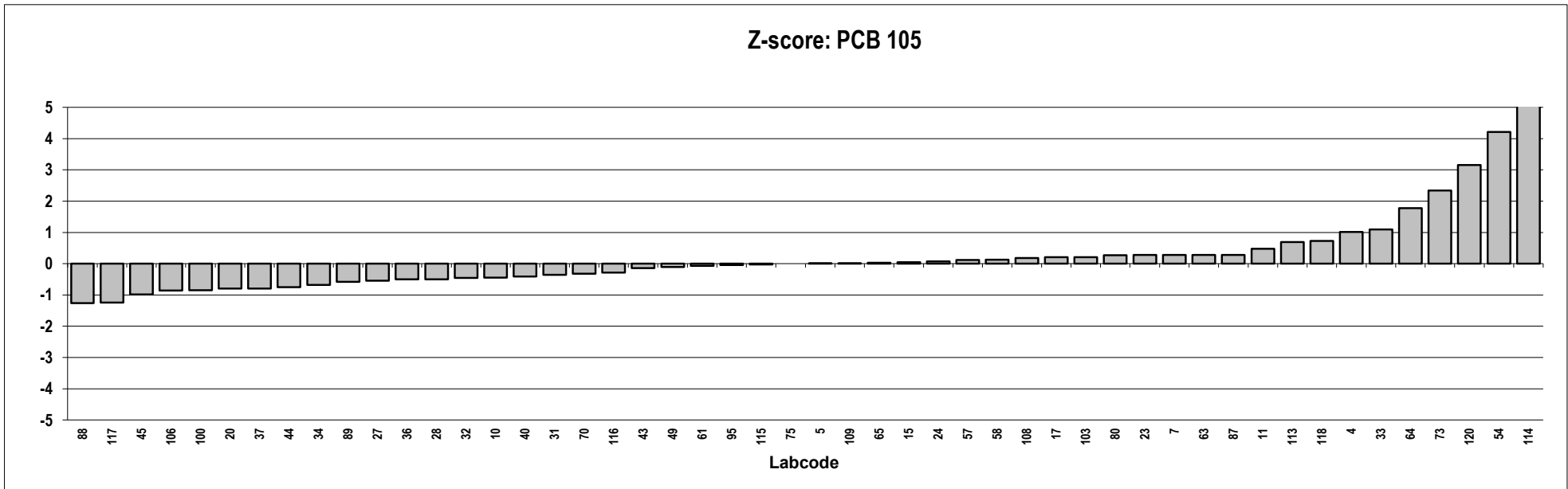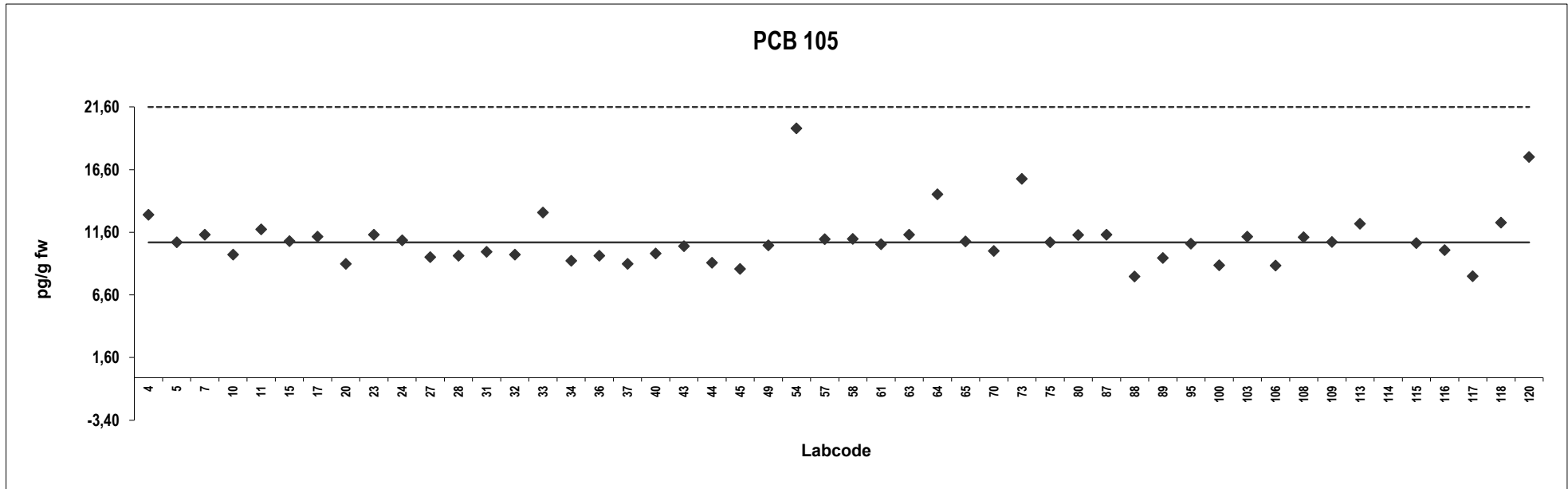
Veal

Congener: PCB 114

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	10	34	Outlier,ND	115	1,3	-0,035	
5	1,3	0,18		116	1,1	-0,54	
7	1,3	0,056		117	1,1	-0,57	
10	1,3	0,13		118	1,4	0,58	
11	1,5	0,86		120	1,7	1,8	
15	1,3	0,095					
17	1,3	0,032					
20	1,2	-0,14					
23	1,4	0,49					
24	1,3	-0,024					
27	1,1	-0,87					
28	0,51	-3,0	ND				
31	1,0	-1,0					
32	1,4	0,31					
33	1,4	0,52					
34	1,0	-0,90					
36	1,1	-0,59					
37	1,1	-0,73					
40	1,3	0,056					
43	1,4	0,45					
44	1,5	0,88					
45	1,2	-0,43					
49	1,1	-0,86					
54	1,3	-0,10					
57	1,2	-0,39					
58	10	34	Outlier,ND				
61	0,81	-1,8					
63	1,3	-0,10					
64	1,9	2,6					
65	1,3	0,00					
70	4,5	13	Outlier,ND				
73	1,8	2,0					
75	1,4	0,49					
80	1,0	-1,1	ND				
87	1,6	1,2					
88	1,0	-0,96					
89	1,0	-1,0					
95	1,6	1,1					
100	1,0	-0,96					
103	1,3	0,12					
106	2,6	5,2	Outlier,ND				
108	1,3	-0,022					
109	1,3	0,064					
113	1,5	1,0					
114	6,8	22	Outlier,ND				

Consenus statistics	
Consensus median, pg/g	1,3
Median all values pg/g	1,3
Consensus mean, pg/g	1,3
Standard deviation, pg/g	0,25
Relative standard deviation, %	20
No. of values reported	50
No. of values removed	5
No. of reported non-detects	7

PCB 114

Z-score: PCB 114
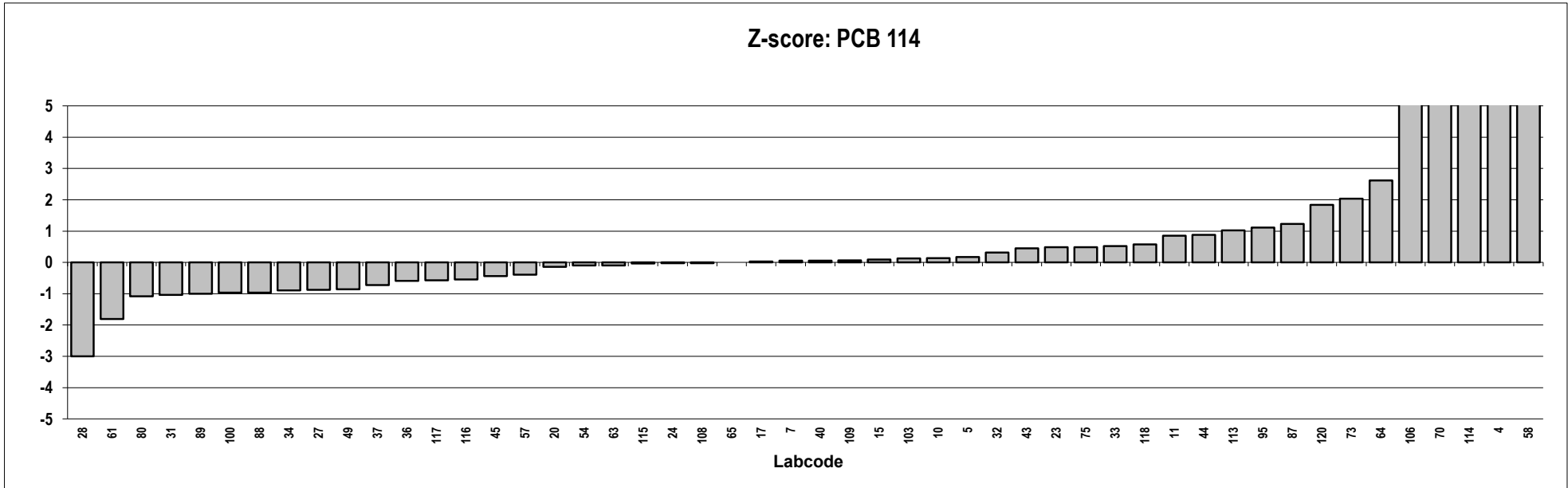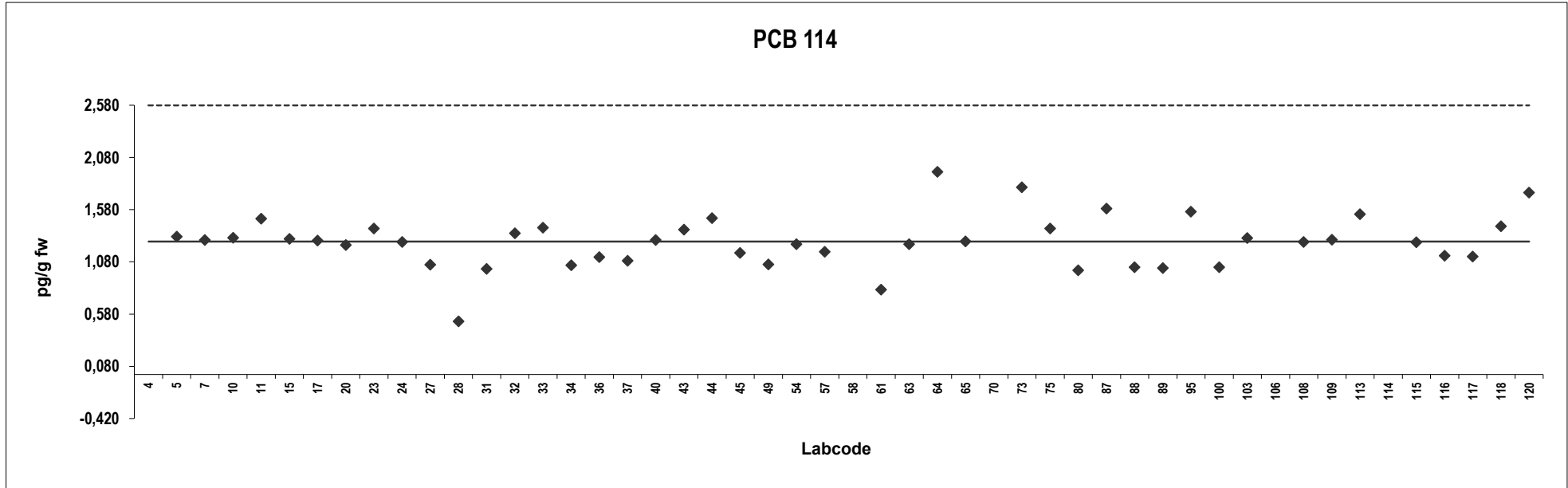
Veal

Congener: PCB 118

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	73	1,2		115	60	0,056	
5	62	0,21		116	56	-0,31	
7	63	0,31		117	46	-1,1	
10	56	-0,27		118	68	0,76	
11	65	0,52		120	88	2,4	
15	61	0,18					
17	65	0,45					
20	63	0,35					
23	66	0,55					
24	60	0,087					
27	56	-0,31					
28	58	-0,15					
31	51	-0,67					
32	59	0,018					
33	66	0,58					
34	51	-0,66					
36	51	-0,69					
37	46	-1,1					
40	54	-0,45					
43	58	-0,098					
44	58	-0,085					
45	51	-0,70					
49	57	-0,16					
54	52	-0,61					
57	59	-0,046					
58	61	0,11					
61	59	0,00					
63	62	0,26					
64	68	0,76					
65	53	-0,50					
70	60	0,094					
73	88	2,4					
75	61	0,16					
80	64	0,40					
87	59	-0,058					
88	48	-0,96					
89	44	-1,3					
95	57	-0,23					
100	54	-0,41					
103	59	0,014					
106	44	-1,3					
108	55	-0,37					
109	66	0,57					
113	78	1,6					
114	230	14	Outlier				

Consenus statistics

Consensus median, pg/g	59
Median all values pg/g	59
Consensus mean, pg/g	60
Standard deviation, pg/g	9,1
Relative standard deviation, %	15
No. of values reported	50
No. of values removed	1
No. of reported non-detects	0

PCB 118

Z-score: PCB 118
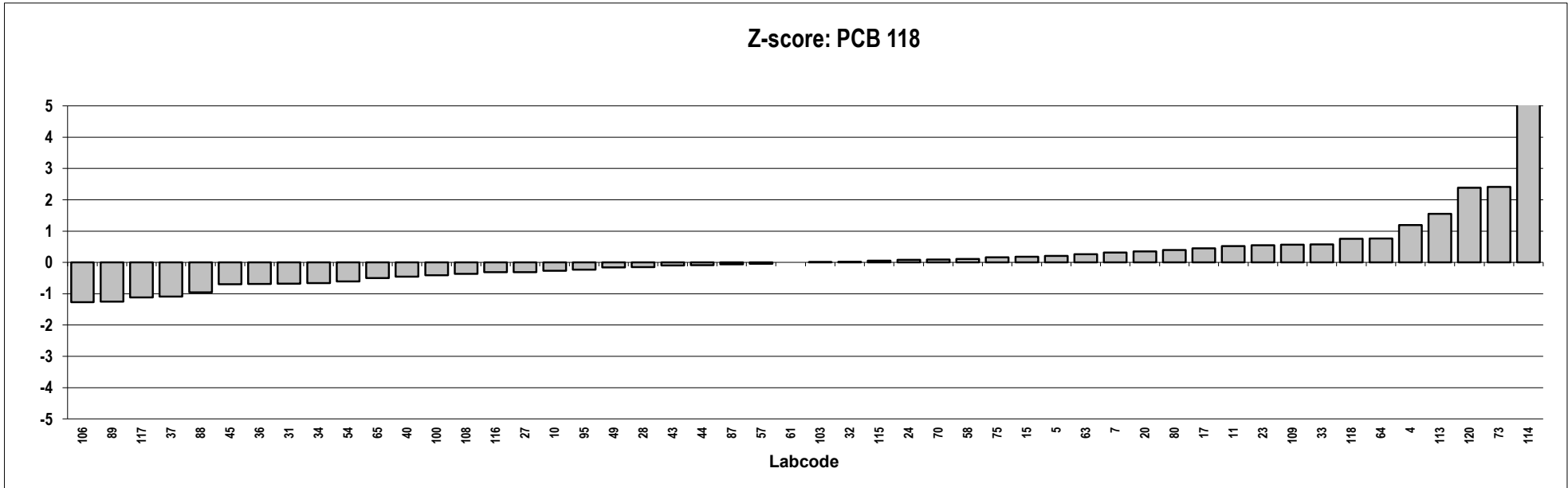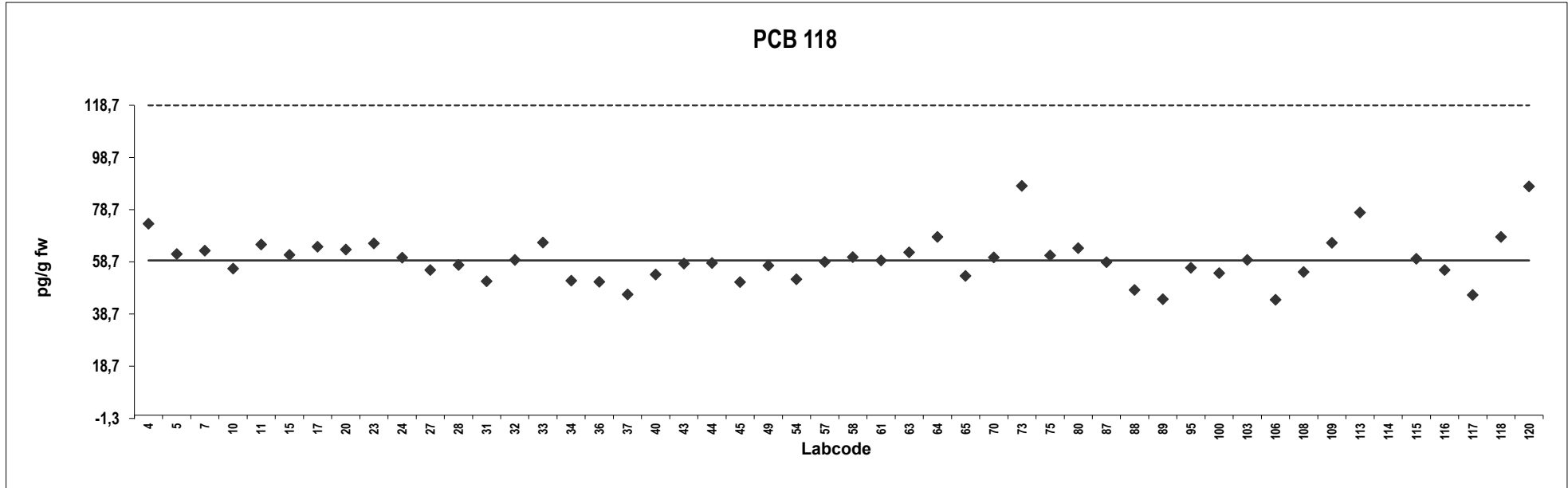
Veal
Congener: PCB 123

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	10	57	Outlier,ND	115	0,91	0,68	
5	0,68	-0,74		116	0,90	0,59	
7	0,98	1,1		117	0,73	-0,47	
10	0,87	0,42		118	0,54	-1,6	
11	0,68	-0,78		120	1,1	1,8	
15	1,1	1,8					
17	2,0	7,5	Outlier				
20	1,5	4,5					
23	1,7	5,3					
24	0,83	0,16					
27	0,85	0,31					
28	0,52	-1,8	ND				
31	0,72	-0,54					
32	1,1	2,0					
33	1,6	5,0					
34	0,44	-2,3					
36	0,51	-1,8					
37	0,58	-1,4					
40	0,64	-1,0					
43	1,6	4,8					
44	2,3	9,3	Outlier				
45	0,31	-3,1					
49	0,53	-1,7					
54	0,74	-0,39					
57	0,0089	-4,9	ND				
58	10	57	Outlier,ND				
61	2,5	11	Outlier				
63	0,94	0,88					
64	1,2	2,8					
65	1,7	5,6					
70	4,9	26	Outlier,ND				
73	3,9	19	Outlier				
75	1,1	1,8					
80	1,0	1,2	ND				
87	0,79	-0,10					
88	0,78	-0,15					
89	0,75	-0,32					
95	0,79	-0,081					
100	0,69	-0,68					
103	0,56	-1,5					
106	3,0	14	Outlier,ND				
108	0,80	0,00					
109	0,97	1,1					
113	1,0	1,4					
114	13	76	Outlier,ND				

Consenus statistics	
Consensus median, pg/g	0,80
Median all values pg/g	0,91
Consensus mean, pg/g	0,87
Standard deviation, pg/g	0,37
Relative standard deviation, %	42
No. of values reported	50
No. of values removed	9
No. of reported non-detects	8

PCB 123

Labcode

pg/g fw

Z-score: PCB 123
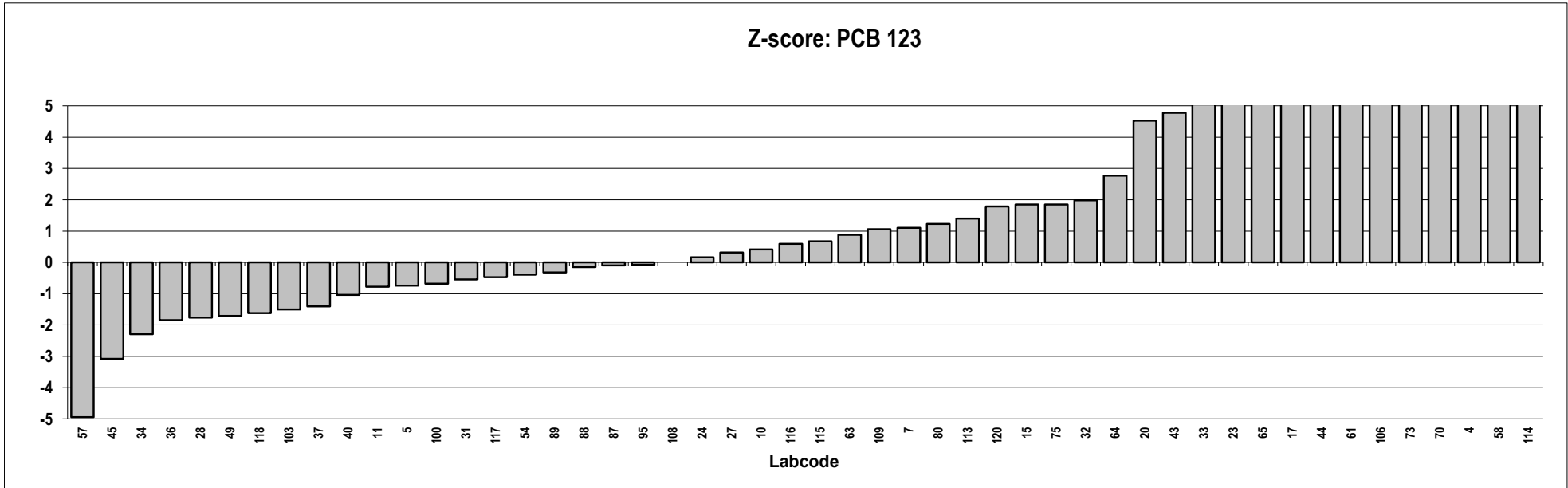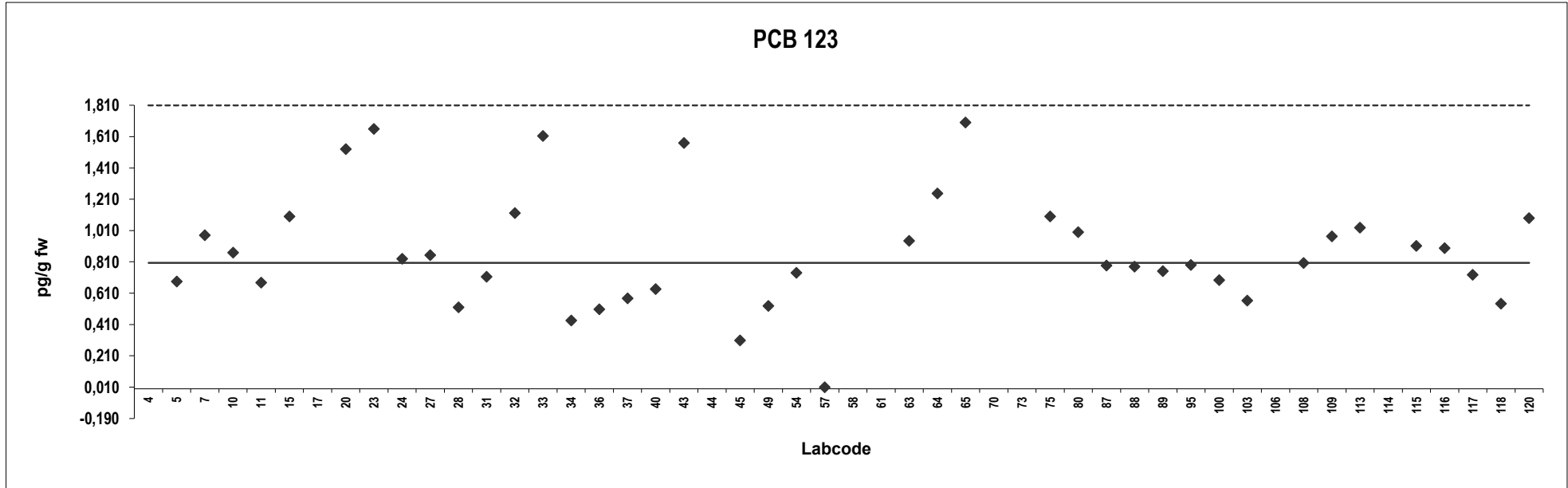
Labcode

Veal
Congener: PCB 156

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	10	3,8	ND	115	6,4	0,64	
5	5,8	0,073		116	6,4	0,61	
7	6,3	0,47		117	4,5	-1,0	
10	5,6	-0,096		118	6,1	0,37	
11	6,2	0,47		120	8,0	2,0	
15	6,1	0,34					
17	6,2	0,46					
20	5,7	0,00					
23	5,5	-0,20					
24	5,4	-0,27					
27	5,4	-0,28					
28	5,2	-0,49					
31	4,9	-0,72					
32	5,5	-0,18					
33	6,0	0,30					
34	4,9	-0,70					
36	5,9	0,15					
37	4,8	-0,82					
40	5,1	-0,50					
43	4,9	-0,69					
44	5,4	-0,32					
45	4,8	-0,84					
49	5,3	-0,37					
54	5,4	-0,30					
57	5,9	0,17					
58	10	3,8	ND				
61	5,6	-0,12					
63	5,8	0,11					
64	6,6	0,81					
65	5,0	-0,62					
70	6,9	1,0	ND				
73	7,2	1,3					
75	6,4	0,60					
80	6,3	0,49					
87	5,9	0,17					
88	4,9	-0,73					
89	4,7	-0,92					
95	5,9	0,16					
100	4,6	-1,0					
103	5,6	-0,082					
106	4,6	-0,96					
108	4,7	-0,93					
109	6,1	0,38					
113	6,2	0,39					
114	19	12	Outlier				

Consenus statistics	
Consensus median, pg/g	5,7
Median all values pg/g	5,8
Consensus mean, pg/g	5,8
Standard deviation, pg/g	1,1
Relative standard deviation, %	19
No. of values reported	50
No. of values removed	1
No. of reported non-detects	3

PCB 156

Z-score: PCB 156
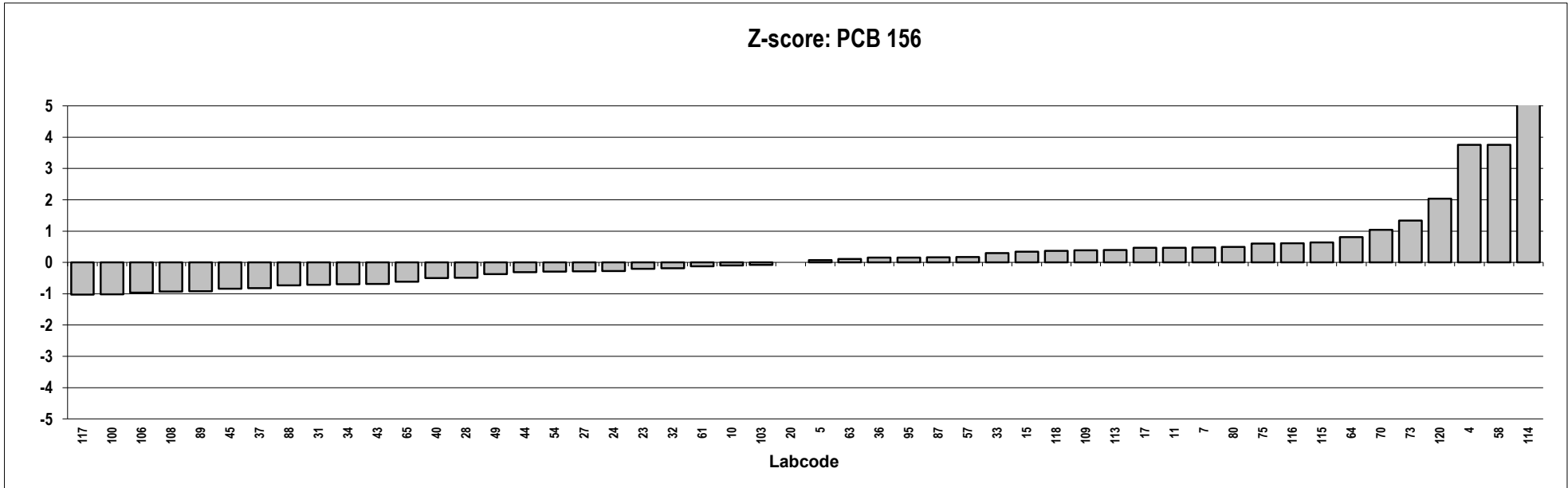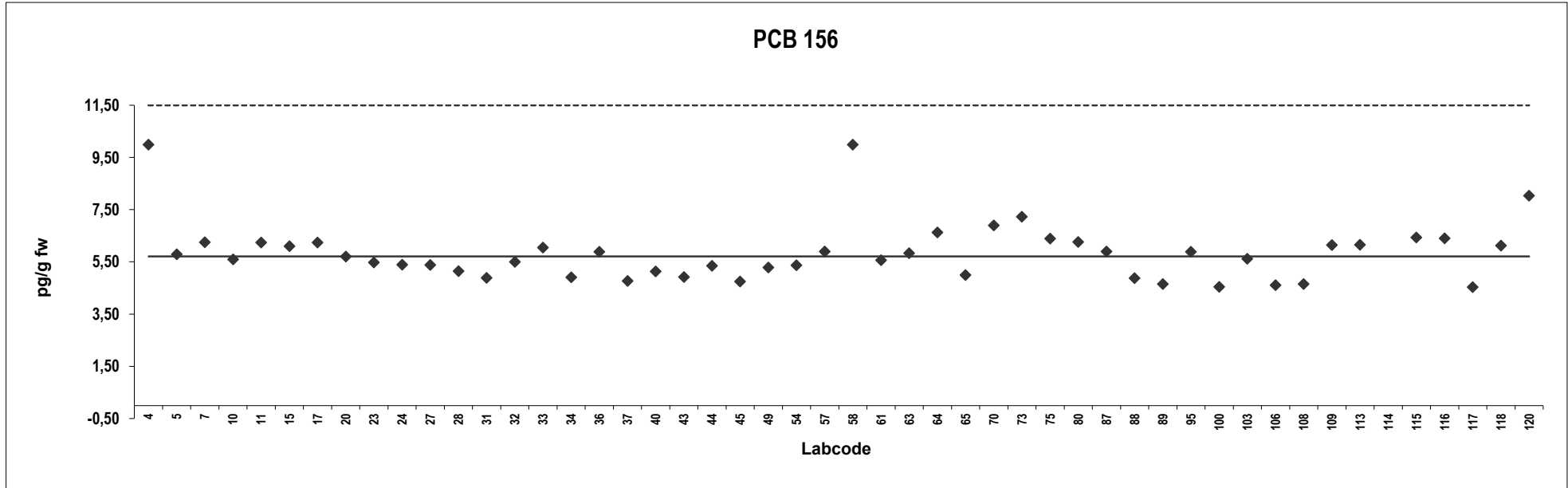
Veal

Congener: PCB 157

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	10	37	Outlier,ND	115	1,6	1,6	
5	1,3	0,26		116	1,2	0,16	
7	1,4	0,81		117	1,2	-0,18	
10	1,3	0,26		118	1,2	0,0072	
11	1,3	0,61		120	1,8	2,5	
15	1,4	0,85					
17	1,3	0,40					
20	1,2	-0,11					
23	0,98	-0,90					
24	1,1	-0,38					
27	1,1	-0,24					
28	1,7	1,9					
31	0,99	-0,88					
32	1,2	-0,0072					
33	1,4	0,94					
34	0,97	-0,93					
36	1,2	-0,038					
37	0,98	-0,93					
40	1,1	-0,28					
43	0,93	-1,1					
44	1,2	0,18					
45	1,2	-0,16					
49	0,98	-0,90					
54	1,2	0,18					
57	1,2	-0,14					
58	10	37	Outlier,ND				
61	0,71	-2,0					
63	1,3	0,43					
64	1,6	1,7					
65	1,2	-0,19					
70	6,9	24	Outlier,ND				
73	1,5	1,3					
75	1,3	0,43					
80	1,3	0,60					
87	1,3	0,35					
88	1,1	-0,47					
89	1,1	-0,30					
95	1,2	0,053					
100	0,96	-0,97					
103	1,4	0,72					
106	1,2	-0,20					
108	1,0	-0,66					
109	1,2	0,17					
113	1,2	-0,15					
114	4,5	14	Outlier,ND				

Consenus statistics

Consensus median, pg/g	1,2
Median all values pg/g	1,2
Consensus mean, pg/g	1,2
Standard deviation, pg/g	0,20
Relative standard deviation, %	17
No. of values reported	50
No. of values removed	4
No. of reported non-detects	4

PCB 157

Z-score: PCB 157
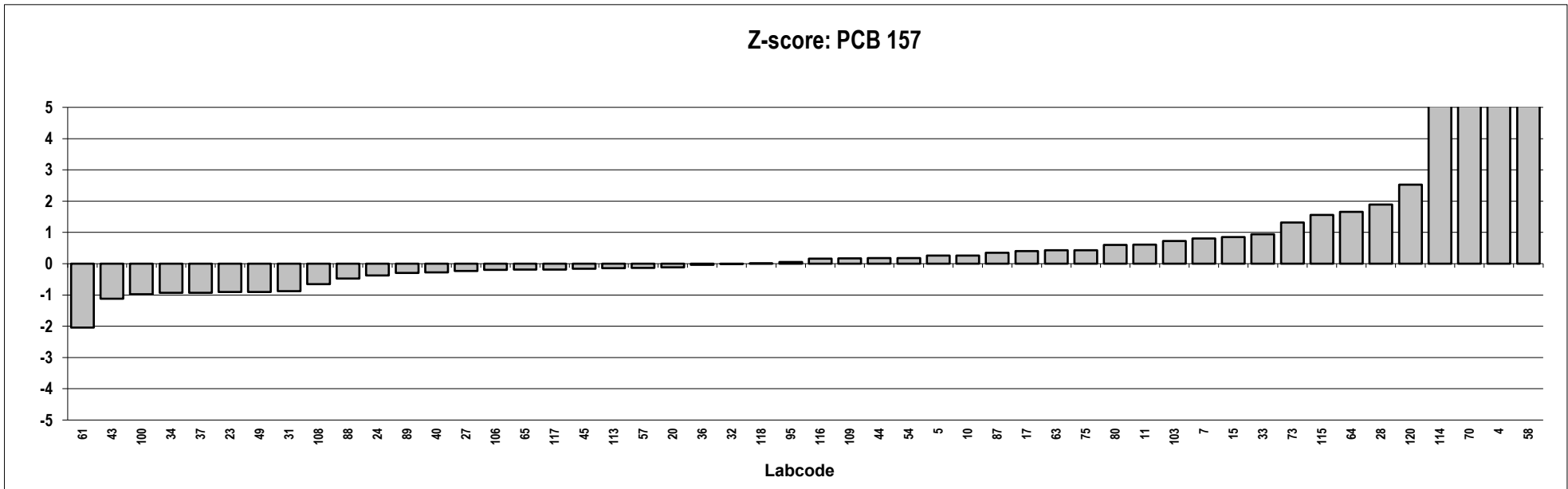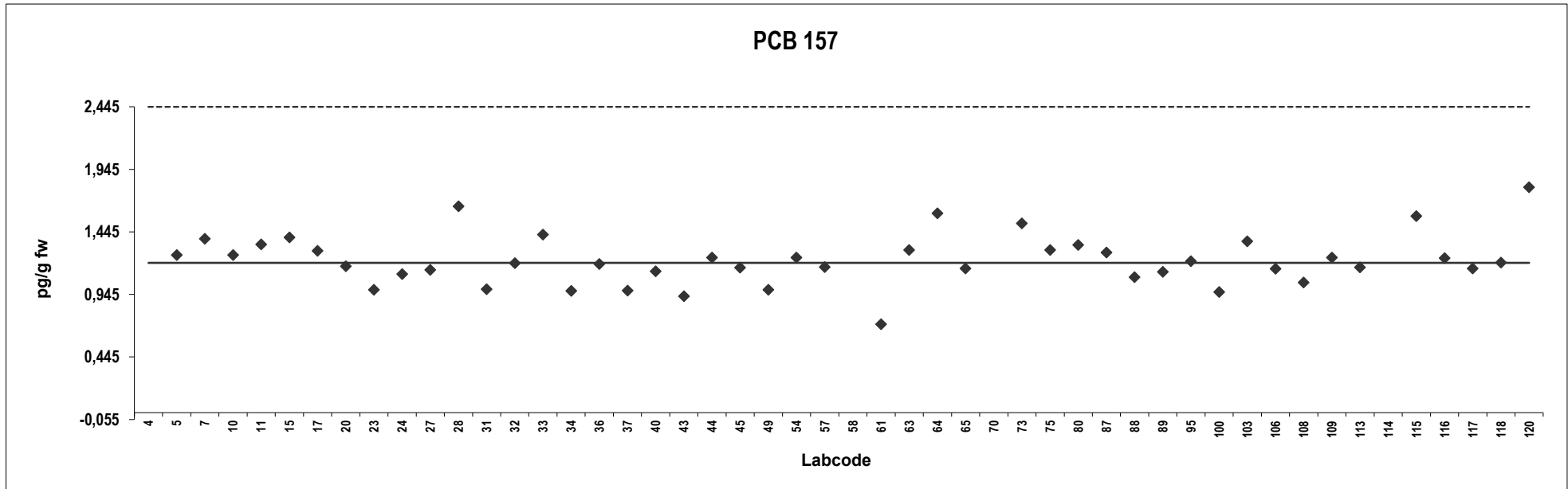
Veal
Congener: PCB 167

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	10	11	Outlier,ND	115	3,5	0,74	
5	3,4	0,56		116	3,2	0,22	
7	4,1	1,7		117	2,3	-1,3	
10	3,4	0,45		118	3,5	0,73	
11	3,4	0,57		120	4,7	2,7	
15	3,6	0,86					
17	3,2	0,15					
20	3,0	-0,17					
23	3,9	1,3					
24	2,9	-0,33					
27	2,7	-0,58					
28	2,2	-1,5					
31	2,9	-0,28					
32	3,0	-0,038					
33	3,4	0,59					
34	2,7	-0,67					
36	2,9	-0,24					
37	2,3	-1,3					
40	2,5	-0,98					
43	2,8	-0,38					
44	3,0	-0,18					
45	2,9	-0,26					
49	3,1	0,038					
54	3,0	-0,068					
57	0,031	-4,9	ND				
58	10	11	Outlier,ND				
61	2,7	-0,60					
63	3,3	0,34					
64	3,5	0,74					
65	2,9	-0,26					
70	6,4	5,4	Outlier,ND				
73	4,2	1,8					
75	3,5	0,70					
80	3,7	1,0					
87	3,4	0,47					
88	2,7	-0,56					
89	2,7	-0,59					
95	3,2	0,16					
100	2,6	-0,82					
103	3,0	-0,083					
106	2,8	-0,41					
108	3,2	0,13					
109	3,3	0,29					
113	3,4	0,55					
114	29	42	Outlier,ND				

Consenus statistics	
Consensus median, pg/g	3,1
Median all values pg/g	3,2
Consensus mean, pg/g	3,1
Standard deviation, pg/g	0,68
Relative standard deviation, %	22
No. of values reported	50
No. of values removed	4
No. of reported non-detects	5

PCB 167

Z-score: PCB 167
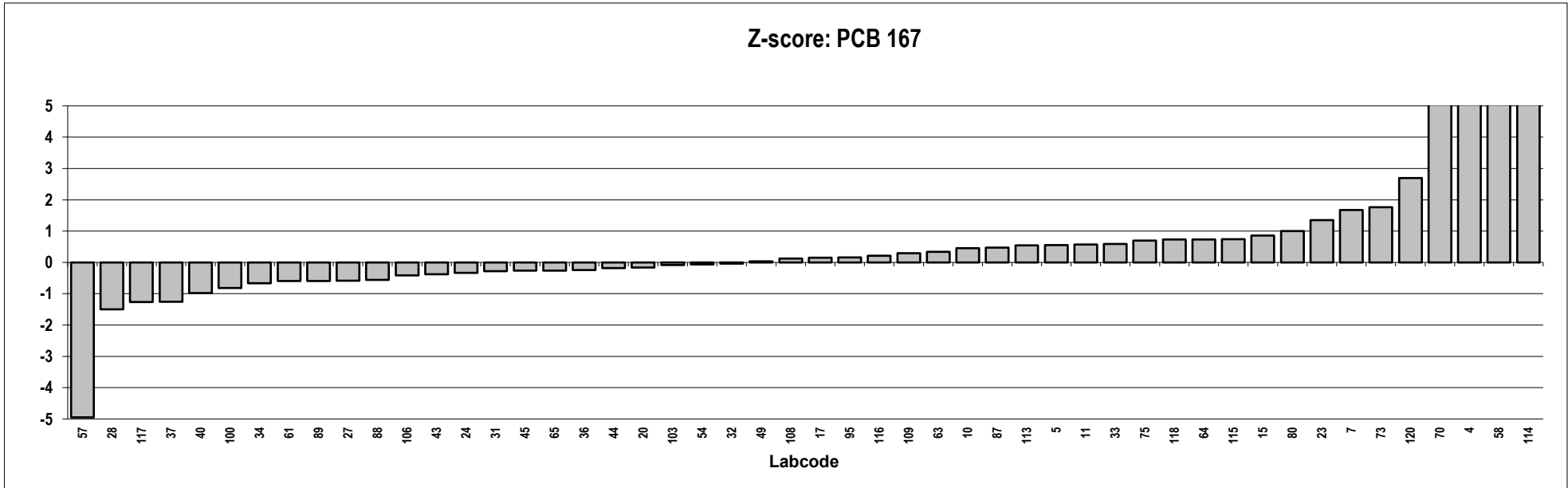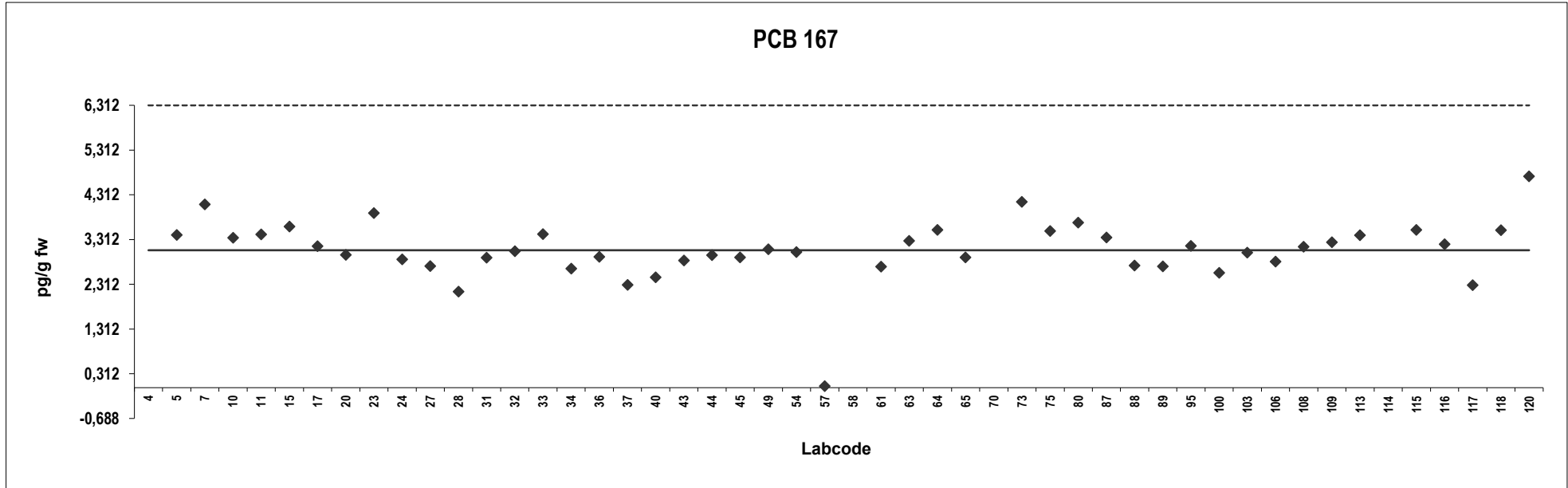
Veal
Congener: PCB 189

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	10	123	Outlier,ND	115	0,43	0,50	
5	0,37	-0,20		116	0,33	-0,76	
7	0,42	0,38		117	0,34	-0,64	
10	0,37	-0,28		118	0,38	-0,084	
11	0,43	0,49		120	0,68	3,7	
15	1,0	7,8	Outlier,ND				
17	0,44	0,58					
20	0,41	0,26					
23	0,38	-0,12					
24	0,35	-0,55					
27	0,87	6,2	Outlier,ND				
28	0,32	-0,90	ND				
31	0,61	2,9	ND				
32	1,0	8,3	Outlier,ND				
33	0,46	0,84					
34	0,36	-0,33					
36	0,38	-0,12					
37	0,39	0,013					
40	0,39	0,00					
43	0,39	0,00					
44	0,38	-0,13					
45	0,33	-0,72					
49	0,98	7,6	Outlier				
54	0,58	2,4					
57	0,41	0,23					
58	10	123	Outlier,ND				
61	0,36	-0,43					
63	0,47	1,1					
64	0,66	3,5					
65	0,40	0,16					
70	0,28	-1,4	ND				
73	0,49	1,3					
75	0,50	1,4	ND				
80	1,0	7,8	Outlier,ND				
87	0,47	1,1					
88	0,37	-0,26					
89	0,38	-0,12					
95	0,51	1,5					
100	0,29	-1,2					
103	0,36	-0,40					
106	1,7	17	Outlier,ND				
108	0,37	-0,27					
109	0,57	2,4					
113	0,38	-0,10					
114	2,5	27	Outlier,ND				

Consensus statistics	
Consensus median, pg/g	0,39
Median all values pg/g	0,41
Consensus mean, pg/g	0,42
Standard deviation, pg/g	0,093
Relative standard deviation, %	22
No. of values reported	50
No. of values removed	9
No. of reported non-detects	12

PCB 189

Z-score: PCB 189
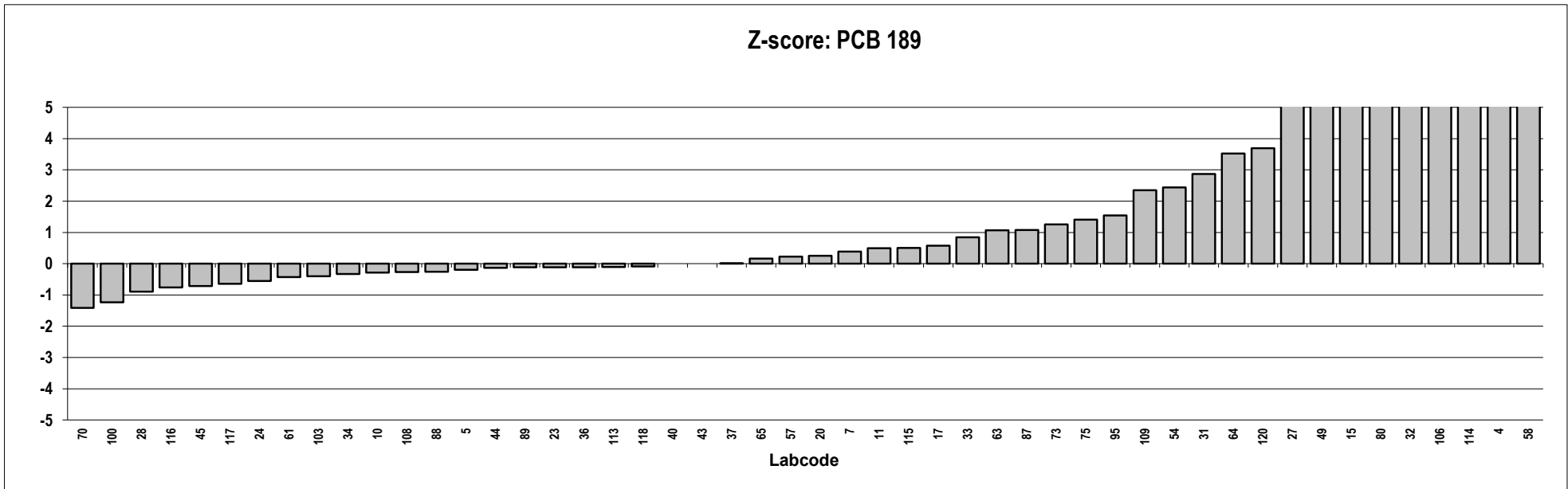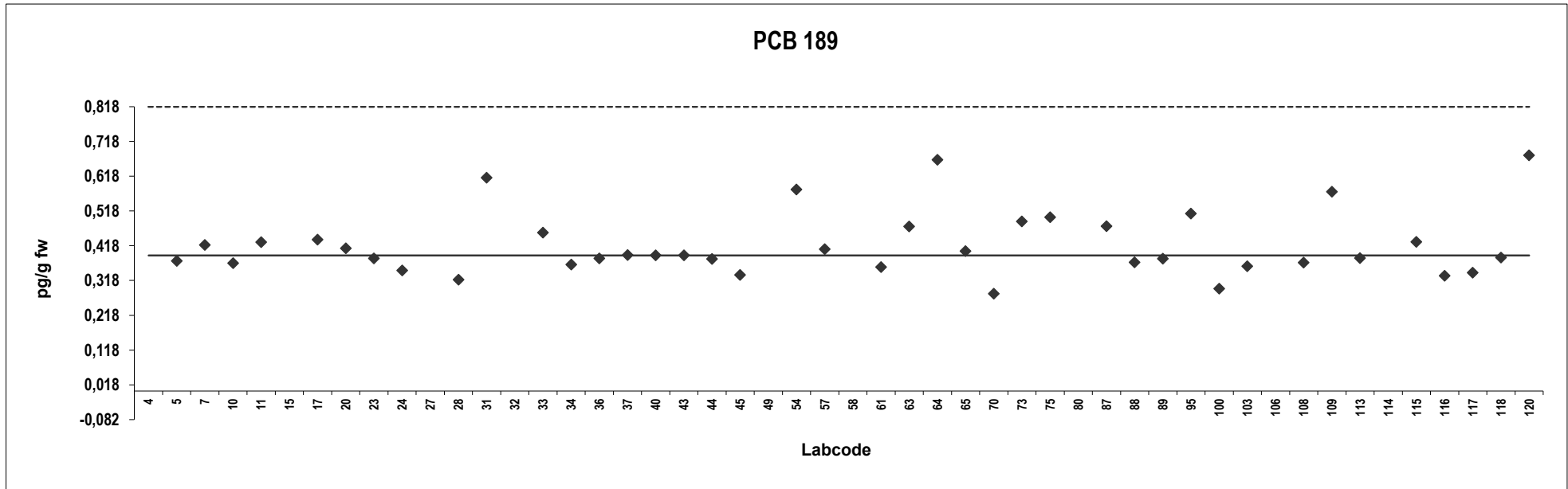
Veal

Congener: PCB 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	32	0,70					
5	32	0,70					
7	50	3,9					
10	35	1,2					
11	43	2,7					
15	42	2,5					
17	24	-0,67					
23	27	-0,22					
24	43	2,6					
27	16	-2,2					
28	27	-0,19					
31	22	-1,1					
32	34	1,11					
34	38	1,7					
37	32	0,78					
40	23	-0,85					
43	10	-3,2	ND				
44	22	-1,1					
45	23	-1,0					
49	21	-1,2					
54	23	-0,95					
57	26	-0,3					
58	50	3,9	ND				
61	77	8,80	Outlier				
63	27	-0,17					
64	26	-0,45					
65	29	0,2					
70	21	-1,3					
75	41	2,3					
80	35	1,2					
87	25	-0,51					
95	30	0,38					
100	22	-1,0					
103	27	-0,19					
105	12	-2,9					
106	23	-0,99					
108	30	0,29					
109	30	0,37					
113	42	2,5					
114	125	17	Outlier				
115	86	10	Outlier				
117	34	1,0					
118	64	6,5	Outlier				
120	31	0,46					

Consenus statistics

Consensus median, pg/g	28
Median all values pg/g	30
Consensus mean, pg/g	29
Standard deviation, pg/g	9,2
Relative standard deviation, %	31
No. of values reported	44
No. of values removed	4
No. of reported non-detects	2

PCB 28

Z-score: PCB 28
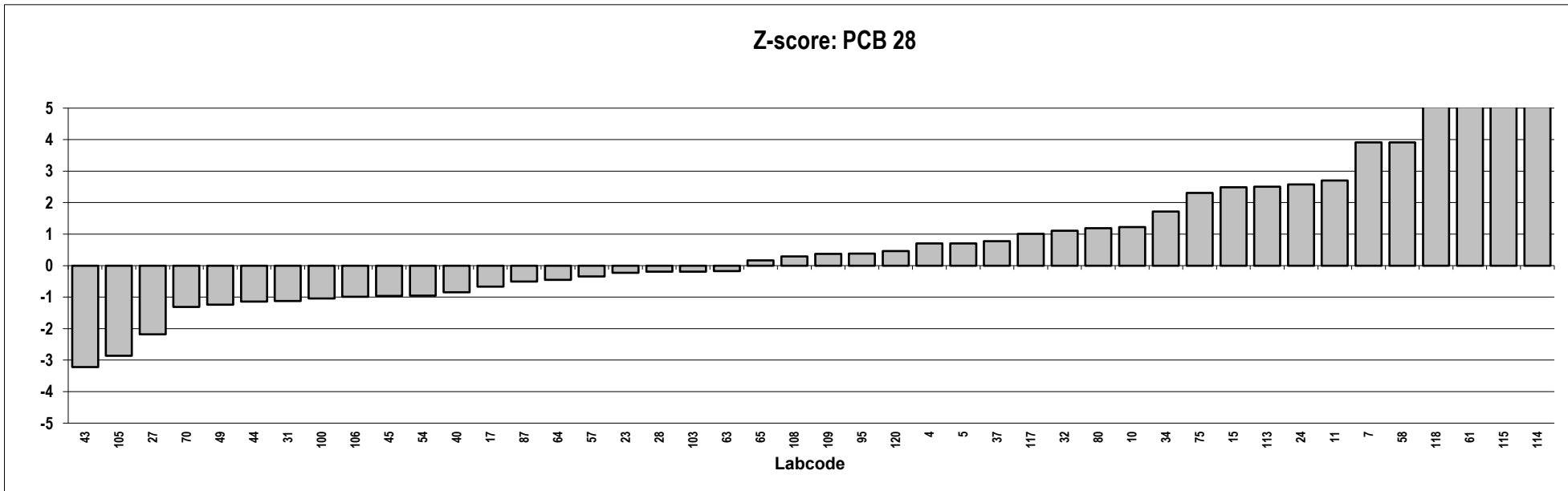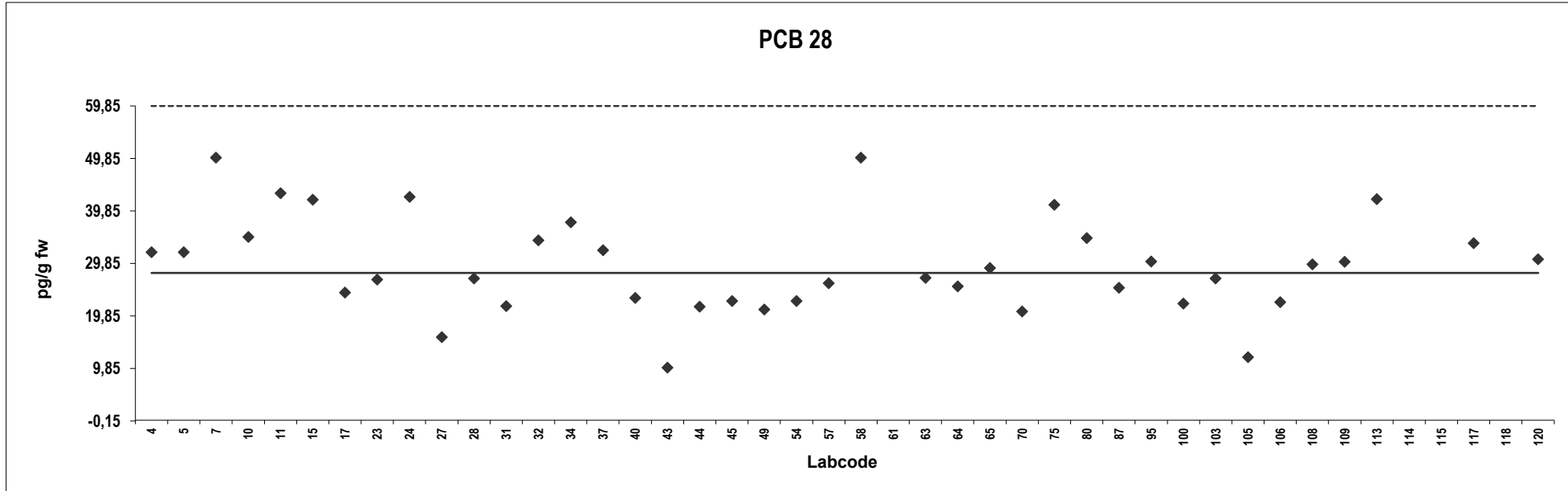
Veal

Congener: PCB 52

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	27	0,85					
5	27	0,85					
7	33	2,1					
10	24	0,22					
11	47	5,1					
15	37	3,0					
17	21	-0,52					
23	25	0,48					
24	27	0,92					
27	19	-0,94					
28	16	-1,6					
31	21	-0,40					
32	37	2,9					
34	19	-0,97					
37	33	2,1					
40	19	-0,90					
43	21	-0,45					
44	23	0,026					
45	18	-1,0					
49	20	-0,75					
54	18	-1,1					
57	22	-0,30					
58	50	5,8	Outlier,ND				
61	28	1,1					
63	23	0,00					
64	21	-0,37					
65	19	-0,92					
70	16	-1,5					
75	35	2,6					
80	25	0,48					
87	22	-0,19					
95	28	0,96					
100	15	-1,7					
103	25	0,42					
105	11	-2,6					
106	19	-0,86					
108	25	0,40					
109	25	0,49					
113	43	4,2					
114	130	23	Outlier				
115	25	0,45					
117	21	-0,45					
118	19	-0,78					
120	74	11	Outlier				

Consenus statistics

Consensus median, pg/g	23
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	7,4
Relative standard deviation, %	31
No. of values reported	44
No. of values removed	3
No. of reported non-detects	1

PCB 52

Z-score: PCB 52
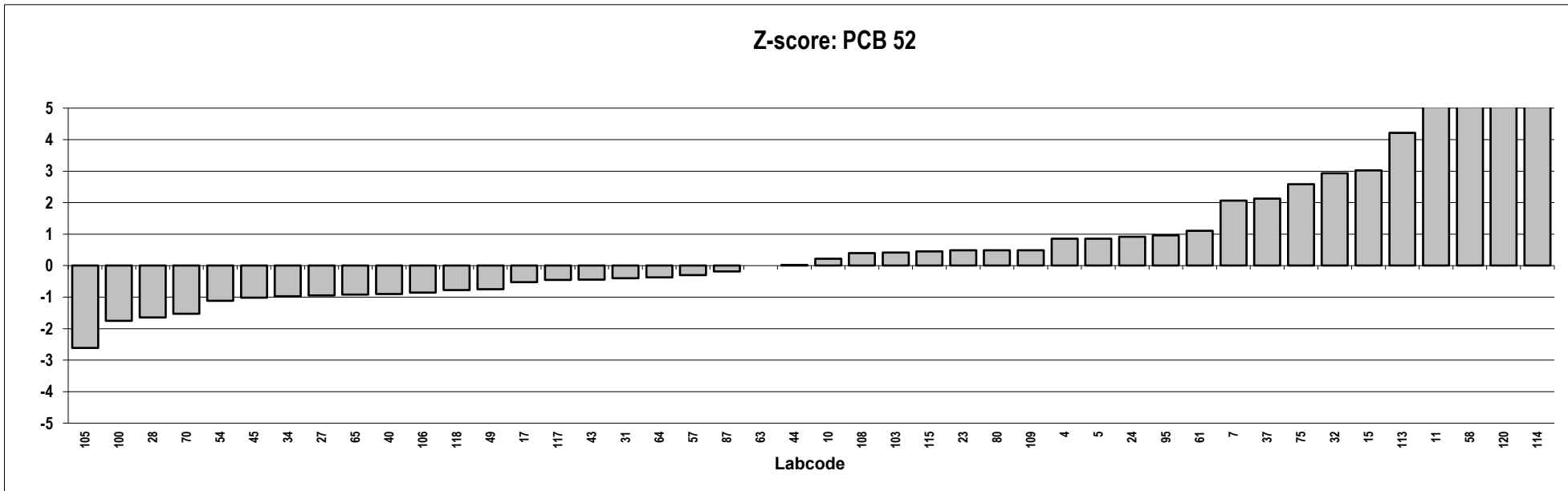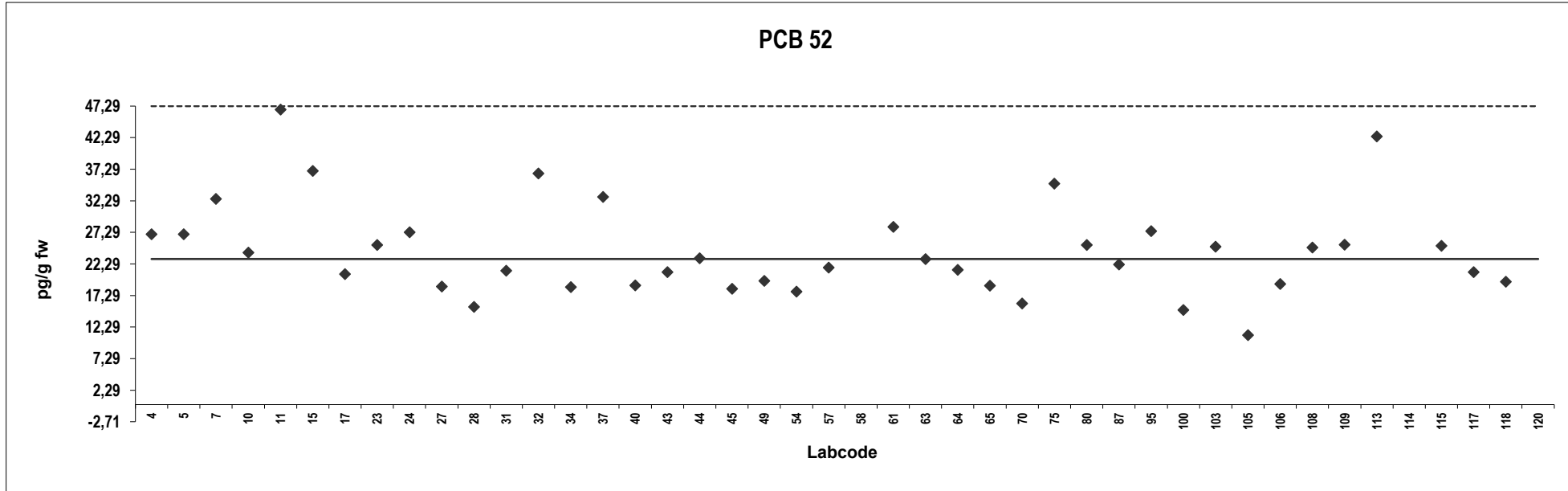
Veal
Congener: PCB 101

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	43	0,80					
5	43	0,80					
7	38	0,16					
10	36	-0,20					
11	50	1,7					
15	50	1,7					
17	37	0,00					
23	42	0,72					
24	36	-0,18					
27	30	-0,93					
28	11	-3,6					
31	38	0,090					
32	43	0,84					
34	33	-0,54					
37	37	-0,066					
40	31	-0,83					
43	34	-0,42					
44	40	0,40					
45	32	-0,75					
49	33	-0,62					
54	36	-0,16					
57	40	0,45					
58	50	1,7	ND				
61	45	1,1					
63	39	0,24					
64	38	0,094					
65	31	-0,85					
70	29	-1,1					
75	51	1,9					
80	44	0,97					
87	37	-0,025					
95	40	0,42					
100	27	-1,4					
103	35	-0,28					
105	13	-3,2					
106	26	-1,6					
108	41	0,51					
109	37	0,014					
113	47	1,4					
114	170	18	Outlier				
115	40	0,43					
117	34	-0,42					
118	34	-0,44					
120	77	5,3	Outlier				

Consensus statistics

Consensus median, pg/g	37
Median all values pg/g	37
Consensus mean, pg/g	37
Standard deviation, pg/g	8,5
Relative standard deviation, %	23
No. of values reported	44
No. of values removed	2
No. of reported non-detects	1

PCB 101

Z-score: PCB 101
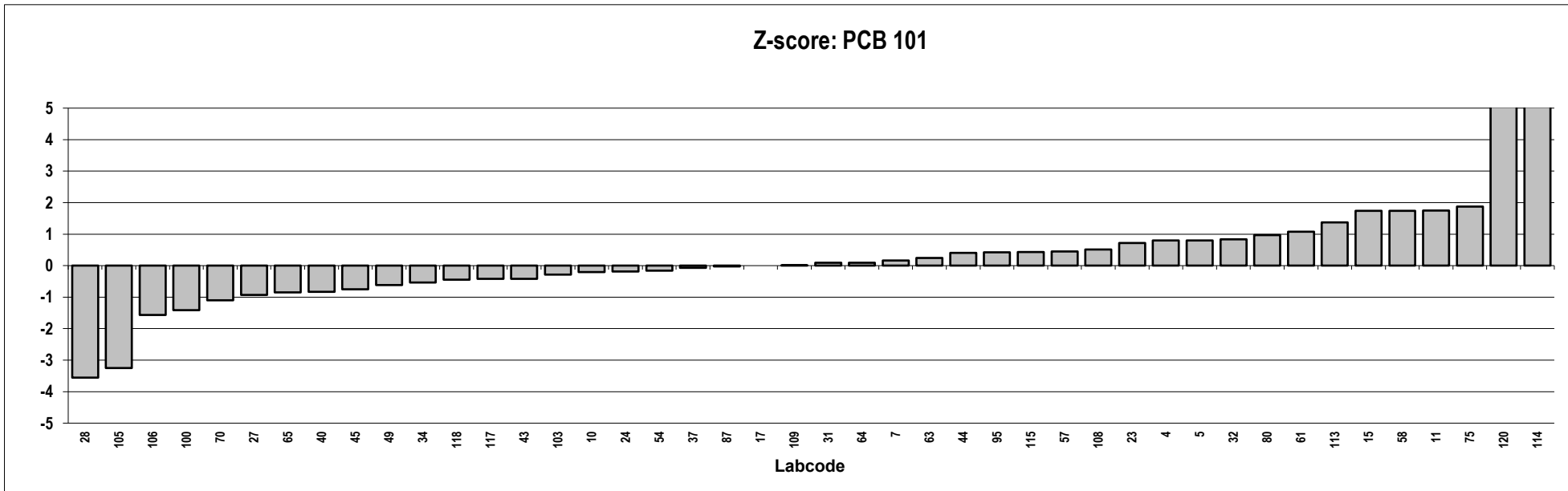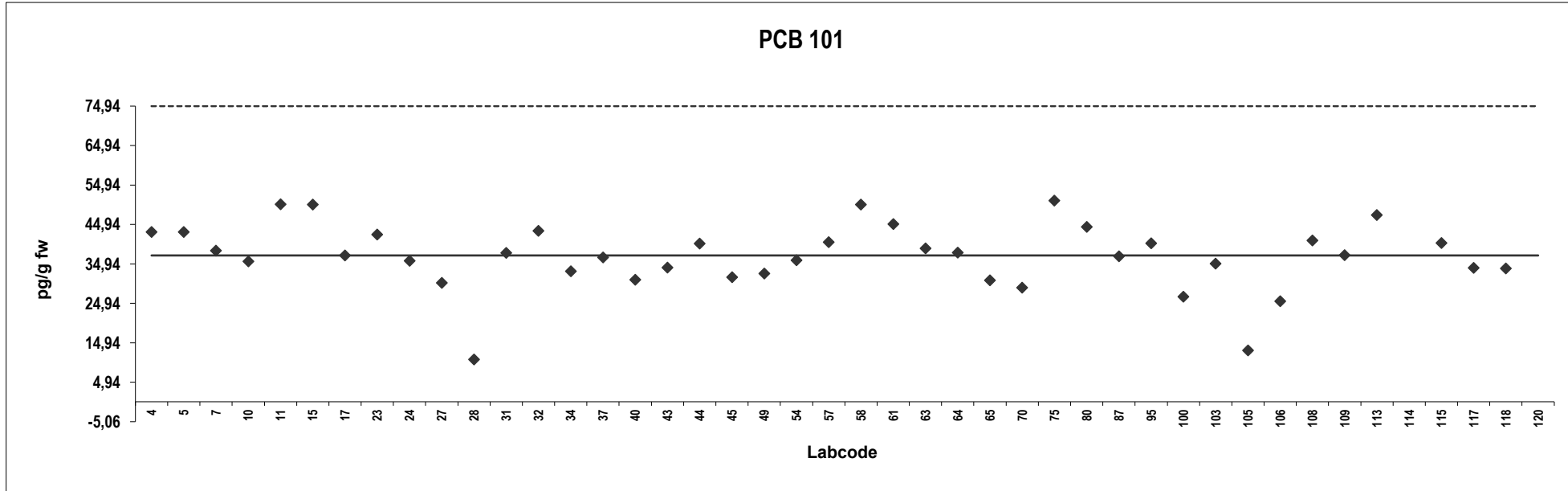
Veal
Congener: PCB 138

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	83	0,39					
5	83	0,39					
7	96	1,2					
10	77	-0,032					
11	94	1,1					
15	95	1,2					
17	117	2,6					
23	78	0,091					
24	74	-0,21					
27	71	-0,41					
28	61	-1,0					
31	74	-0,21					
32	62	-0,95					
34	71	-0,38					
37	66	-0,75					
40	70	-0,47					
43	122	2,9					
44	79	0,11					
45	70	-0,43					
49	66	-0,69					
54	81	0,28					
57	90	0,85					
58	72	-0,32					
61	129	3,4					
63	83	0,38					
64	65	-0,80					
65	56	-1,3					
70	84	0,42					
75	97	1,3					
80	77	0,00					
87	84	0,47					
95	80	0,19					
100	73	-0,27					
103	75	-0,13					
105	23	-3,5					
106	65	-0,77					
108	72	-0,36					
109	81	0,23					
113	99	1,4					
114	310	15	Outlier				
115	88	0,68					
117	69	-0,51					
118	98	1,3					
120	67	-0,66					

Consenus statistics

Consensus median, pg/g	77
Median all values pg/g	78
Consensus mean, pg/g	79
Standard deviation, pg/g	18
Relative standard deviation, %	23
No. of values reported	44
No. of values removed	1
No. of reported non-detects	0

PCB 138

Z-score: PCB 138
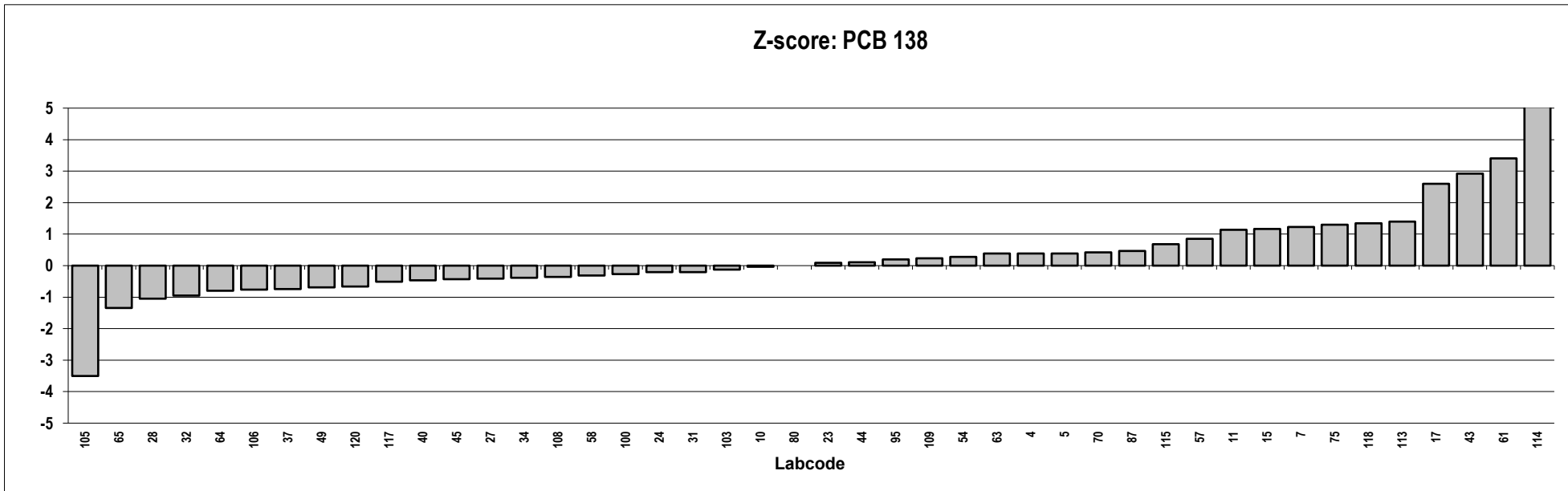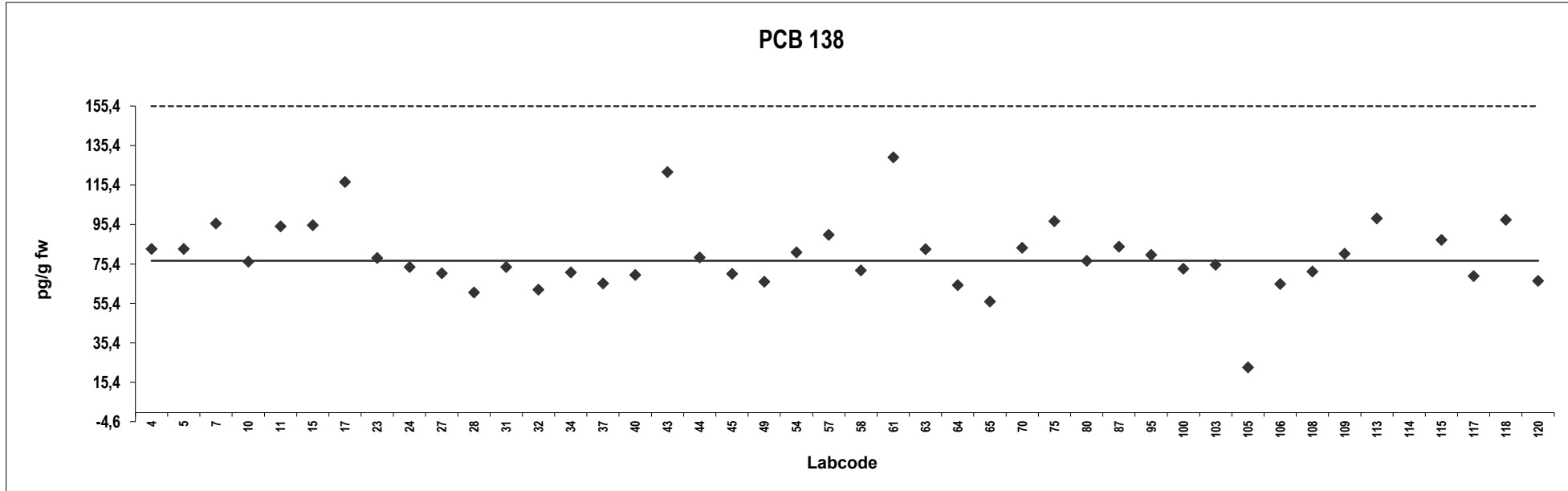
Veal
Congener: PCB 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	137	1,4					
5	137	1,4					
7	125	0,85					
10	107	0,0061					
11	116	0,41					
15	120	0,61					
17	107	0,023					
23	114	0,33					
24	110	0,14					
27	105	-0,074					
28	93	-0,65					
31	108	0,073					
32	101	-0,27					
34	110	0,15					
37	94	-0,61					
40	92	-0,68					
43	88	-0,88					
44	104	-0,15					
45	83	-1,1					
49	88	-0,87					
54	105	-0,087					
57	112	0,25					
58	95	-0,56					
61	146	1,8					
63	114	0,34					
64	114	0,35					
65	79	-1,3					
70	89	-0,82					
75	124	0,80					
80	105	-0,11					
87	112	0,24					
95	112	0,24					
100	93	-0,63					
103	97	-0,46					
105	41	-3,1					
106	82	-1,2					
108	105	-0,087					
109	108	0,056					
113	125	0,85					
114	360	12	Outlier				
115	68	-1,8					
117	90	-0,79					
118	127	0,92					
120	107	0,00					

Consenus statistics

Consensus median, pg/g	107
Median all values pg/g	107
Consensus mean, pg/g	104
Standard deviation, pg/g	19
Relative standard deviation, %	18
No. of values reported	44
No. of values removed	1
No. of reported non-detects	0

PCB 153

Z-score: PCB 153
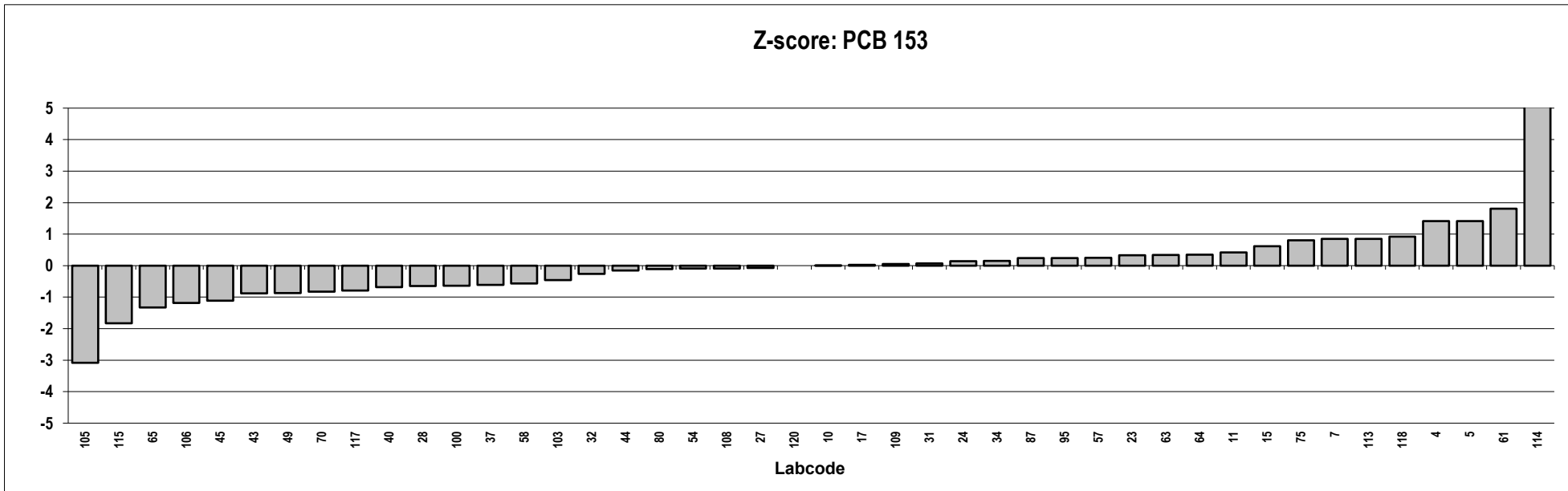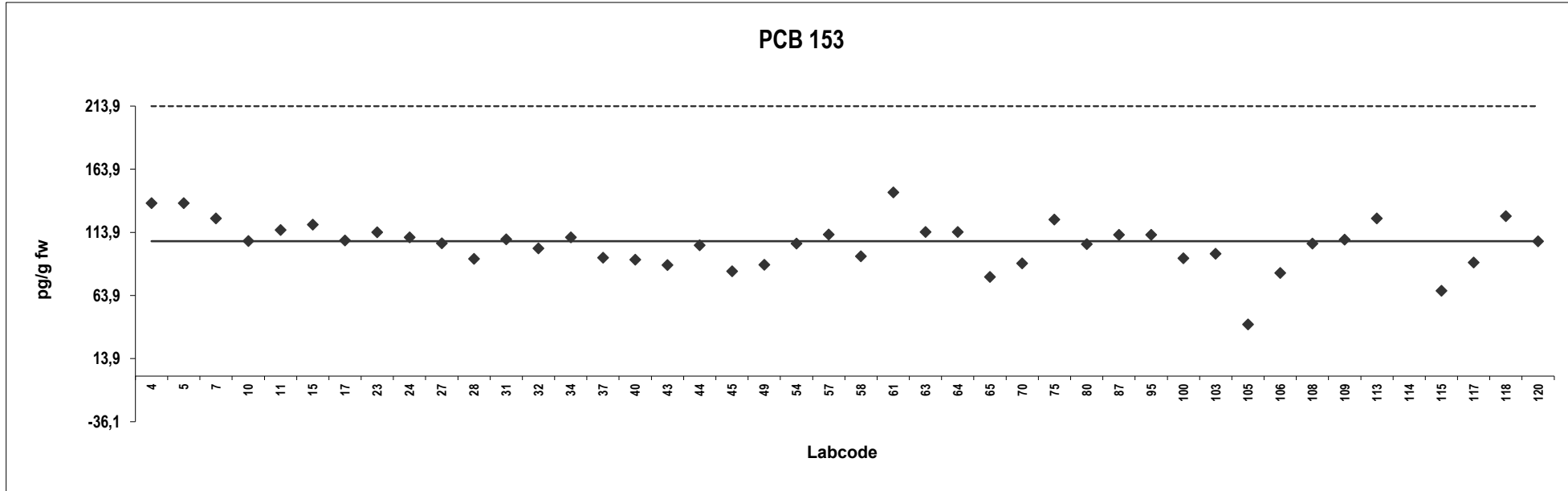
Veal
Congener: PCB 180

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	30	0,38					
5	30	0,38					
7	25	-0,57					
10	30	0,39					
11	31	0,54					
15	32	0,73					
17	28	-0,069					
23	29	0,18					
24	29	0,19					
27	19	-1,6					
28	28	-0,055					
31	26	-0,34					
32	31	0,56					
34	26	-0,27					
37	24	-0,66					
40	24	-0,63					
43	18	-1,8					
44	26	-0,36					
45	24	-0,70					
49	26	-0,27					
54	31	0,57					
57	27	-0,14					
58	50	4,0	ND				
61	40	2,2					
63	30	0,39					
64	30	0,39					
65	21	-1,2					
70	22	-1,1					
75	33	0,91					
80	30	0,34					
87	28	-0,00090					
95	29	0,20					
100	22	-1,0					
103	29	0,20					
105	6,8	-3,8					
106	21	-1,3					
108	28	0,017					
109	33	0,88					
113	31	0,61					
114	100	13	Outlier				
115	23	-0,85					
117	27	-0,17					
118	35	1,2					
120	28	0,00090					

Consenus statistics

Consensus median, pg/g	28
Median all values pg/g	28
Consensus mean, pg/g	28
Standard deviation, pg/g	6,4
Relative standard deviation, %	23
No. of values reported	44
No. of values removed	1
No. of reported non-detects	1

PCB 180

Z-score: PCB 180
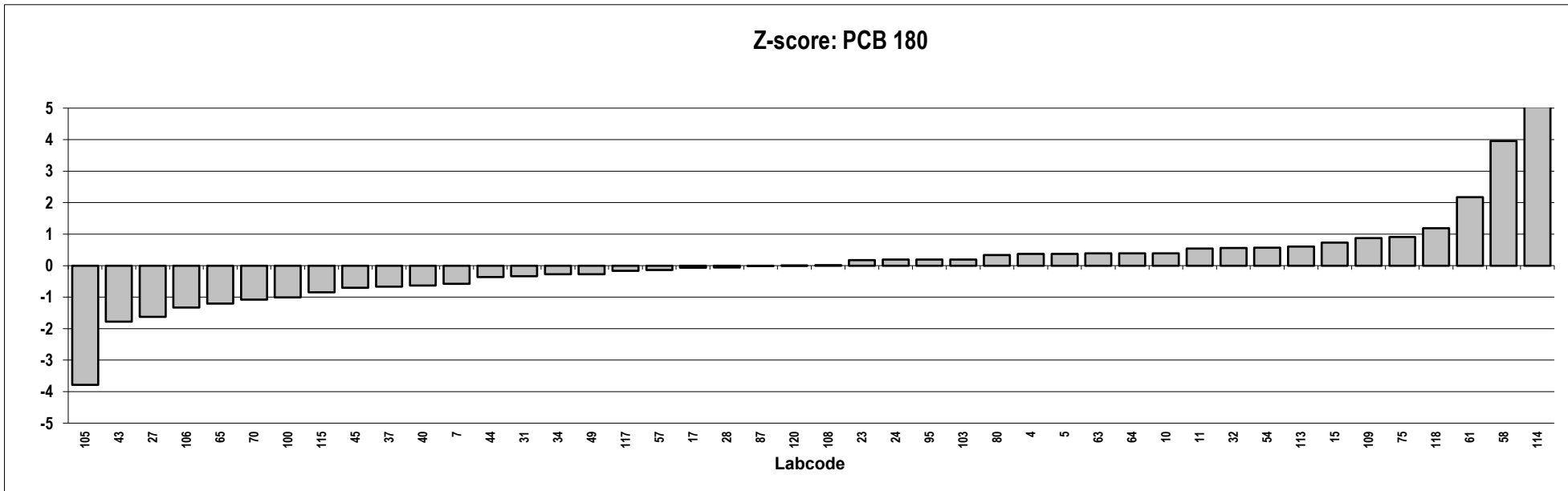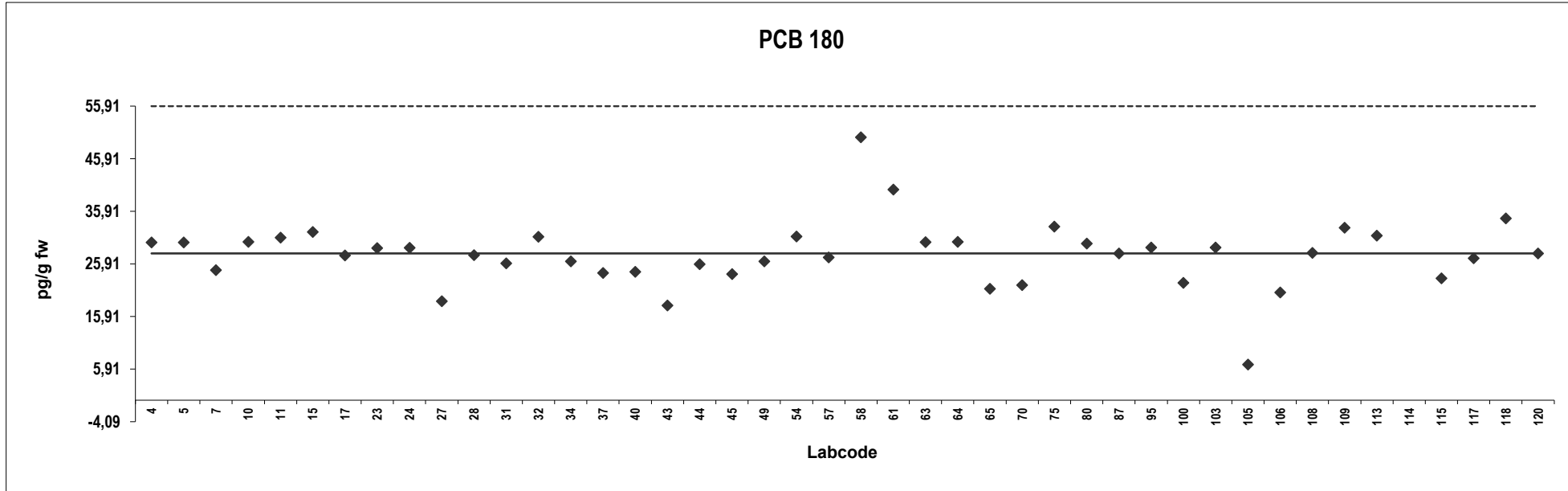
Veal
Congener: PBDE 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	0,96	27	Outlier,ND				
23	0,15	0,069					
31	0,77	21	Outlier,ND				
36	0,25	3,4					
37	0,13	-0,61					
40	0,35	6,8					
43	1,0	29	Outlier,ND				
49	0,043	-3,5	ND				
54	0,15	0,069					
57	0,13	-0,48					
63	2,6	82	Outlier				
65	0,15	-0,069					
95	0,080	-2,3	ND				
108	2,2	68	Outlier				
113	0,81	22	Outlier				
115	0,62	16	Outlier				
116	0,10	-1,5					

Consensus statistics

Consensus median, pg/g	0,15
Median all values pg/g	0,25
Consensus mean, pg/g	0,15
Standard deviation, pg/g	0,088
Relative standard deviation, %	57
No. of values reported	17
No. of values removed	7
No. of reported non-detects	5

PBDE 28

Z-score: PBDE 28
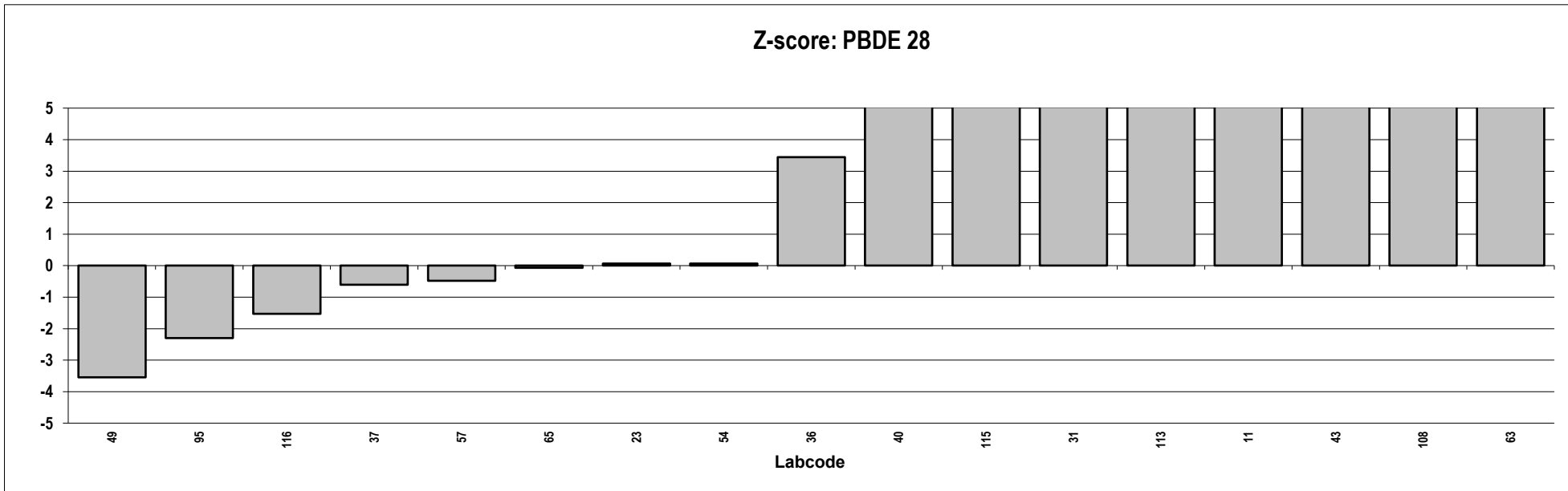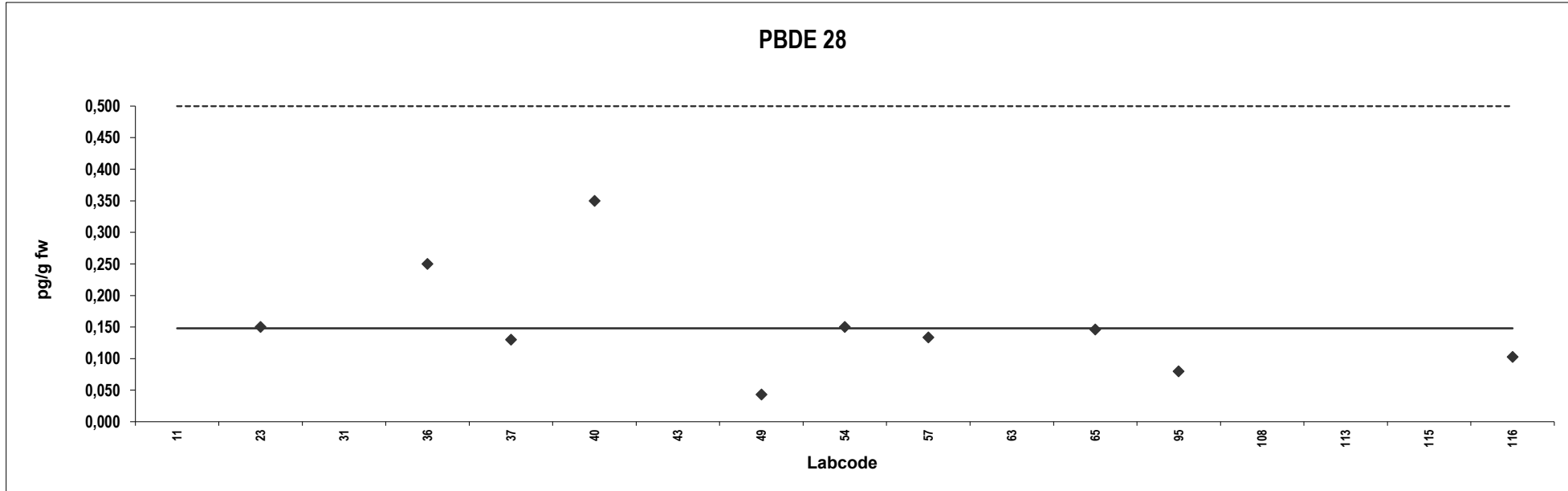
Veal
Congener: PBDE 47

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	2,9	0,37					
23	3,7	1,9					
31	3,1	0,68	ND				
36	3,3	1,0					
37	0,31	-4,4					
40	2,2	-1,0					
43	13	19	Outlier				
49	2,7	0,00					
54	2,3	-0,80					
57	3,8	2,0					
63	12	17	Outlier				
65	2,4	-0,61					
95	2,6	-0,17					
108	6,6	7,2	Outlier				
113	3,5	1,5					
115	4,4	3,1					
116	2,1	-1,1					

Consenus statistics

Consensus median, pg/g	2,7
Median all values pg/g	3,1
Consensus mean, pg/g	2,8
Standard deviation, pg/g	0,98
Relative standard deviation, %	35
No. of values reported	17
No. of values removed	3
No. of reported non-detects	1

PBDE 47

Z-score: PBDE 47
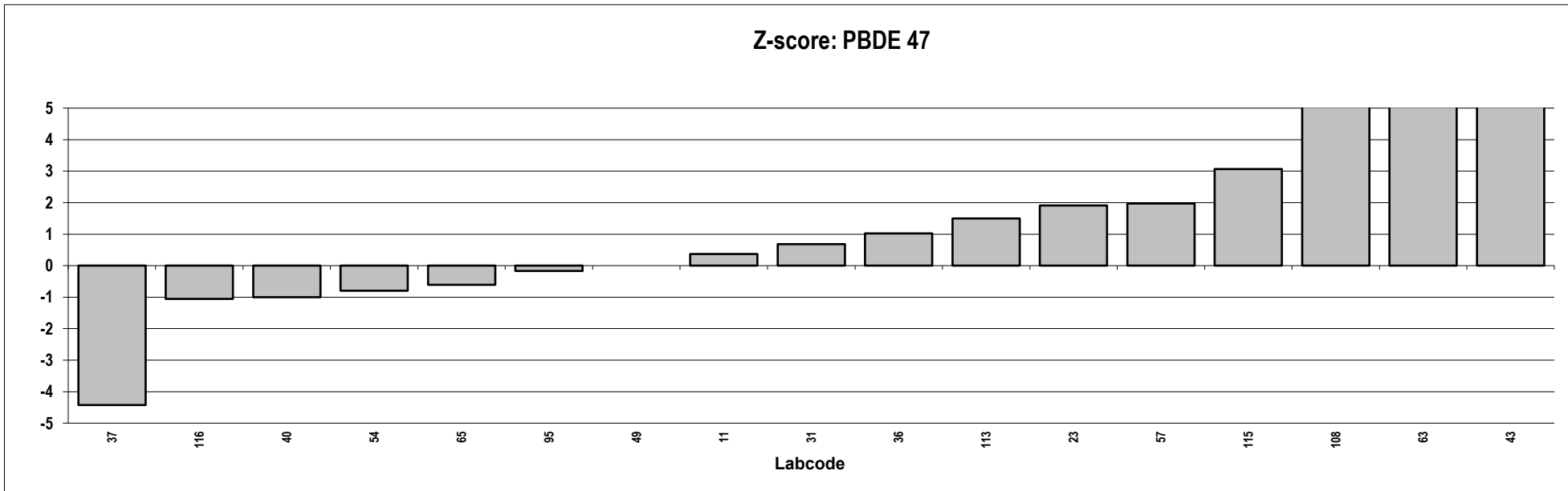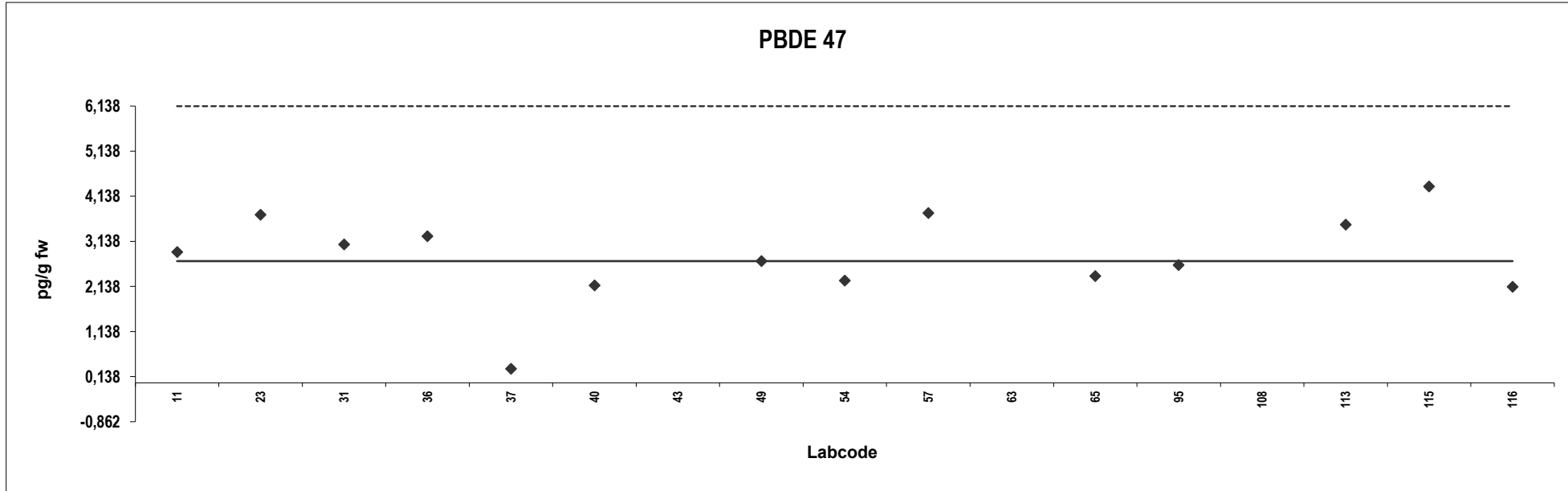
Veal
Congener: PBDE 99

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	2,4	4,1					
23	3,3	7,5	Outlier				
31	1,5	0,84	ND				
36	1,5	0,86					
37	0,54	-2,9					
40	1,3	-0,016					
43	1,0	-1,2	ND				
49	2,9	5,9					
54	1,1	-0,89					
57	1,9	2,3					
63	4,9	13	Outlier				
65	1,3	0,00					
95	1,1	-0,74					
108	29	104	Outlier				
113	0,14	-4,5					
115	1,7	1,3					
116	3,6	8,6	Outlier				

Consenus statistics

Consensus median, pg/g	1,3
Median all values pg/g	1,5
Consensus mean, pg/g	1,4
Standard deviation, pg/g	0,72
Relative standard deviation, %	51
No. of values reported	17
No. of values removed	4
No. of reported non-detects	2

PBDE 99

pg/g fw

Labcode

Z-score: PBDE 99
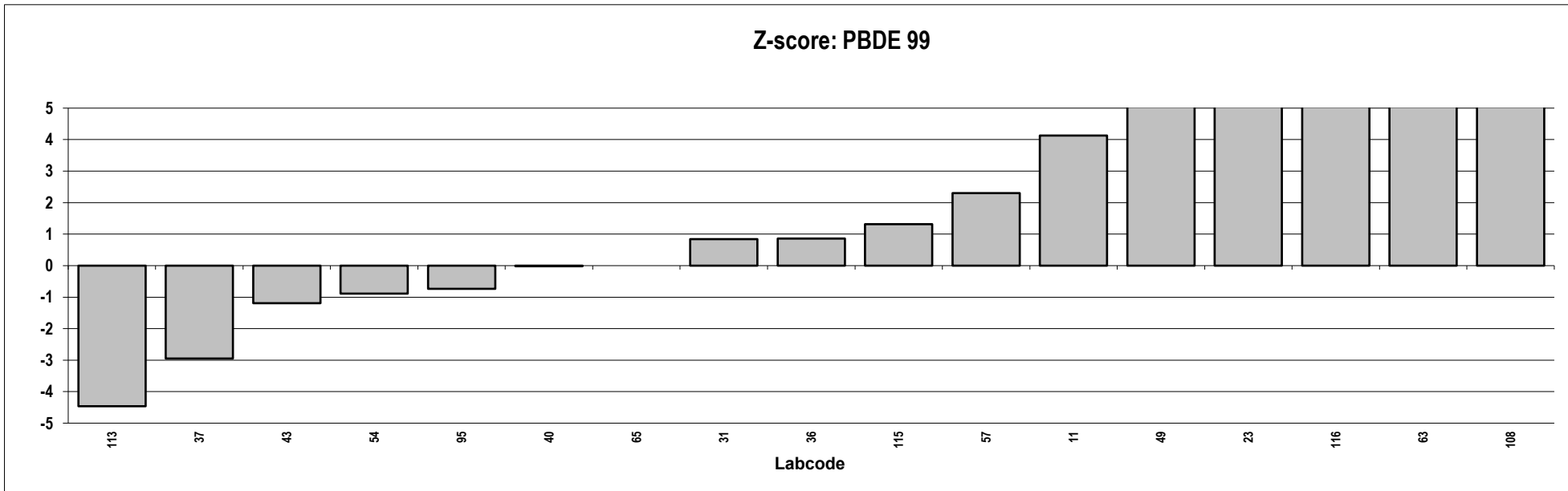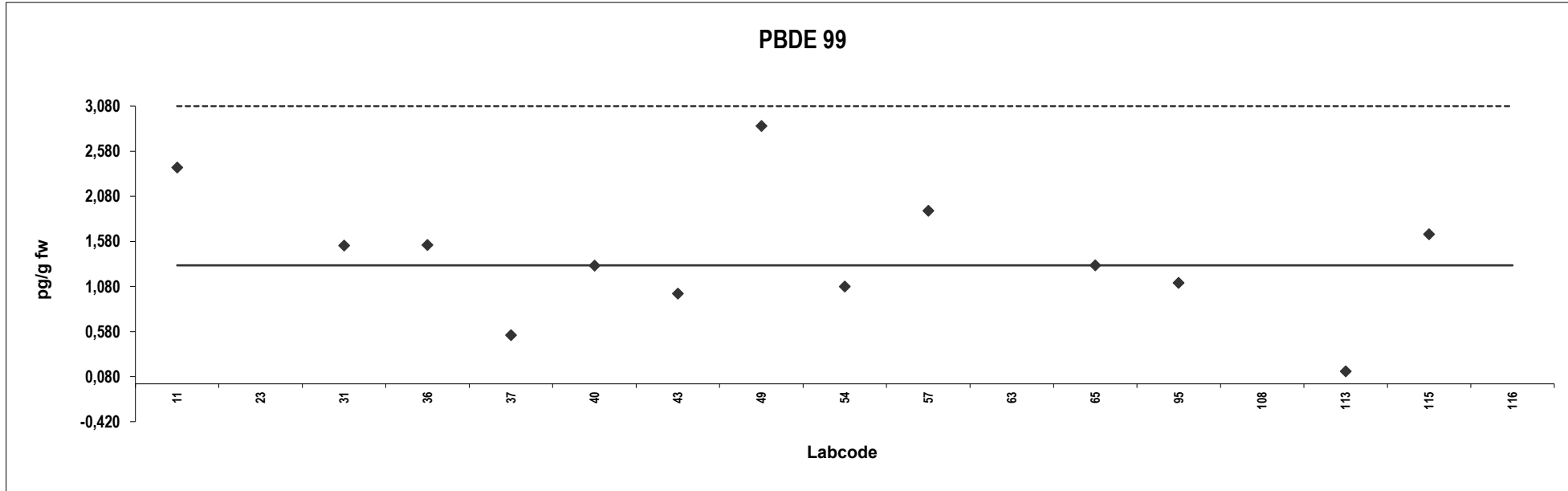
Labcode

Veal

Congener: PBDE 100

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	1,9	16	Outlier,ND				
23	0,69	2,6					
31	1,5	12	Outlier,ND				
36	0,43	-0,28					
37	0,20	-2,8					
40	0,71	2,8					
43	2,9	27	Outlier				
49	0,94	5,3					
54	0,24	-2,4					
57	0,48	0,28					
63	1,8	15	Outlier				
65	0,37	-0,92					
95	0,35	-1,2					
108	3,8	36	Outlier				
113	0,14	-3,5					
115	0,56	1,1					
116	0,56	1,2					

Consenus statistics

Consensus median, pg/g	0,46
Median all values pg/g	0,56
Consensus mean, pg/g	0,47
Standard deviation, pg/g	0,23
Relative standard deviation, %	49
No. of values reported	17
No. of values removed	5
No. of reported non-detects	2

PBDE 100

Z-score: PBDE 100
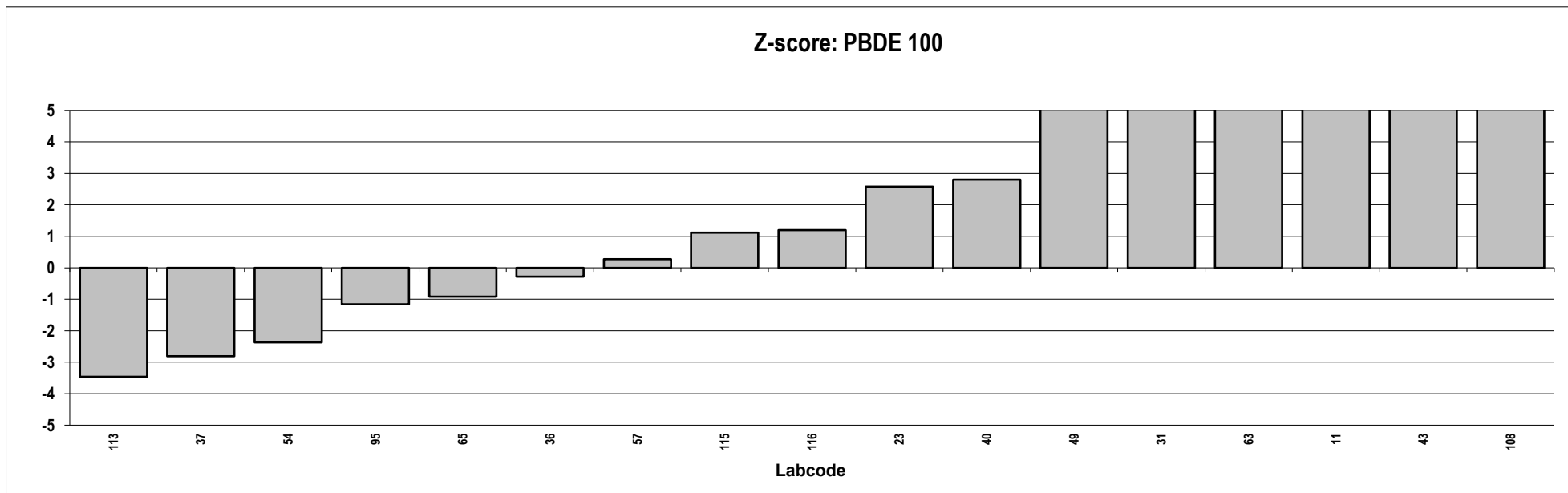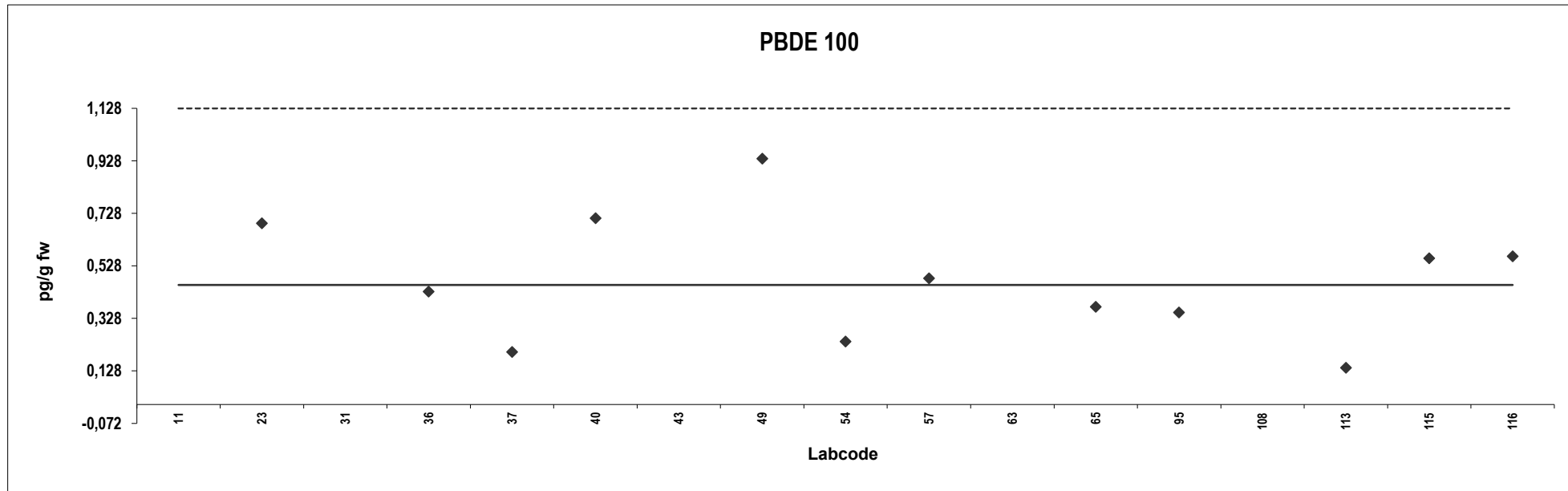
Veal
Congener: PBDE 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	2,9	29	Outlier,ND				
23	0,57	1,8					
31	0,77	4,2	ND				
36	0,39	-0,34					
37	0,21	-2,5					
40	2,4	24	Outlier				
43	1,0	7,0	ND				
49	0,45	0,39					
54	0,36	-0,70					
57	0,42	0,062					
63	2,6	25	Outlier,ND				
65	0,42	0,00					
95	0,47	0,62					
108	7,4	84	Outlier				
113	0,14	-3,3					
115	2,0	19	Outlier				
116	1,4	11	Outlier				

Consenus statistics

Consensus median, pg/g	0,42
Median all values pg/g	0,57
Consensus mean, pg/g	0,47
Standard deviation, pg/g	0,24
Relative standard deviation, %	51
No. of values reported	17
No. of values removed	6
No. of reported non-detects	4

PBDE 153
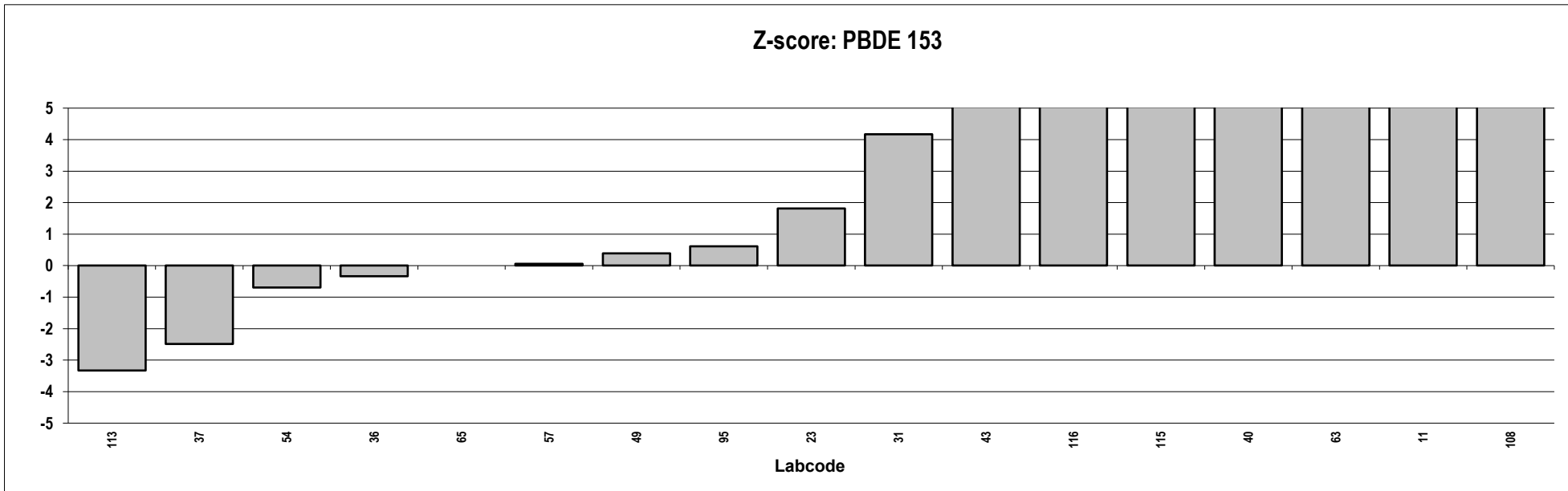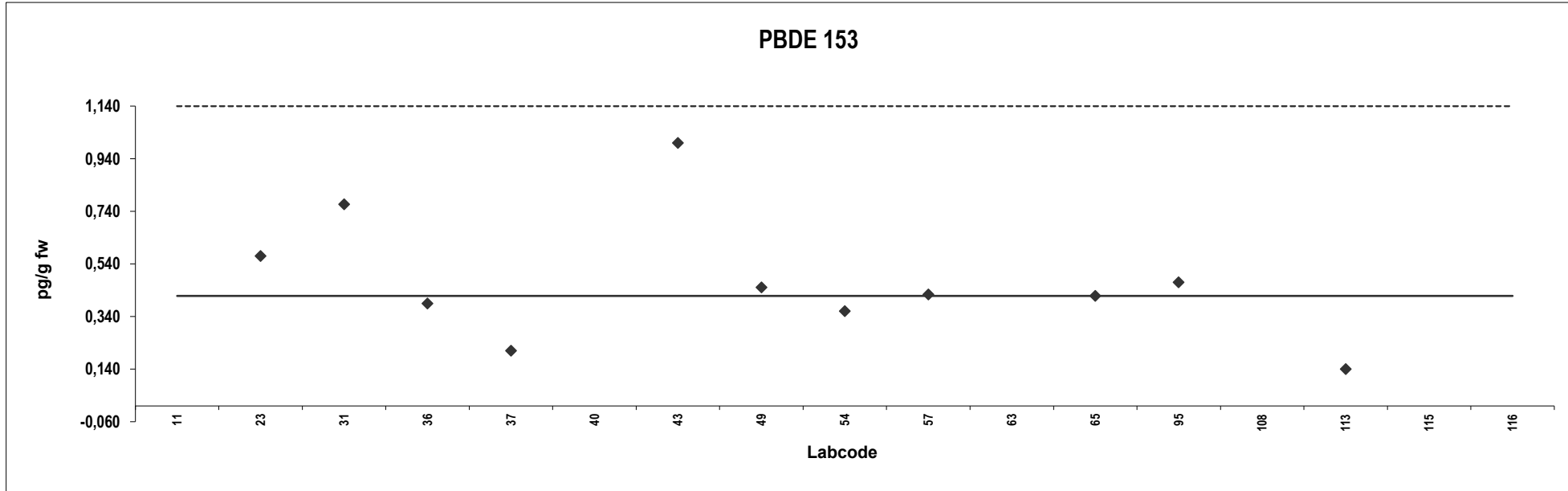
Z-score: PBDE 153

Veal
Congener: PBDE 154

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	2,9	52	Outlier,ND				
23	0,41	3,1					
31	0,77	10	ND				
36	0,25	-0,068					
37	0,21	-0,86					
40	1,9	33	Outlier				
43	1,0	15	Outlier,ND				
49	0,28	0,46					
54	0,22	-0,66					
57	0,31	1,2					
63	2,3	40	Outlier,ND				
65	0,25	0,00					
95	0,12	-2,6					
108	4,7	88	Outlier				
113	0,14	-2,2					
115	0,56	6,0					
116	0,77	10					

Consenus statistics

Consensus median, pg/g	0,25
Median all values pg/g	0,41
Consensus mean, pg/g	0,36
Standard deviation, pg/g	0,22
Relative standard deviation, %	63
No. of values reported	17
No. of values removed	5
No. of reported non-detects	4

PBDE 154

Z-score: PBDE 154
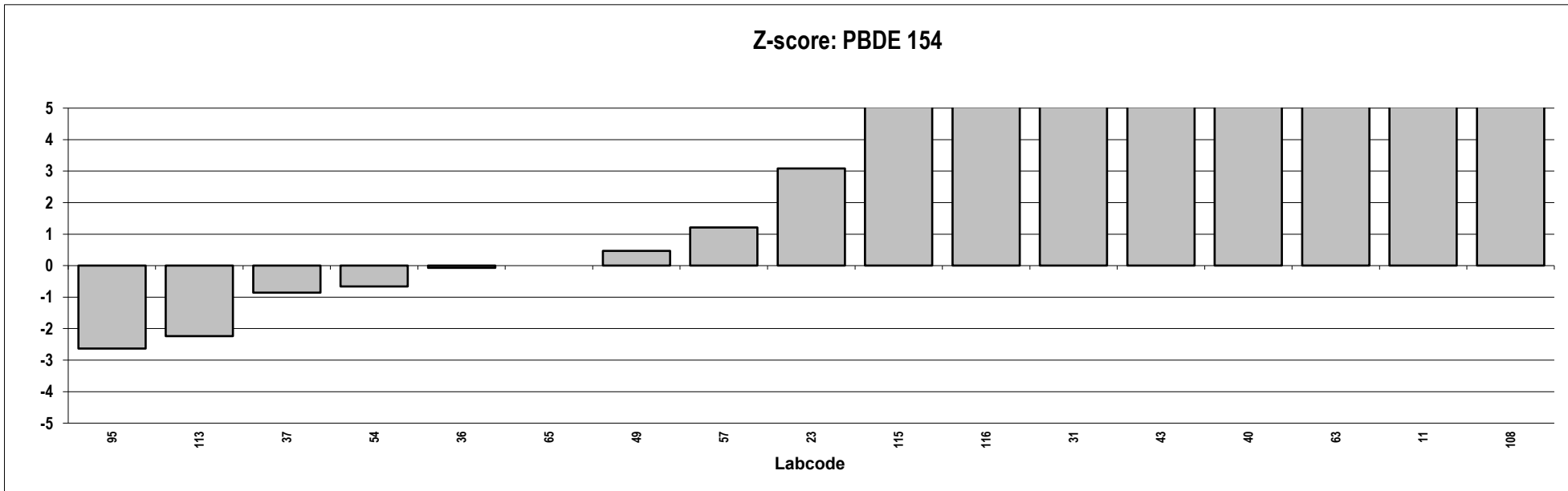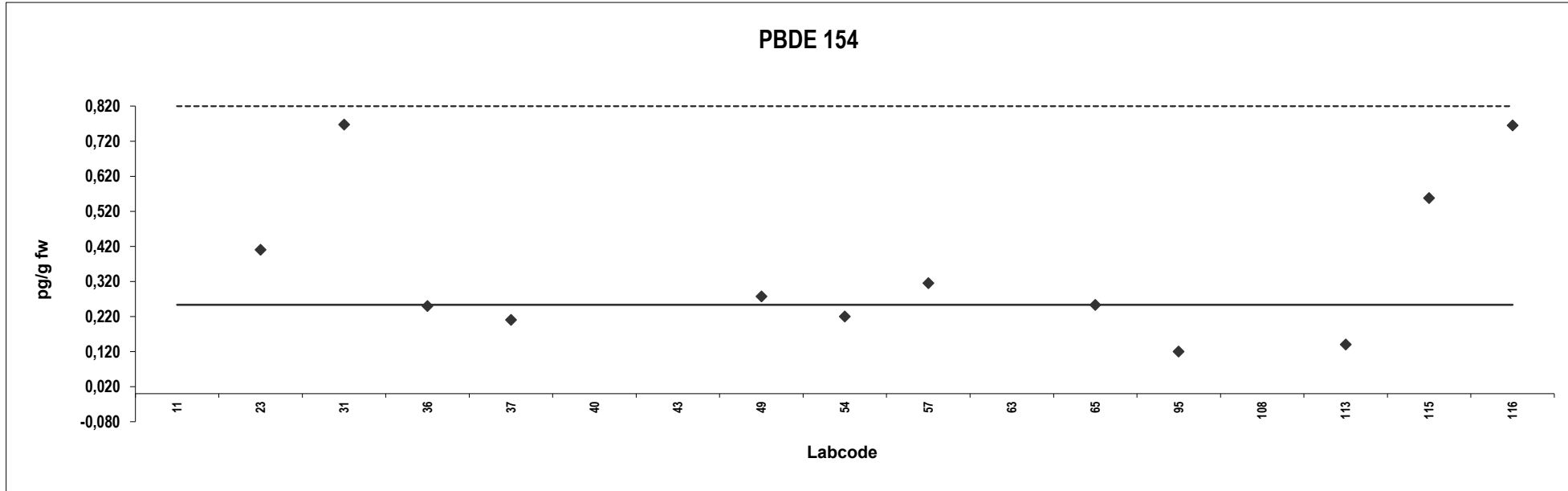
Veal
Congener: PBDE 183

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	4,8	81	Outlier,ND				
23	0,16	-2,1					
31	0,77	8,8	Outlier,ND				
36	0,37	1,6					
37	0,56	5,1					
40	4,1	69	Outlier				
43	1,0	13	Outlier,ND				
49	0,23	-0,80					
54	0,32	0,75					
57	0,16	-2,2					
63	1,7	25	Outlier,ND				
65	0,28	0,00					
95	0,44	2,9					
108	0,33	0,93					
113	0,14	-2,5					
115	1,8	28	Outlier				
116	0,14	-2,4					

Consenus statistics	
Consensus median, pg/g	0,28
Median all values pg/g	0,37
Consensus mean, pg/g	0,28
Standard deviation, pg/g	0,14
Relative standard deviation, %	48
No. of values reported	17
No. of values removed	6
No. of reported non-detects	4

PBDE 183

Z-score: PBDE 183
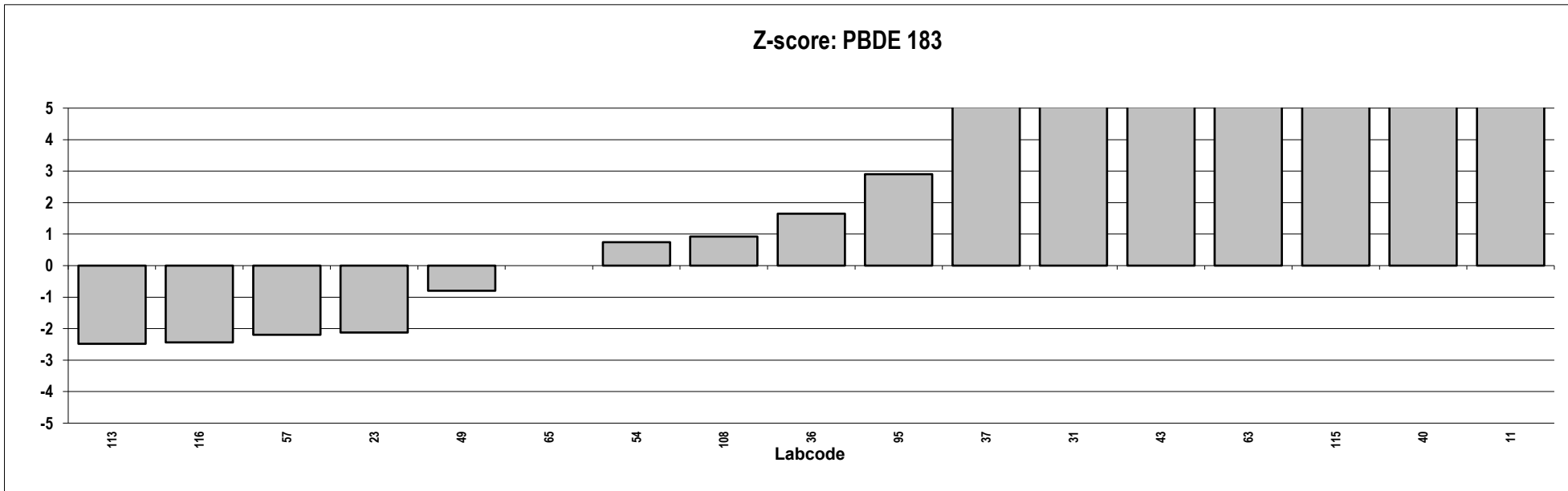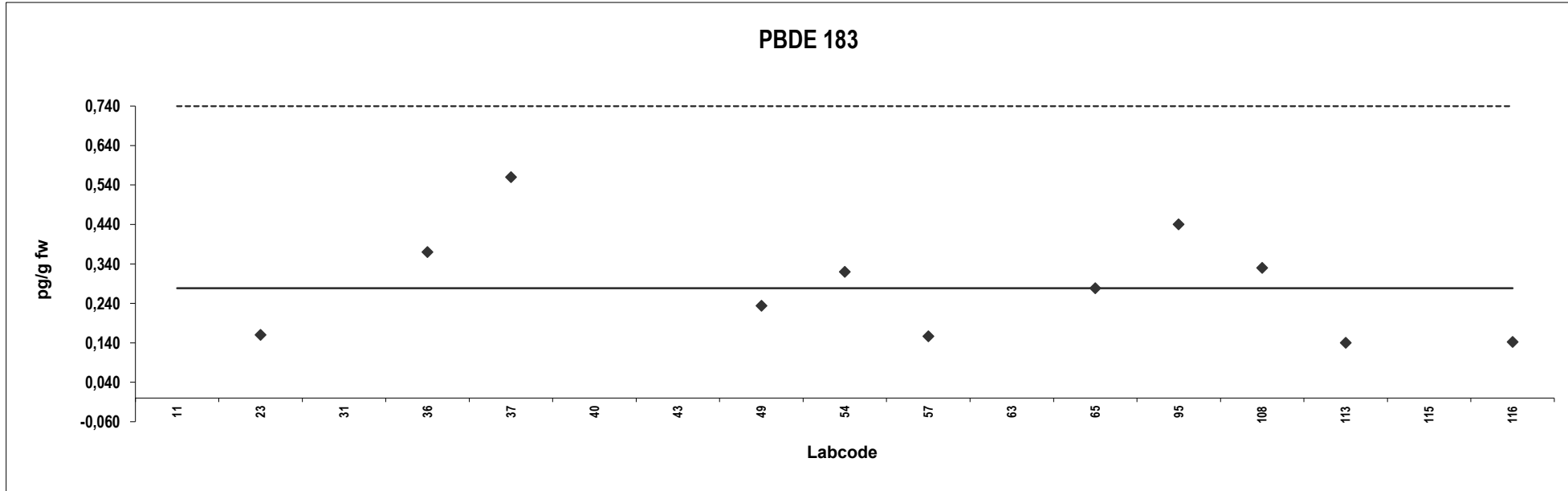
Veal

Congener: PBDE 209

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	181	68	Outlier				
23	10	-0,83					
31	61	20	Outlier,ND				
36	27	5,9	ND				
37	13	0,061					
43	1,0	-4,6	ND				
57	4,2	-3,3					
63	191	72	Outlier,ND				
65	28	6,3					
95	12	-0,061					
108	17	2,0					
113	25	5,0					
115	1007	403	Outlier				
116	11	-0,38					

Consenus statistics

Consensus median, pg/g	12
Median all values pg/g	21
Consensus mean, pg/g	15
Standard deviation, pg/g	9,3
Relative standard deviation, %	62
No. of values reported	14
No. of values removed	4
No. of reported non-detects	4

PBDE 209

Z-score: PBDE 209
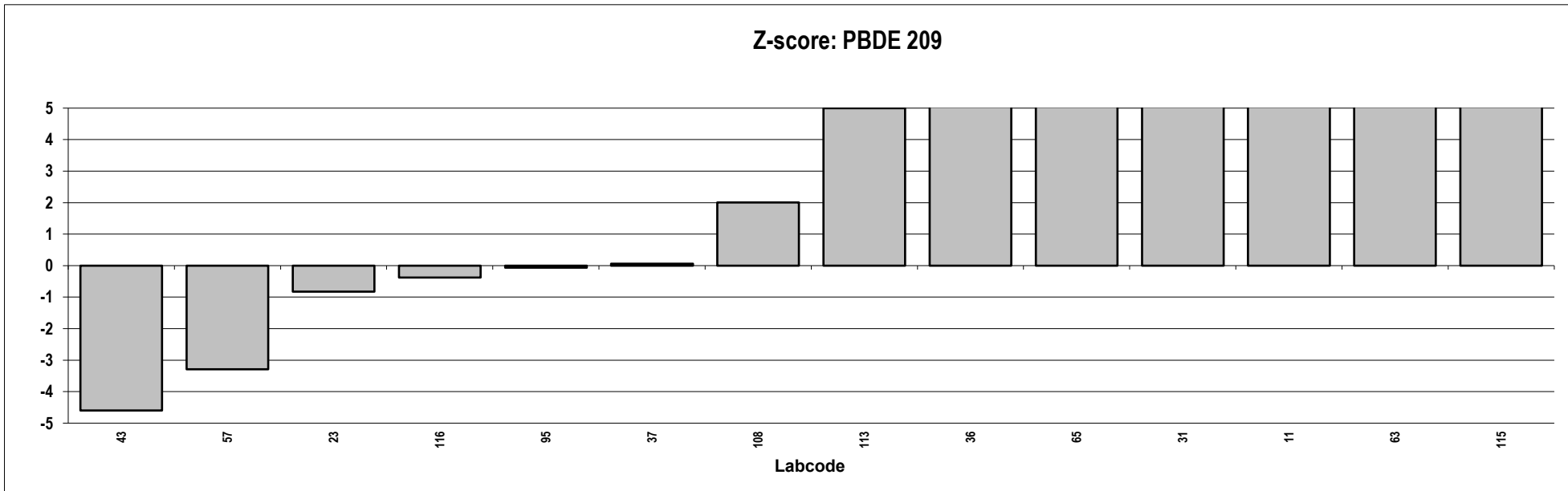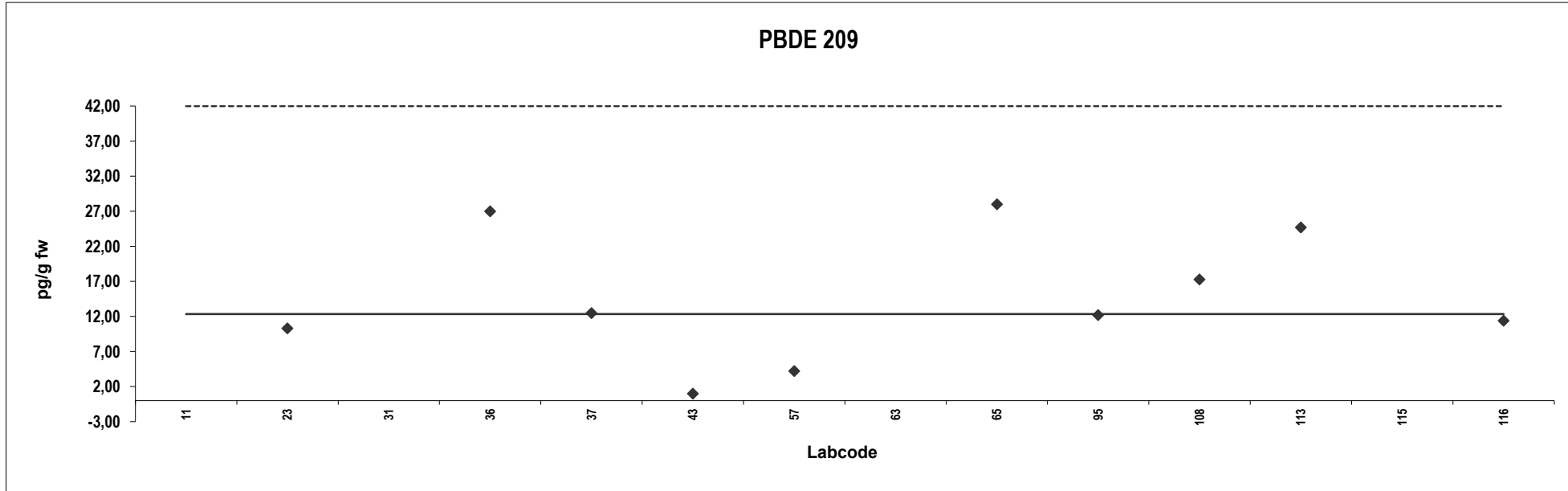
Veal

Congener: α-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	6,0	-1,3	ND				
17	14	3,5					
49	15	4,4	ND				
65	2,4	-3,5					
95	10	1,2	ND				

Consenus statistics

Consensus median, pg/g	8,0
Median all values pg/g	10
Consensus mean, pg/g	9,4
Standard deviation, pg/g	5,2
Relative standard deviation, %	56
No. of values reported	5
No. of values removed	0
No. of reported non-detects	3
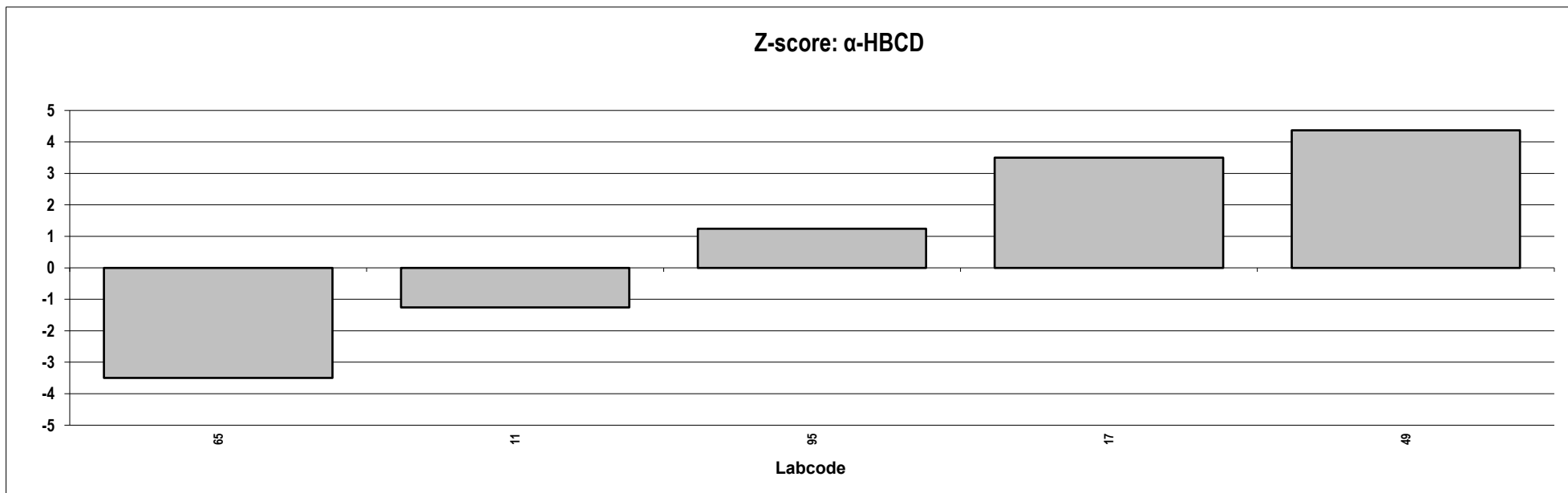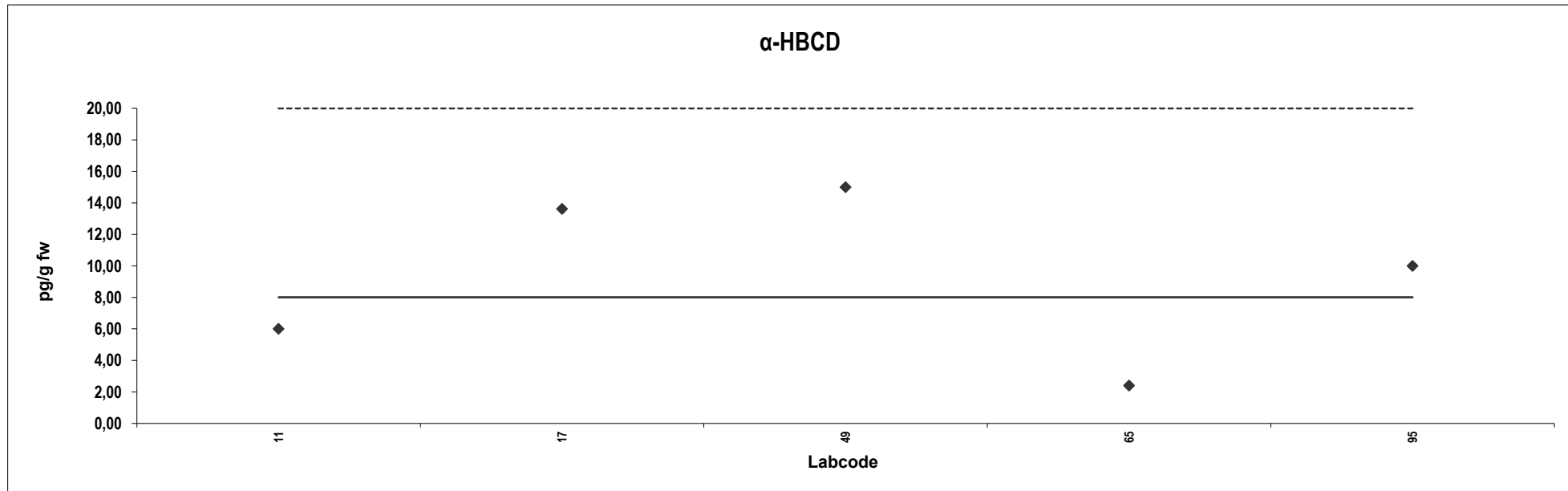
Veal

Congener: β-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	6,0	4,6	ND				
17	5,7	4,0					
49	15	19	Outlier,ND				
65	0,60	-4,0					
95	5,0	3,0	ND				

Consenus statistics

Consensus median, pg/g	3,1
Median all values pg/g	5,7
Consensus mean, pg/g	4,3
Standard deviation, pg/g	2,5
Relative standard deviation, %	58
No. of values reported	5
No. of values removed	1
No. of reported non-detects	3

β-HBCD

Z-score: β-HBCD
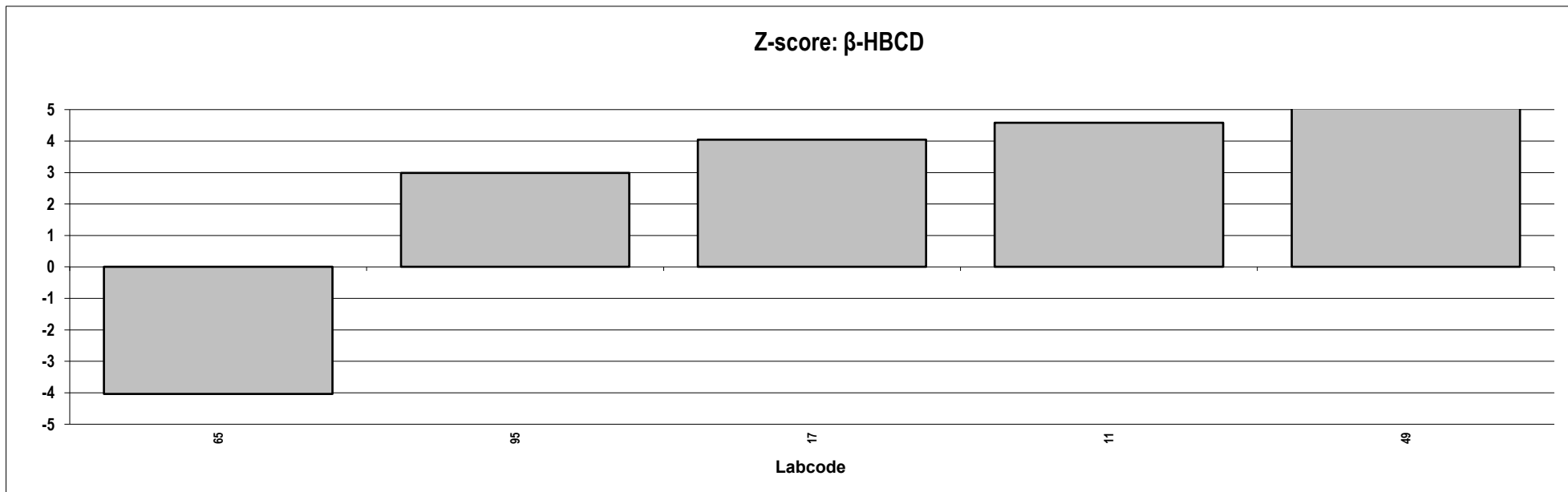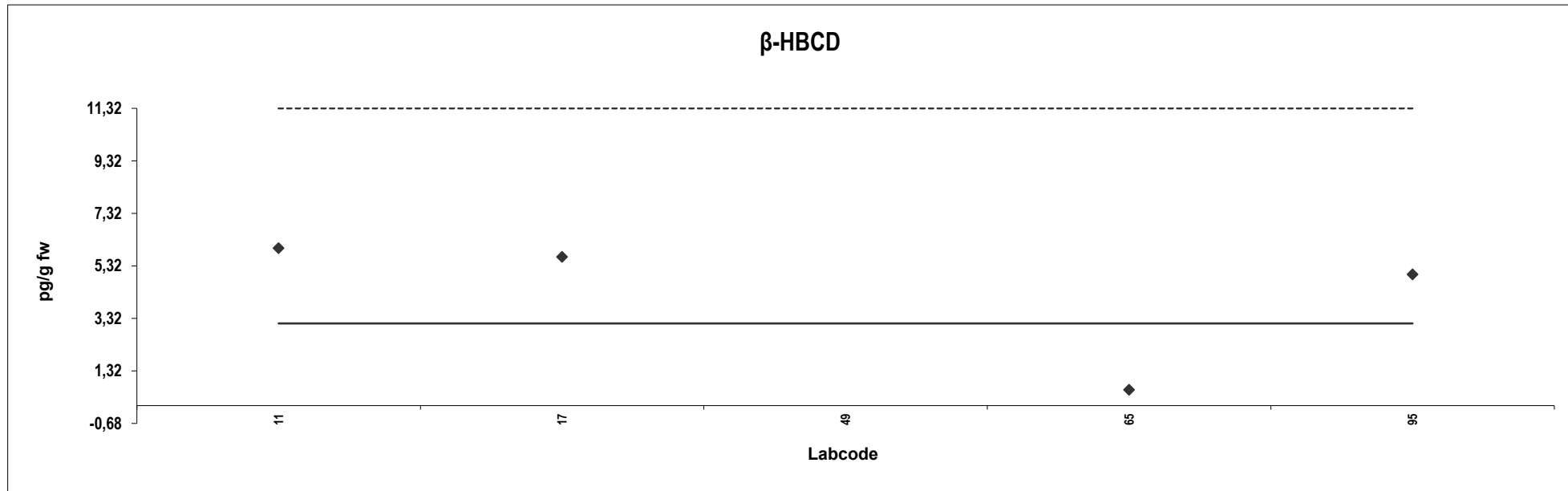
Veal
Congener: γ-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	6,0	-0,51	ND				
17	11	3,3					
49	15	6,2	ND				
65	2,3	-3,3					
95	10	2,5	ND				

Consenus statistics

Consensus median, pg/g	6,7
Median all values pg/g	10
Consensus mean, pg/g	8,9
Standard deviation, pg/g	4,9
Relative standard deviation, %	55
No. of values reported	5
No. of values removed	0
No. of reported non-detects	3

γ-HBCD

Z-score: γ-HBCD
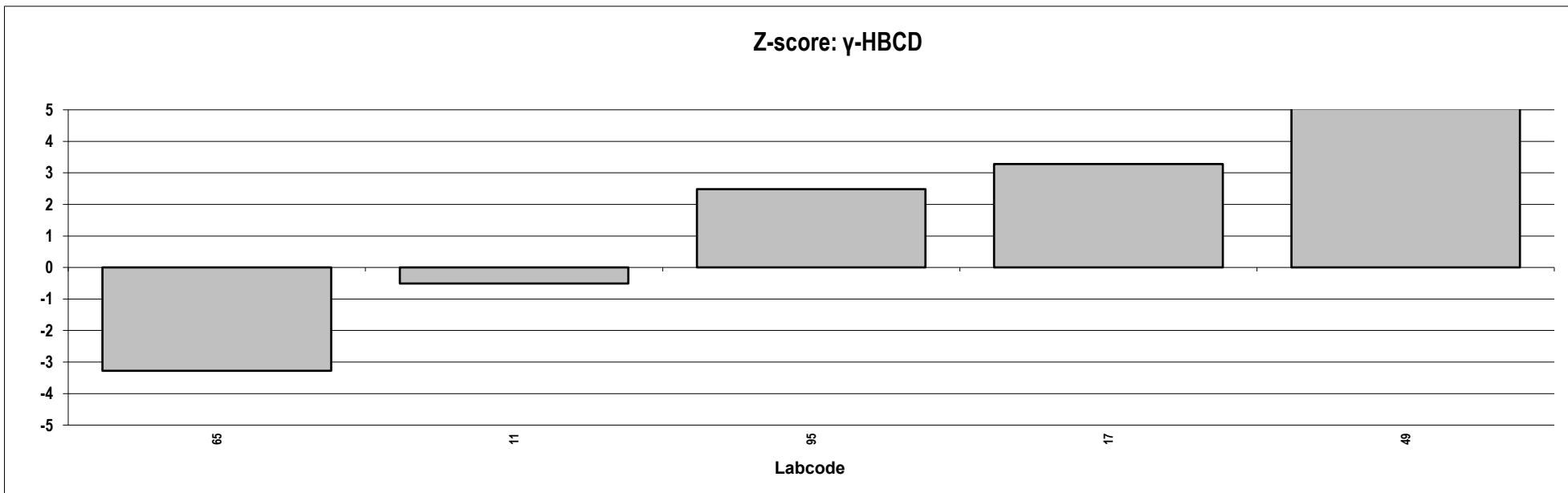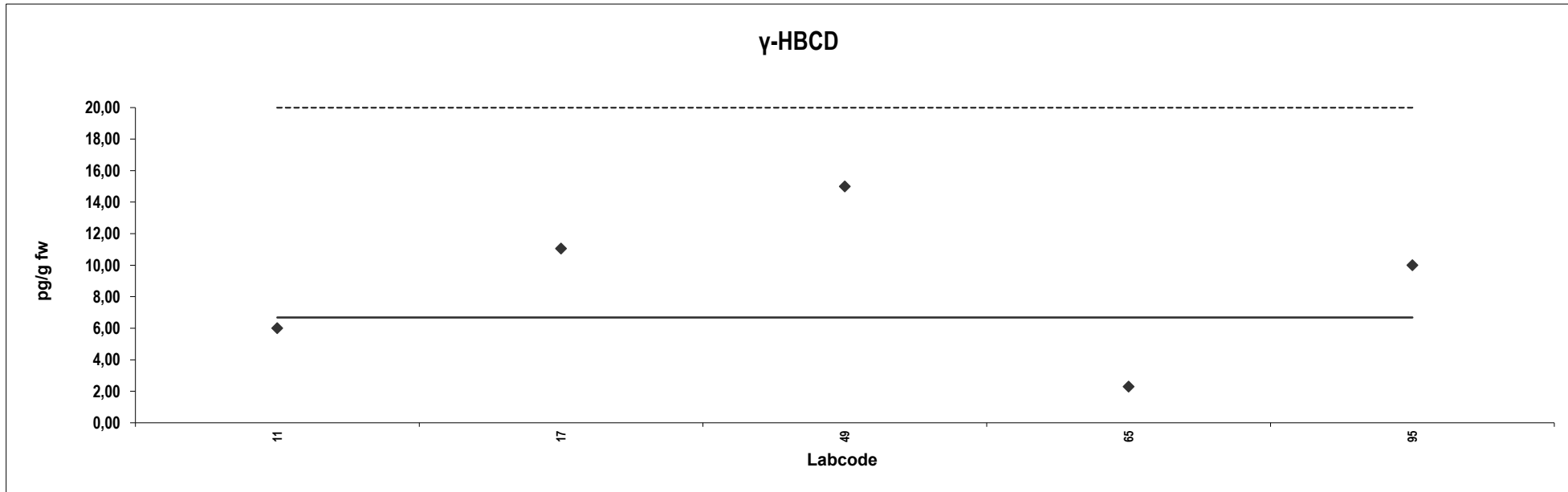
Veal

Congener: total HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
17	30	34	Outlier				
65	5,2	1,7					
108	2,5	-1,7					

Consenus statistics

Consensus median, pg/g	3,9
Median all values pg/g	5,2
Consensus mean, pg/g	3,9
Standard deviation, pg/g	1,9
Relative standard deviation, %	49
No. of values reported	3
No. of values removed	1
No. of reported non-detects	0

total HBCD

pg/g fw

10,40

8,40

6,40

4,40

2,40

0,40

-1,60

17　　　　　　　　65　　　　　　　　108

Labcode

Z-score: total HBCD

5

4

3

2

1

0

-1

-2

-3

-4

-5

108　　　　　　　　65　　　　　　　　17

Labcode
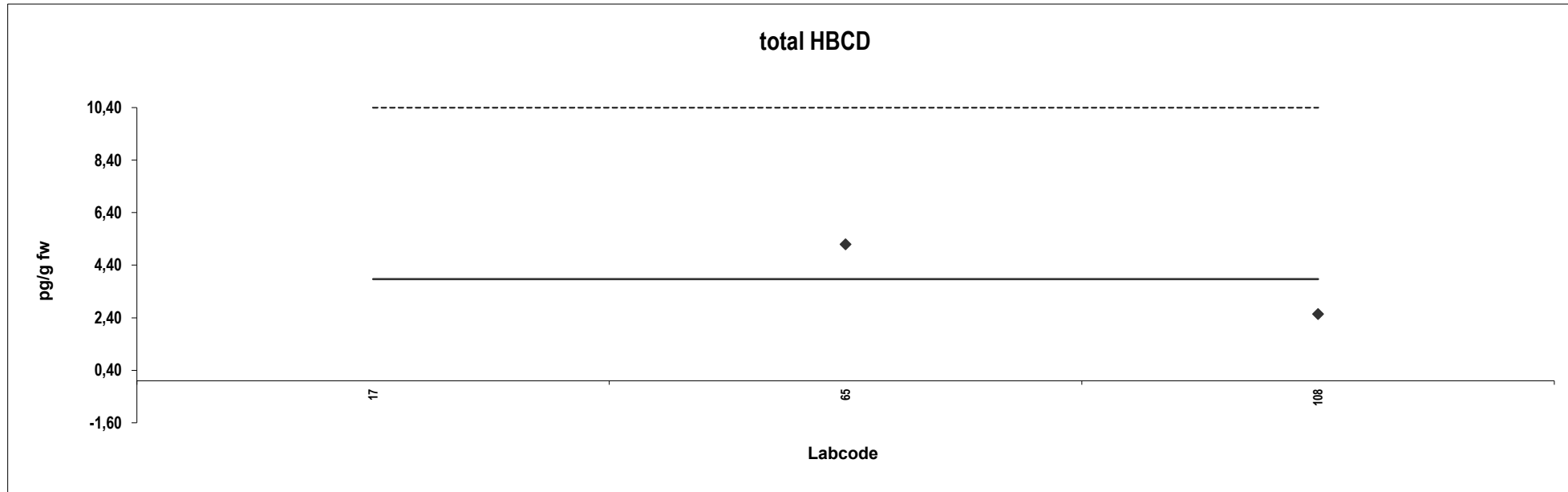
Appendix 3:

Presentation of results for
Herring-2019

Appendix 3: Presentation of results: Herring-2019

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 × 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 × 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 × 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 ± 20% from the consensus value.

Herring
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,10	1,2		90	0,072	-0,54	
5	0,10	1,5		92	0,078	-0,14	
7	0,081	0,034		95	0,074	-0,40	
11	0,079	-0,072		100	0,031	-3,1	
12	0,088	0,46		102	0,10	1,2	
15	0,089	0,53		103	0,069	-0,71	
17	0,096	0,94		106	0,076	-0,26	
19	0,079	-0,096		108	0,064	-1,0	
20	0,079	-0,072		109	0,076	-0,28	
23	0,082	0,12		110	0,060	-1,3	
24	0,085	0,25		113	0,080	-0,028	
25	0,040	-2,5		114	0,0082	-4,5	
27	0,085	0,31		115	0,066	-0,87	
28	0,20	7,4	Outlier,ND	116	0,10	1,2	
30	0,089	0,53		117	0,068	-0,77	
31	0,082	0,092		118	0,080	-0,0067	
32	0,076	-0,28		119	0,066	-0,91	
33	0,075	-0,31		120	0,080	-0,011	
34	0,093	0,80					
36	0,084	0,22					
37	0,059	-1,3					
38	0,10	1,2					
40	0,031	-3,1	ND				
42	0,086	0,34					
43	0,070	-0,65					
44	0,13	2,8					
45	0,093	0,77					
48	0,083	0,16					
49	0,089	0,53					
54	0,076	-0,28					
57	0,084	0,20					
58	0,087	0,41					
61	0,077	-0,23					
63	0,080	-0,028					
64	0,049	-1,9					
65	0,080	-0,059					
71	0,072	-0,53					
73	0,083	0,13					
75	0,087	0,41					
78	0,085	0,27	ND				
80	0,091	0,66					
84	0,081	0,0067					
87	0,11	1,7					
88	0,093	0,78					
89	0,089	0,52					

Consenus statistics

Consensus median, pg/g	0,080
Median all values pg/g	0,081
Consensus mean, pg/g	0,079
Standard deviation, pg/g	0,019
Relative standard deviation, %	24
No. of values reported	63
No. of values removed	1
No. of reported non-detects	3

2,3,7,8 TCDD
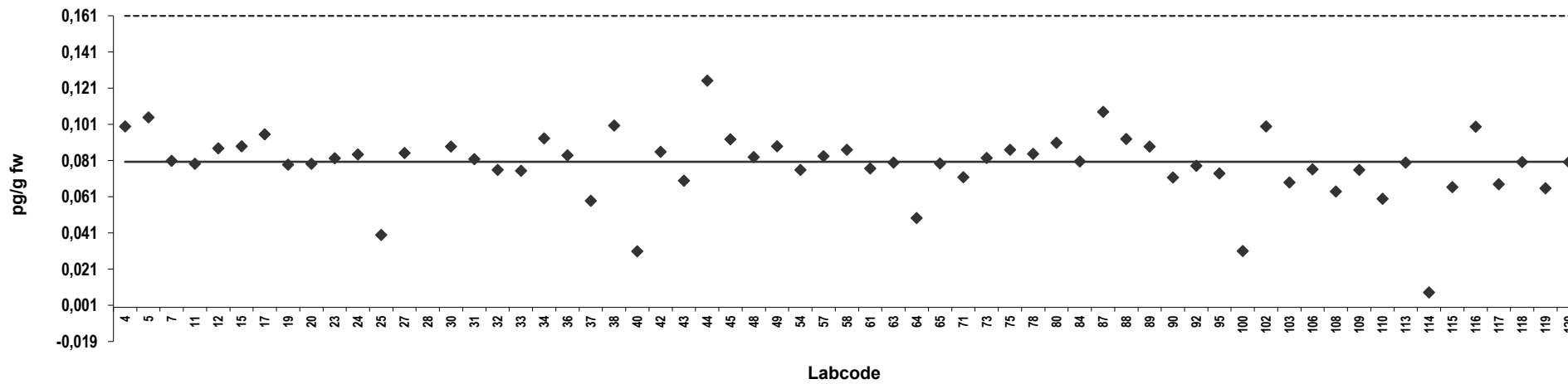
Z-score: 2,3,7,8 TCDD
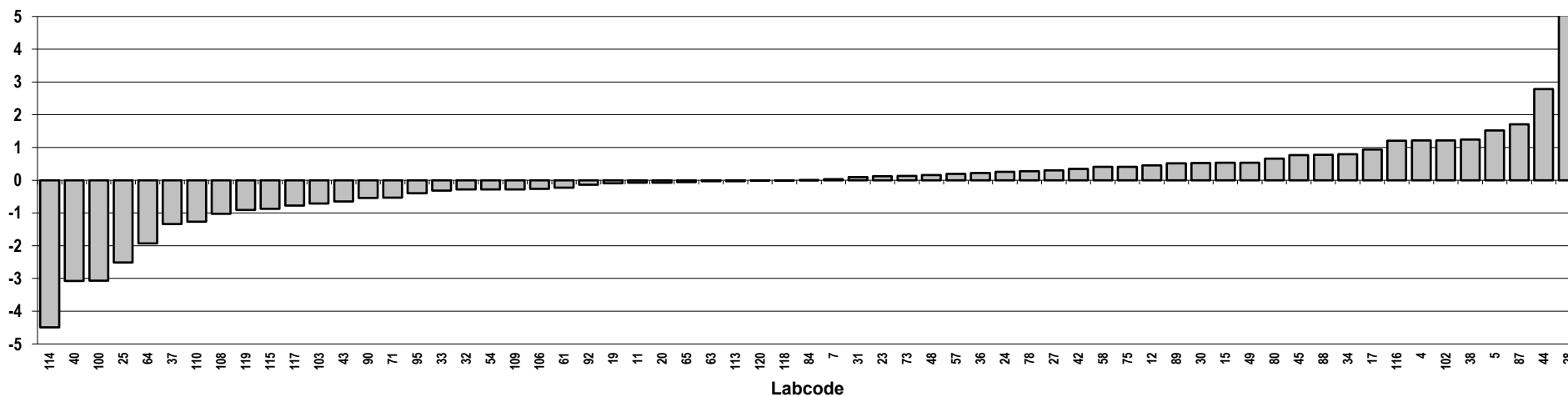
Herring
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,31	2,0		90	0,20	-0,43	
5	0,24	0,34		92	0,31	2,1	
7	0,22	-0,045		95	0,21	-0,29	
11	0,23	0,061		100	0,17	-1,2	
12	0,21	-0,23		102	0,25	0,58	
15	0,24	0,27		103	0,20	-0,52	
17	0,23	0,21		106	0,19	-0,78	
19	0,18	-1,1		108	0,19	-0,85	
20	0,22	-0,16		109	0,22	-0,045	
23	0,23	0,22		110	0,22	0,00	
24	0,23	0,26		113	0,26	0,83	
25	0,18	-0,86		114	0,030	-4,3	
27	0,24	0,34		115	0,21	-0,24	
28	0,11	-2,5	ND	116	0,21	-0,20	
30	0,25	0,65		117	0,21	-0,40	
31	0,20	-0,56		118	0,25	0,61	
32	0,23	0,15		119	0,18	-0,95	
33	0,25	0,51		120	0,22	-0,13	
34	0,22	-0,081					
36	0,24	0,38					
37	0,19	-0,75					
38	0,28	1,2					
40	0,27	1,1					
42	0,25	0,61					
43	0,22	-0,067					
44	0,22	-0,081					
45	0,21	-0,27					
48	0,20	-0,52					
49	0,22	-0,067					
54	0,26	0,83					
57	0,24	0,36					
58	0,23	0,083					
61	0,26	0,93					
63	0,22	0,00					
64	0,33	2,4					
65	0,24	0,33					
71	0,21	-0,27					
73	0,21	-0,32					
75	0,23	0,18					
78	0,17	-1,2					
80	0,26	0,85					
84	0,24	0,28					
87	0,26	0,83					
88	0,23	0,090					
89	0,23	0,26					

Consenus statistics	
Consensus median, pg/g	0,22
Median all values pg/g	0,22
Consensus mean, pg/g	0,22
Standard deviation, pg/g	0,043
Relative standard deviation, %	19
No. of values reported	63
No. of values removed	0
No. of reported non-detects	1

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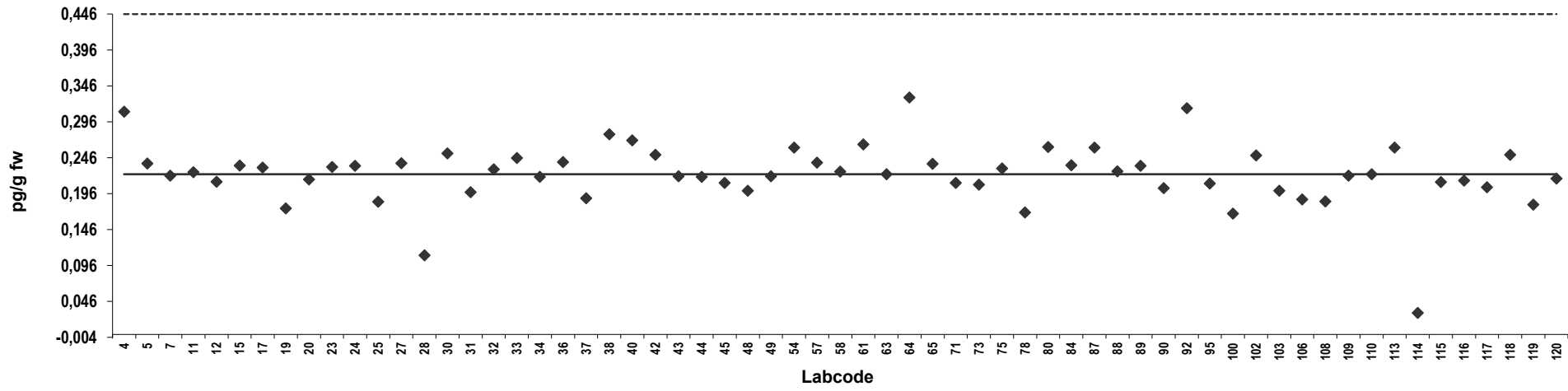
Z-score: 1,2,3,7,8 PeCDD
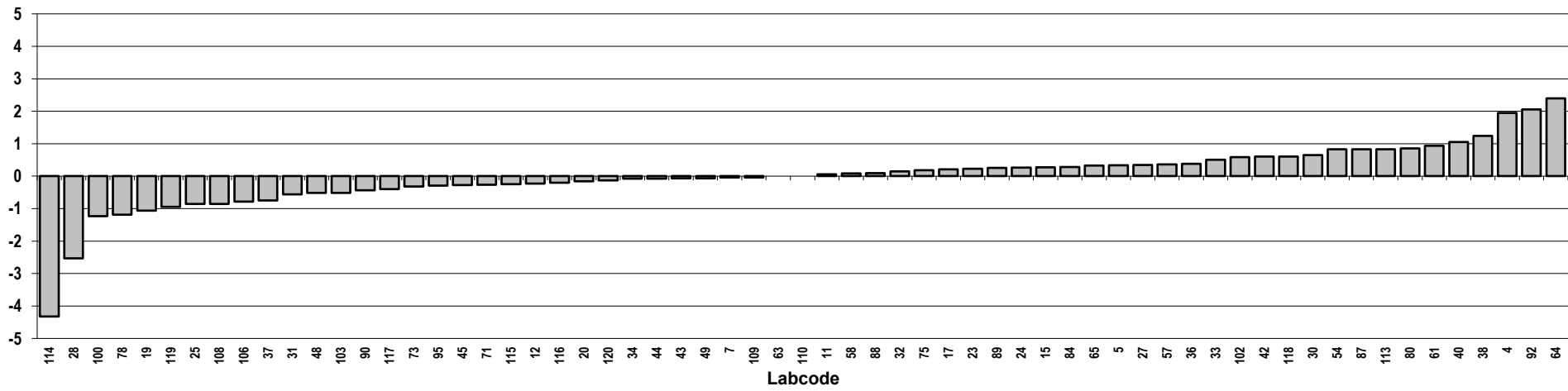
Herring
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,060	3,8		90	0,028	-0,91	
5	0,019	-2,2		92	0,036	0,25	
7	0,042	1,1		95	0,035	0,12	
11	0,035	0,11		100	0,020	-2,0	ND
12	0,027	-1,1		102	0,035	0,12	
15	0,036	0,27		103	0,031	-0,47	
17	0,029	-0,70		106	0,042	1,1	
19	0,010	-3,5	ND	108	0,027	-1,1	
20	0,032	-0,39		109	0,039	0,66	
23	0,026	-1,2		110	0,040	0,85	
24	0,034	-0,073		113	0,027	-1,1	
25	0,036	0,27		114	0,0050	-4,3	ND
27	0,034	0,00		115	0,032	-0,31	
28	0,16	18	Outlier,ND	116	0,025	-1,3	
30	0,048	2,0		117	0,030	-0,61	
31	0,036	0,27		118	0,033	-0,19	
32	0,029	-0,79		119	0,032	-0,32	
33	0,033	-0,20		120	0,035	0,051	
34	0,030	-0,55					
36	0,037	0,41					
37	0,046	1,7					
38	0,10	9,6	Outlier,ND				
40	0,077	6,3	Outlier				
42	0,039	0,70					
43	0,030	-0,61					
44	0,036	0,21					
45	0,038	0,49					
48	0,033	-0,17					
49	0,039	0,70					
54	0,041	1,0					
57	0,029	-0,83					
58	0,050	2,3	ND				
61	0,028	-0,91					
63	0,031	-0,47					
64	0,028	-0,93					
65	0,034	-0,058					
71	0,021	-2,0					
73	0,037	0,34					
75	0,037	0,41					
78	0,077	6,3	Outlier,ND				
80	0,043	1,3					
84	0,042	1,2					
87	0,054	2,9					
88	0,038	0,56					
89	0,036	0,23					

Consenus statistics	
Consensus median, pg/g	0,034
Median all values pg/g	0,035
Consensus mean, pg/g	0,034
Standard deviation, pg/g	0,0090
Relative standard deviation, %	27
No. of values reported	63
No. of values removed	4
No. of reported non-detects	7

1,2,3,4,7,8 HxCDD
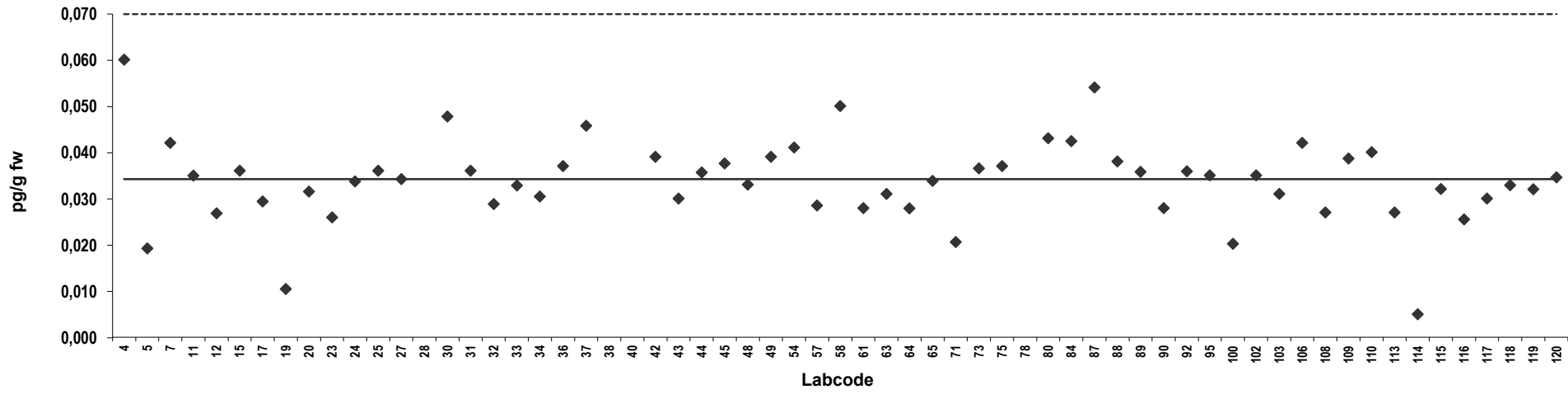
Z-score: 1,2,3,4,7,8 HxCDD
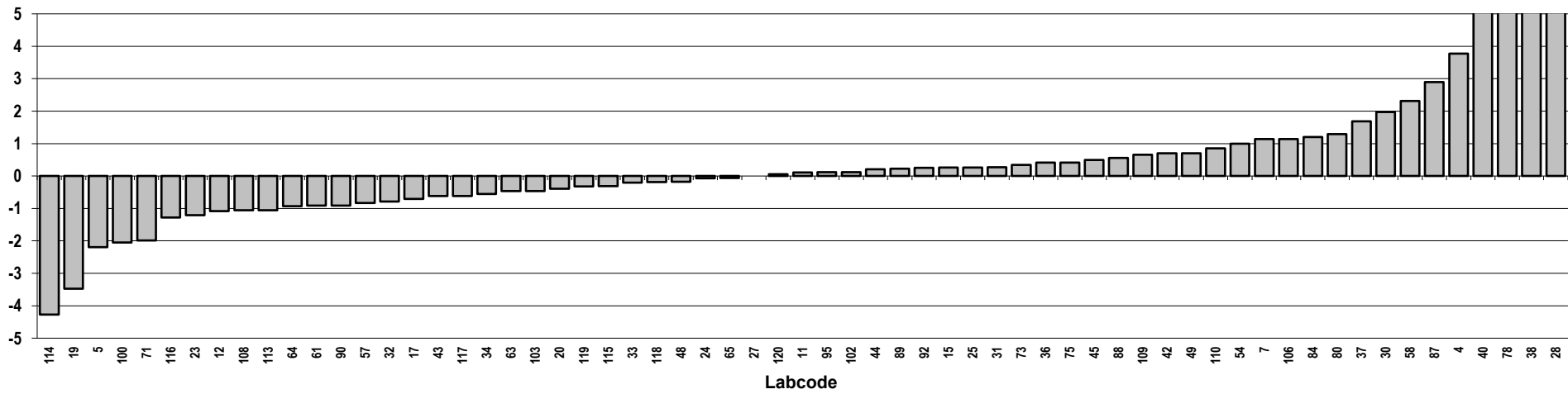
Herring
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,17	0,57		90	0,13	-0,76	
5	0,17	0,52		92	0,18	0,74	
7	0,17	0,70		95	0,12	-1,1	
11	0,15	0,047		100	0,082	-2,3	
12	0,16	0,15		102	0,12	-1,1	
15	0,15	-0,15		103	0,18	0,90	
17	0,16	0,12		106	0,15	-0,022	
19	0,11	-1,5		108	0,13	-0,87	
20	0,15	-0,25		109	0,13	-0,62	
23	0,075	-2,5		110	0,13	-0,74	
24	0,15	-0,19		113	0,16	0,24	
25	0,13	-0,84		114	0,015	-4,5	
27	0,15	-0,014		115	0,15	0,00	
28	0,31	5,0		116	0,13	-0,72	
30	0,12	-1,1		117	0,13	-0,84	
31	0,16	0,39		118	0,16	0,29	
32	0,14	-0,37		119	0,12	-1,0	
33	0,15	0,054		120	0,15	-0,072	
34	0,16	0,23					
36	0,17	0,51					
37	0,13	-0,71					
38	0,10	-1,7	ND				
40	0,17	0,57					
42	0,17	0,57					
43	0,13	-0,74					
44	0,18	0,79					
45	0,16	0,23					
48	0,15	-0,084					
49	0,18	0,90					
54	0,17	0,57					
57	0,15	-0,12					
58	0,18	0,87					
61	0,071	-2,7					
63	0,17	0,44					
64	0,15	-0,17					
65	0,16	0,28					
71	0,16	0,31					
73	0,20	1,5					
75	0,15	-0,25					
78	0,083	-2,3	ND				
80	0,15	0,014					
84	0,16	0,17					
87	0,18	0,74					
88	0,15	0,047					
89	0,15	0,075					

Consenus statistics	
Consensus median, pg/g	0,15
Median all values pg/g	0,15
Consensus mean, pg/g	0,15
Standard deviation, pg/g	0,037
Relative standard deviation, %	25
No. of values reported	63
No. of values removed	0
No. of reported non-detects	2

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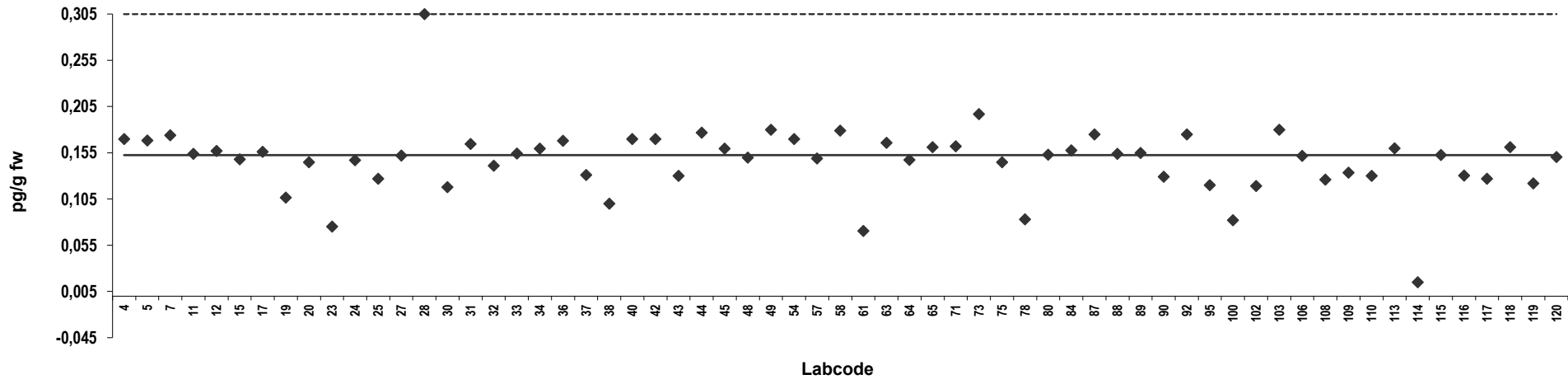
Z-score: 1,2,3,6,7,8 HxCDD
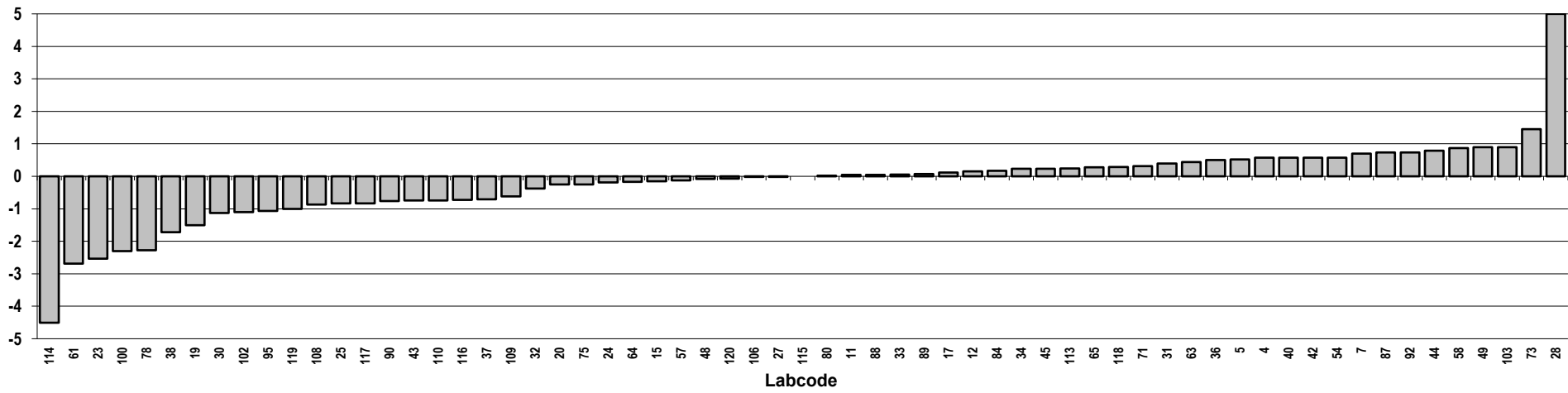
Herring

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	4,3	ND	90	0,023	-0,80	
5	0,029	0,35		92	0,077	9,3	Outlier
7	0,025	-0,36		95	0,033	1,1	
11	0,028	0,11		100	0,021	-1,0	ND
12	0,039	2,2	ND	102	0,028	0,20	ND
15	0,026	-0,17		103	0,033	1,1	
17	0,028	0,13		106	0,033	1,1	
19	0,016	-2,0	ND	108	0,021	-1,1	
20	0,030	0,50		109	0,028	0,20	
23	0,019	-1,4	ND	110	0,060	6,1	Outlier,ND
24	0,023	-0,65		113	0,037	1,9	
25	0,024	-0,48		114	0,0052	-4,0	ND
27	0,031	0,70		115	0,021	-1,0	
28	0,23	38	Outlier	116	0,020	-1,3	
30	0,045	3,4		117	0,026	-0,17	
31	0,028	0,13		118	0,027	0,036	
32	0,025	-0,39		119	0,025	-0,45	
33	0,034	1,4		120	0,027	-0,015	
34	0,024	-0,51					
36	0,024	-0,56					
37	0,021	-1,1					
38	0,10	14	Outlier,ND				
40	0,037	1,9					
42	0,033	1,1					
43	0,030	0,57	ND				
44	0,040	2,4					
45	0,025	-0,29					
48	0,027	0,015					
49	0,029	0,39					
54	0,028	0,20					
57	0,024	-0,51					
58	0,050	4,3	ND				
61	0,040	2,5					
63	0,026	-0,17					
64	0,025	-0,39					
65	0,024	-0,57					
71	0,017	-1,9					
73	0,016	-2,0					
75	0,026	-0,17					
78	0,087	11	Outlier,ND				
80	0,028	0,20					
84	0,028	0,17					
87	0,048	3,9					
88	0,023	-0,73					
89	0,021	-1,1					

Consenus statistics	
Consensus median, pg/g	0,027
Median all values pg/g	0,028
Consensus mean, pg/g	0,028
Standard deviation, pg/g	0,0083
Relative standard deviation, %	30
No. of values reported	63
No. of values removed	5
No. of reported non-detects	12

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

Z-score: 1,2,3,7,8,9 HxCDD
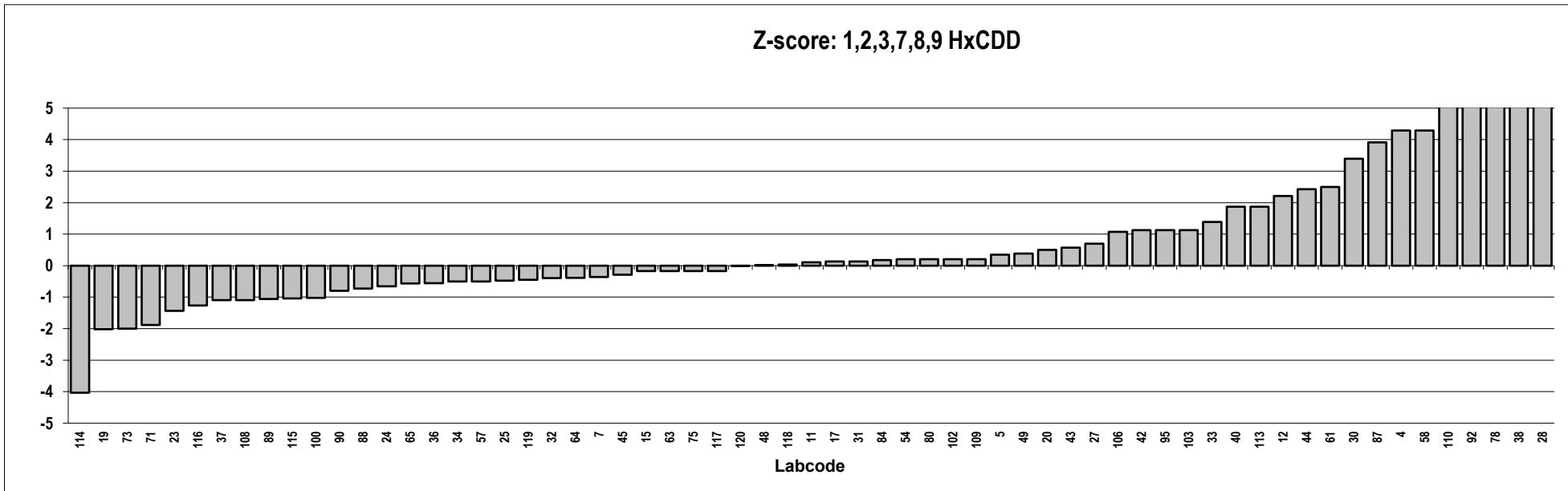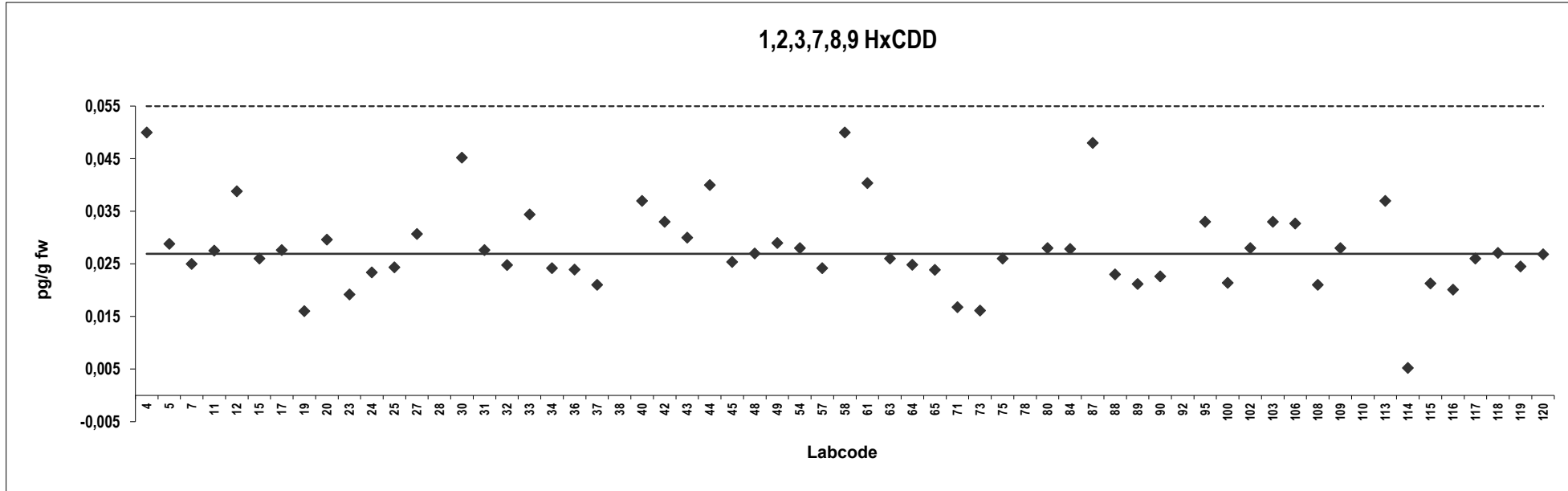
Herring
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,070	3,8		90	0,033	-0,83	
5	0,073	4,1		92	0,65	77	Outlier
7	0,027	-1,6		95	0,039	-0,13	
11	0,040	-0,063		100	0,032	-0,96	ND
12	0,033	-0,87		102	0,030	-1,3	ND
15	0,045	0,63		103	0,054	1,8	
17	0,039	-0,18		106	0,073	4,1	
19	0,049	1,1	ND	108	0,030	-1,3	
20	0,063	2,8		109	0,037	-0,42	
23	0,045	0,58	ND	110	0,060	2,5	ND
24	0,035	-0,67		113	0,042	0,25	
25	0,047	0,88		114	0,014	-3,3	
27	0,041	0,12		115	0,057	2,1	
28	0,53	61	Outlier	116	0,011	-3,6	ND
30	0,040	-0,013		117	0,040	0,00	
31	0,032	-1,0	ND	118	0,038	-0,29	
32	0,032	-1,0		119	0,048	1,1	
33	0,037	-0,41		120	0,066	3,2	
34	0,038	-0,21					
36	0,040	-0,063					
37	0,053	1,7					
38	0,10	7,5	Outlier,ND				
40	0,064	3,0					
42	0,051	1,4					
43	0,030	-1,3					
44	0,039	-0,13					
45	0,038	-0,25					
48	0,032	-1,0					
49	0,040	0,00					
54	0,041	0,13					
57	0,030	-1,2					
58	0,050	1,3	ND				
61	0,052	1,5					
63	0,045	0,63					
64	0,12	10	Outlier				
65	0,037	-0,40					
71	0,00039	-5,0	ND				
73	0,057	2,1					
75	0,046	0,75					
78	0,42	48	Outlier				
80	0,054	1,8					
84	0,037	-0,36					
87	0,058	2,3					
88	0,051	1,4					
89	0,042	0,19					

Consensus statistics

Consensus median, pg/g	0,040
Median all values pg/g	0,041
Consensus mean, pg/g	0,043
Standard deviation, pg/g	0,014
Relative standard deviation, %	33
No. of values reported	63
No. of values removed	5
No. of reported non-detects	10

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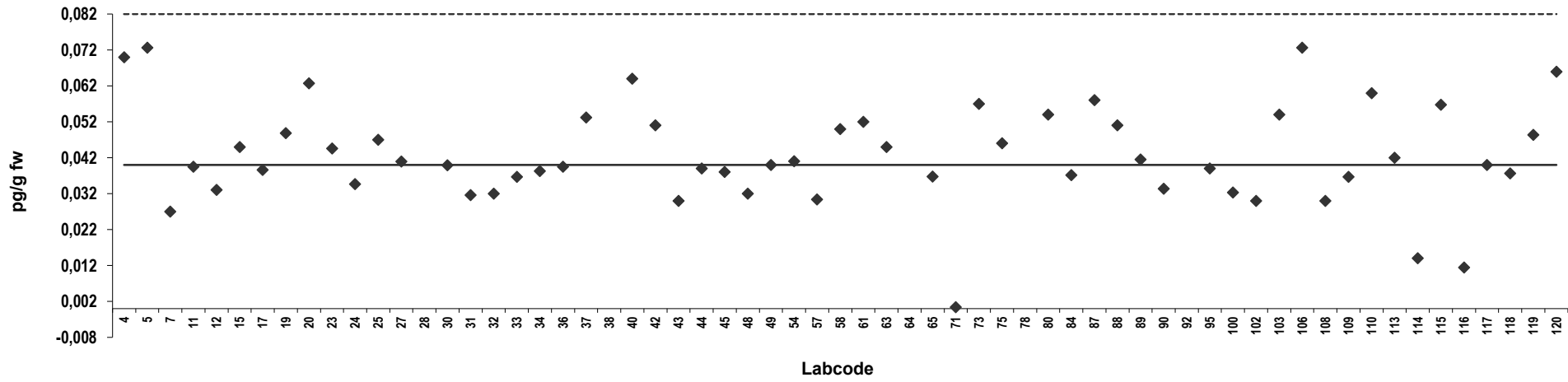
Z-score: 1,2,3,4,6,7,8 HpCDD
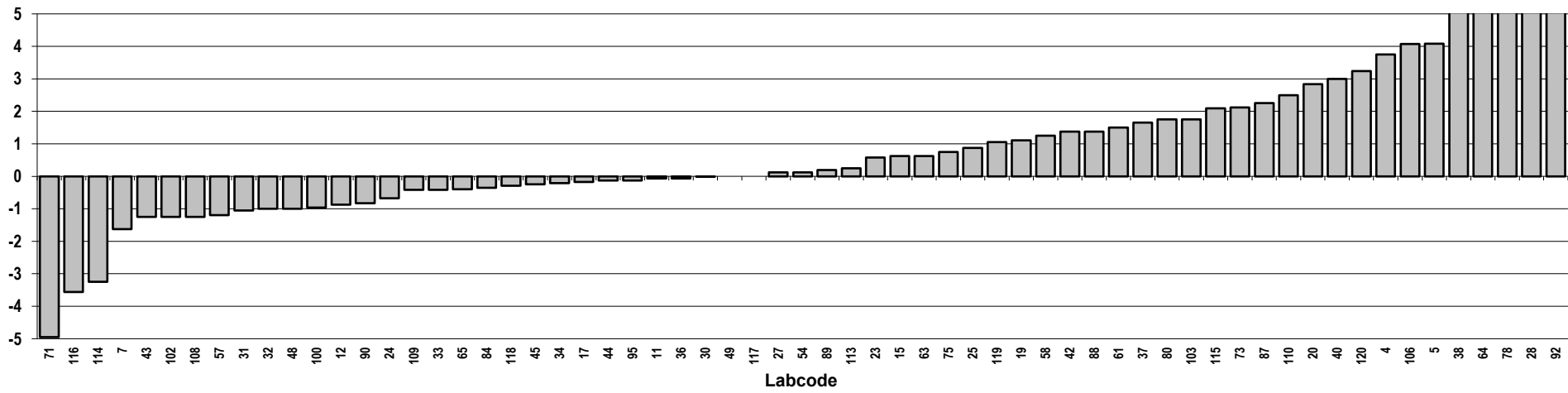
Herring

Congener: OCDD

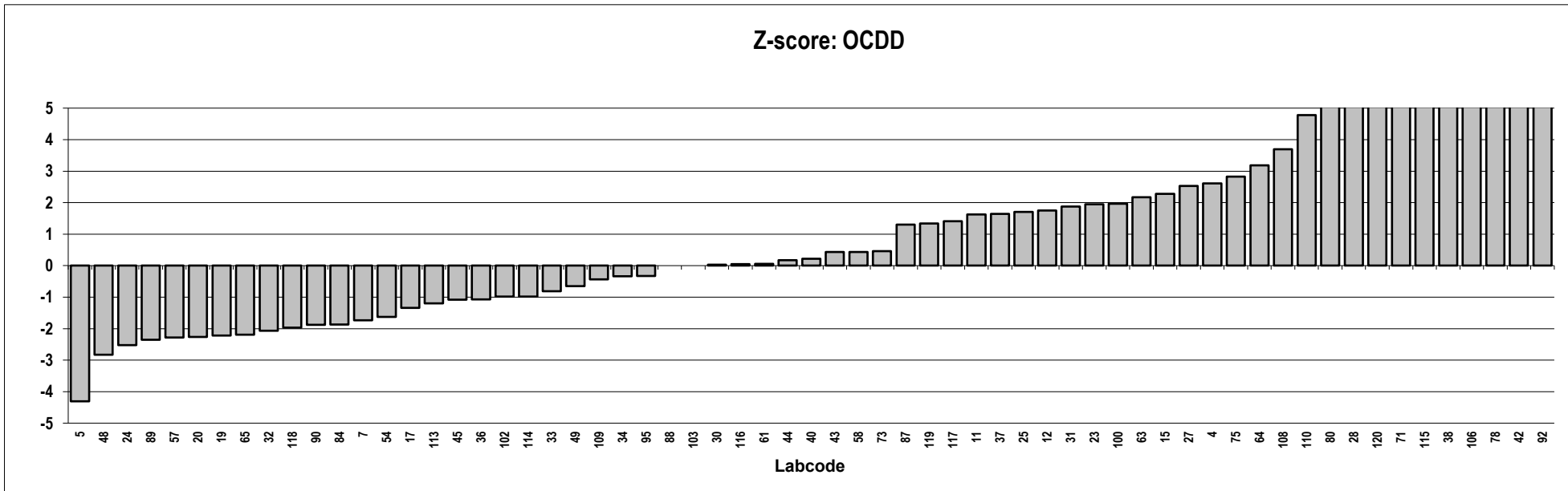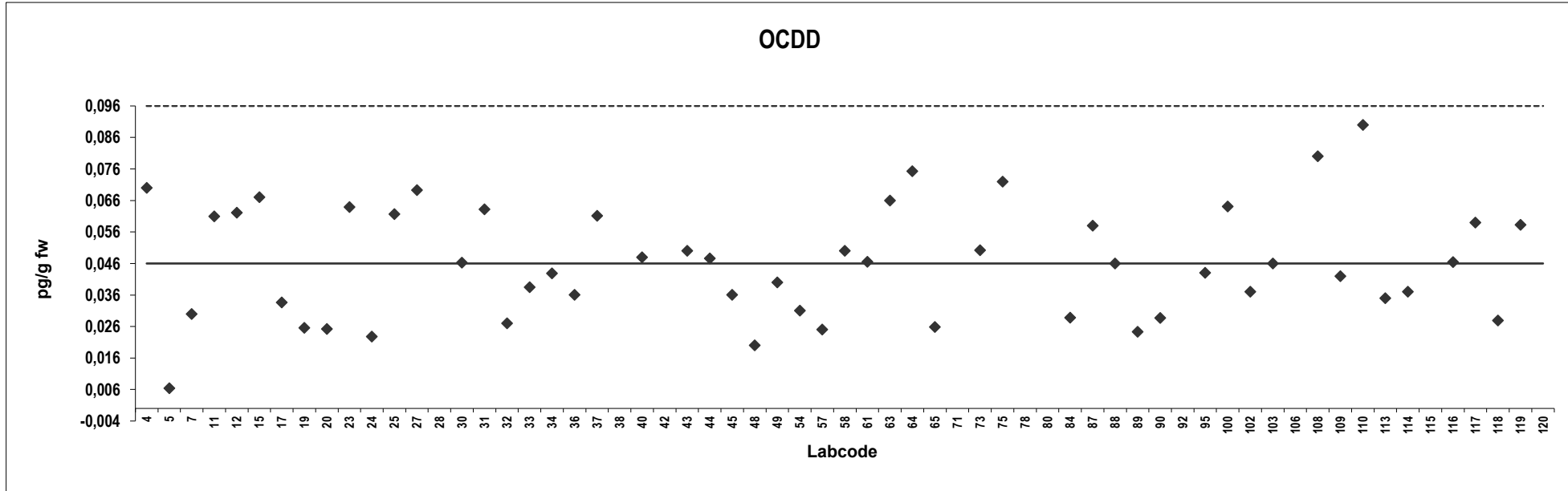| Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,070	2,6		90	0,029	-2	
5	0,0064	-4,3		92	2,3	247	Outlier
7	0,030	-1,7		95	0,043	-0,33	
11	0,061	1,6		100	0,064	2,0	
12	0,062	1,7		102	0,037	-0,98	ND
15	0,067	2,3		103	0,046	0,00	
17	0,034	-1,3		106	0,23	20	Outlier
19	0,026	-2,2	ND	108	0,080	3,7	ND
20	0,025	-2,3		109	0,042	-0,43	
23	0,064	1,9		110	0,090	4,8	
24	0,023	-2,5		113	0,035	-1,2	
25	0,062	1,7		114	0,037	-0,98	
27	0,069	2,5		115	0,20	16	Outlier
28	0,13	9,1	Outlier,ND	116	0,046	0,048	ND
30	0,046	0,033		117	0,059	1,4	
31	0,063	1,9	ND	118	0,028	-2,0	
32	0,027	-2,1		119	0,058	1,3	
33	0,039	-0,82		120	0,16	12	Outlier
34	0,043	-0,34					
36	0,036	-1,1					
37	0,061	1,6					
38	0,20	17	Outlier,ND				
40	0,048	0,22	ND				
42	0,38	36	Outlier,ND				
43	0,050	0,43	ND				
44	0,048	0,17					
45	0,036	-1,1					
48	0,020	-2,8					
49	0,040	-0,65					
54	0,031	-1,6					
57	0,025	-2,3					
58	0,050	0,43	ND				
61	0,047	0,061					
63	0,066	2,2					
64	0,075	3,2					
65	0,026	-2,2					
71	0,18	14	Outlier				
73	0,050	0,46					
75	0,072	2,8					
78	0,30	28	Outlier,ND				
80	0,10	5,9	Outlier,ND				
84	0,029	-1,9					
87	0,058	1,3					
88	0,046	0,00					
89	0,024	-2,4					

Consenus statistics	
Consensus median, pg/g	0,046
Median all values pg/g	0,048
Consensus mean, pg/g	0,046
Standard deviation, pg/g	0,018
Relative standard deviation, %	39
No. of values reported	63
No. of values removed	10
No. of reported non-detects	13

OCDD

Z-score: OCDD

Herring

Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	1,3	-0,39		90	1,3	-0,44	
5	1,8	1,3		92	1,7	0,69	
7	1,6	0,36		95	1,5	0,093	
11	1,4	-0,30		100	1,1	-1,2	
12	2,0	1,8		102	1,3	-0,63	
15	1,5	0,27		103	1,6	0,64	
17	1,4	-0,34		106	1,3	-0,42	
19	1,5	0,13		108	1,1	-1,1	
20	1,6	0,55		109	1,3	-0,57	
23	1,6	0,54		110	1,2	-0,77	
24	1,4	-0,025		113	1,6	0,44	
25	1,2	-0,88		114	0,21	-4,3	
27	1,6	0,36		115	1,3	-0,36	
28	1,2	-0,84		116	1,5	0,0099	
30	1,2	-0,87		117	1,3	-0,54	
31	1,5	0,029		118	1,5	0,13	
32	1,6	0,62		119	1,1	-1,3	
33	1,5	0,19		120	1,4	-0,10	
34	1,2	-0,85					
36	1,5	0,32					
37	1,2	-0,73					
38	1,4	-0,060					
40	2,0	1,7					
42	1,5	0,16					
43	1,3	-0,56					
44	2,0	1,9					
45	1,4	-0,11					
48	1,5	0,16					
49	1,5	0,30					
54	1,5	0,024					
57	1,5	0,014					
58	1,5	0,26					
61	1,3	-0,62					
63	1,7	0,68					
64	1,0	-1,4					
65	1,5	-0,0099					
71	1,8	1,3					
73	1,6	0,38					
75	1,5	0,30					
78	1,3	-0,42					
80	1,5	0,12					
84	1,4	-0,27					
87	7,8	22	Outlier				
88	1,4	-0,29					
89	1,3	-0,52					

Consenus statistics	
Consensus median, pg/g	1,5
Median all values pg/g	1,5
Consensus mean, pg/g	1,4
Standard deviation, pg/g	0,26
Relative standard deviation, %	18
No. of values reported	63
No. of values removed	1
No. of reported non-detects	0

2,3,7,8 TCDF

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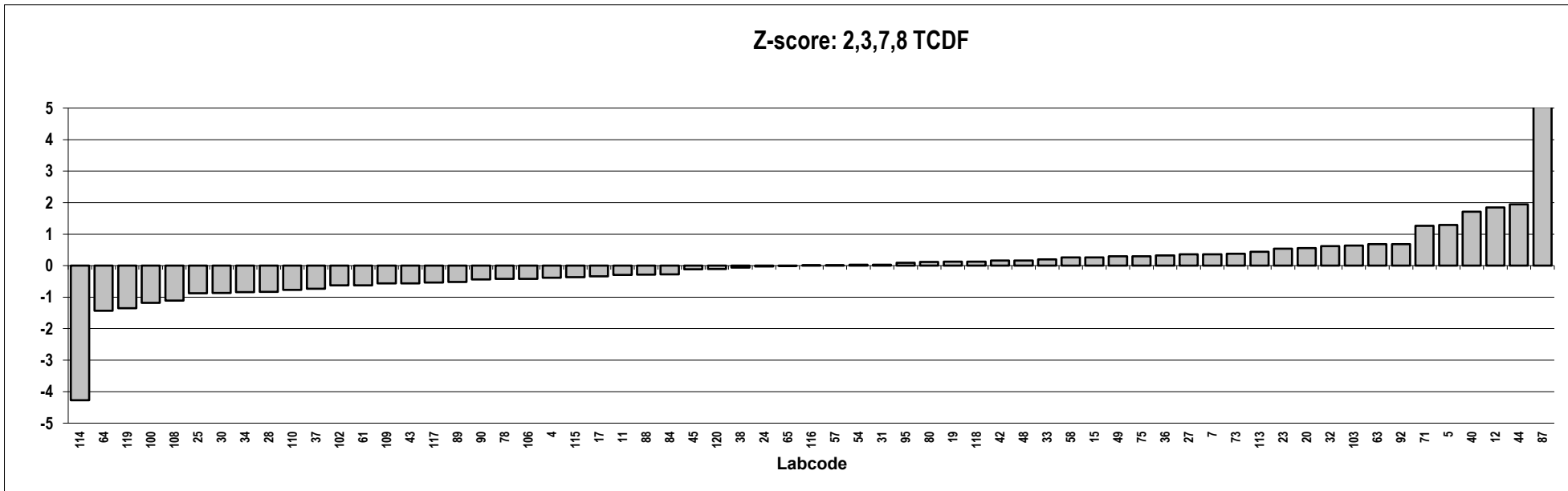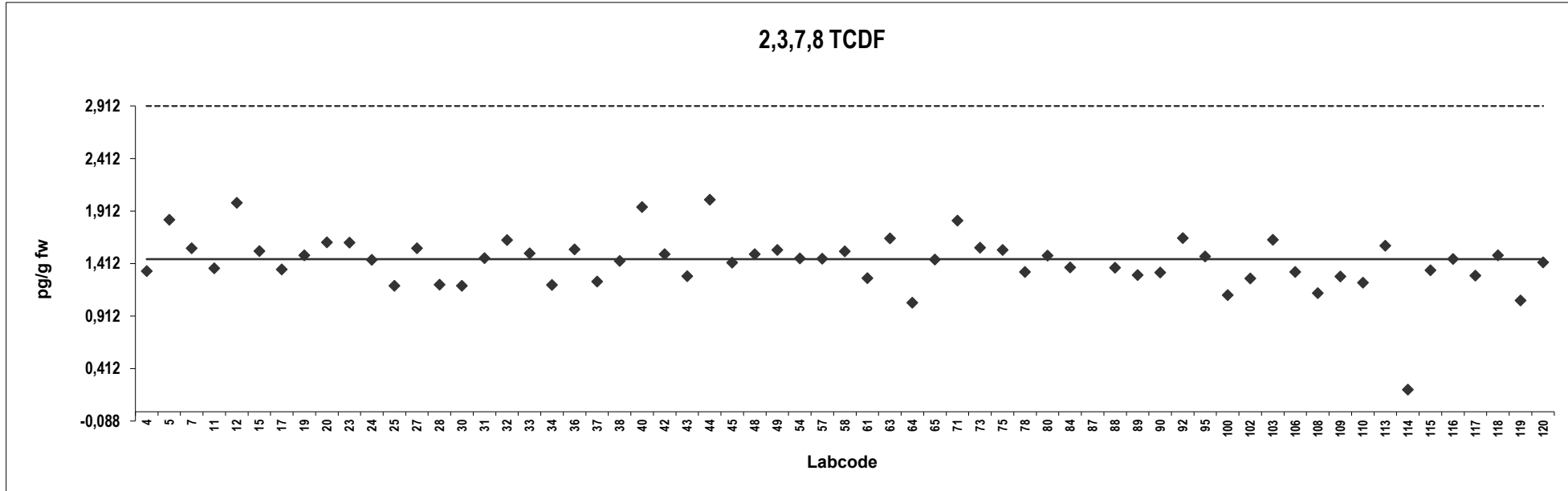
Herring

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,42	1,2		90	0,32	-0,31	
5	0,52	2,7		92	0,49	2,2	
7	0,34	0,0089		95	0,34	0,024	
11	0,32	-0,29		100	0,24	-1,4	
12	0,35	0,14		102	0,33	-0,17	
15	0,38	0,67		103	0,56	3,2	
17	0,37	0,49		106	0,33	-0,080	
19	0,30	-0,55		108	0,26	-1,2	
20	0,35	0,24		109	0,28	-0,92	
23	0,32	-0,23		110	0,32	-0,27	
24	0,34	0,037		113	0,35	0,17	
25	0,29	-0,68		114	0,10	-3,5	
27	0,40	0,85		115	0,33	-0,12	
28	0,57	3,4		116	0,34	0,066	
30	0,33	-0,18		117	0,32	-0,29	
31	0,36	0,29		118	0,40	0,87	
32	0,38	0,64		119	0,27	-1,1	
33	0,33	-0,12		120	0,33	-0,14	
34	0,31	-0,36					
36	0,38	0,58					
37	0,30	-0,61					
38	0,40	0,90					
40	0,40	0,97					
42	0,38	0,61					
43	0,31	-0,42					
44	0,41	1,1					
45	0,32	-0,20					
48	0,33	-0,12					
49	0,33	-0,12					
54	0,42	1,2					
57	0,34	0,096					
58	0,37	0,47					
61	0,27	-1,0					
63	0,31	-0,48					
64	0,25	-1,4					
65	0,32	-0,26					
71	0,85	7,6	Outlier				
73	0,39	0,79					
75	0,38	0,60					
78	0,060	-4,1					
80	0,34	0,024					
84	0,33	-0,098					
87	0,37	0,42					
88	0,41	1,1					
89	0,34	-0,0089					

Consensus statistics	
Consensus median, pg/g	0,34
Median all values pg/g	0,34
Consensus mean, pg/g	0,34
Standard deviation, pg/g	0,080
Relative standard deviation, %	23
No. of values reported	63
No. of values removed	1
No. of reported non-detects	0
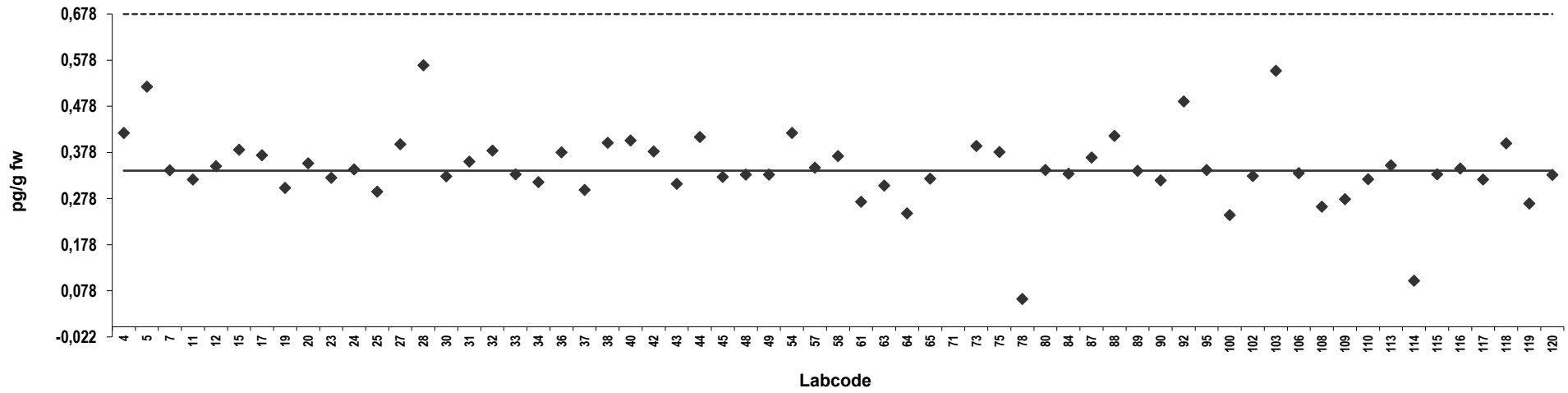
1,2,3,7,8 PeCDF

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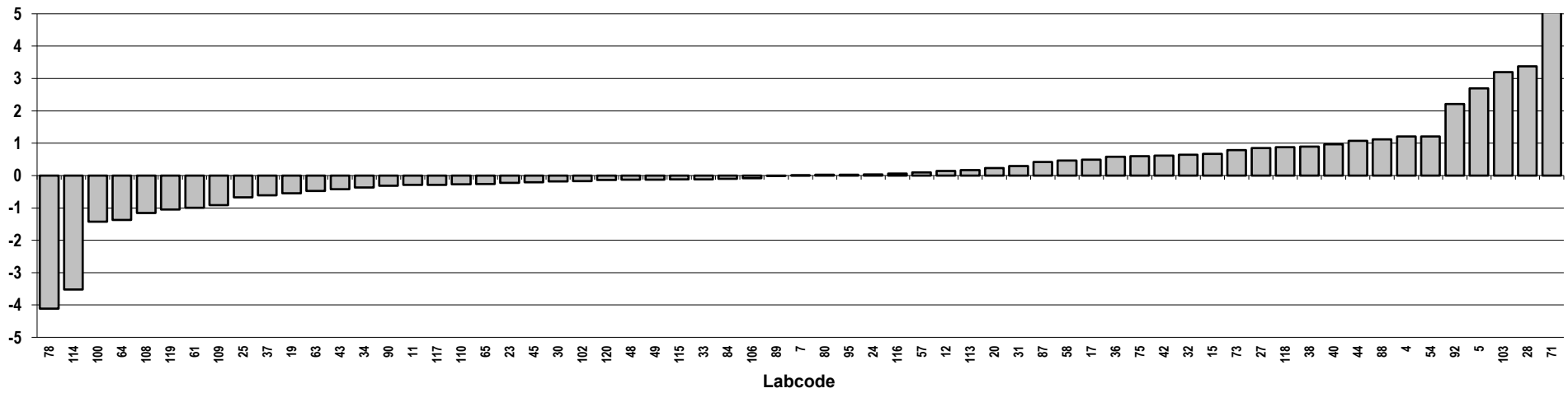
Herring

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	1,8	1,3		90	1,2	-0,71	
5	1,8	1,4		92	1,5	0,13	
7	1,6	0,66		95	1,3	-0,47	
11	1,5	0,13		100	0,92	-1,8	
12	1,7	1,0		102	1,4	-0,16	
15	1,4	-0,014		103	1,9	1,6	
17	1,4	0,049		106	1,3	-0,31	
19	1,3	-0,27		108	1,2	-0,72	
20	1,4	-0,056		109	1,3	-0,49	
23	1,4	0,021		110	1,3	-0,47	
24	1,5	0,17		113	1,5	0,45	
25	1,1	-0,94		114	0,18	-4,4	
27	1,4	-0,20		115	1,3	-0,49	
28	1,3	-0,44		116	1,2	-0,63	
30	1,3	-0,51		117	1,3	-0,50	
31	1,4	-0,012		118	1,4	0,086	
32	1,4	-0,015		119	1,1	-1,1	
33	1,4	-0,071		120	1,4	0,00	
34	1,3	-0,28					
36	1,6	0,51					
37	1,2	-0,75					
38	1,4	0,037					
40	1,6	0,59					
42	1,5	0,30					
43	1,3	-0,30					
44	1,6	0,80					
45	1,5	0,42					
48	1,5	0,30					
49	1,5	0,37					
54	1,4	-0,12					
57	1,5	0,28					
58	1,5	0,46					
61	1,2	-0,84					
63	1,4	0,021					
64	0,87	-1,9					
65	1,5	0,14					
71	1,8	1,2					
73	1,5	0,35					
75	1,4	-0,050					
78	0,99	-1,5					
80	1,4	0,050					
84	1,5	0,25					
87	1,4	0,071					
88	1,4	0,021					
89	1,4	0,11					

Consenus statistics	
Consensus median, pg/g	1,4
Median all values pg/g	1,4
Consensus mean, pg/g	1,4
Standard deviation, pg/g	0,24
Relative standard deviation, %	18
No. of values reported	63
No. of values removed	0
No. of reported non-detects	0
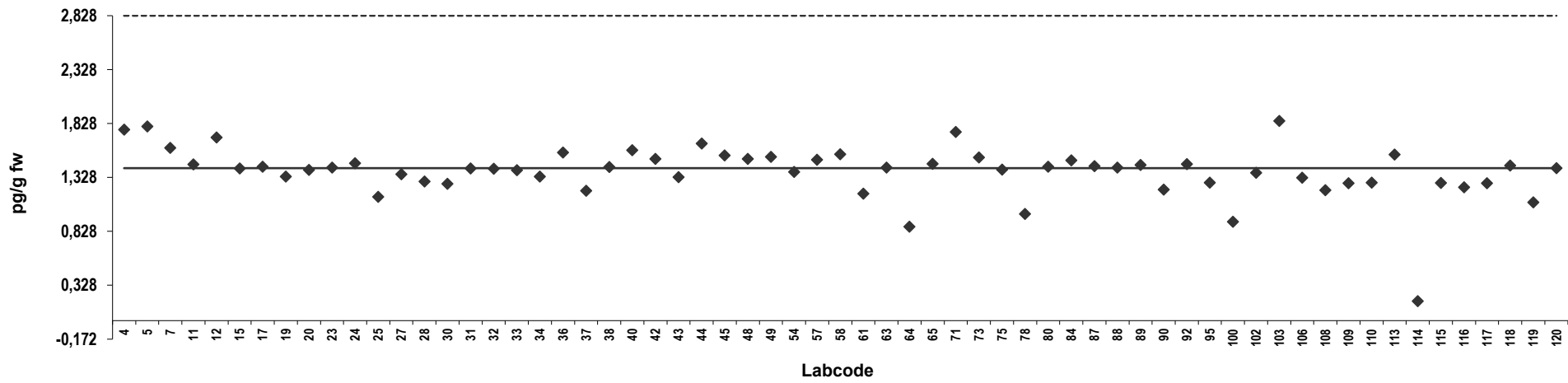
2,3,4,7,8 PeCDF

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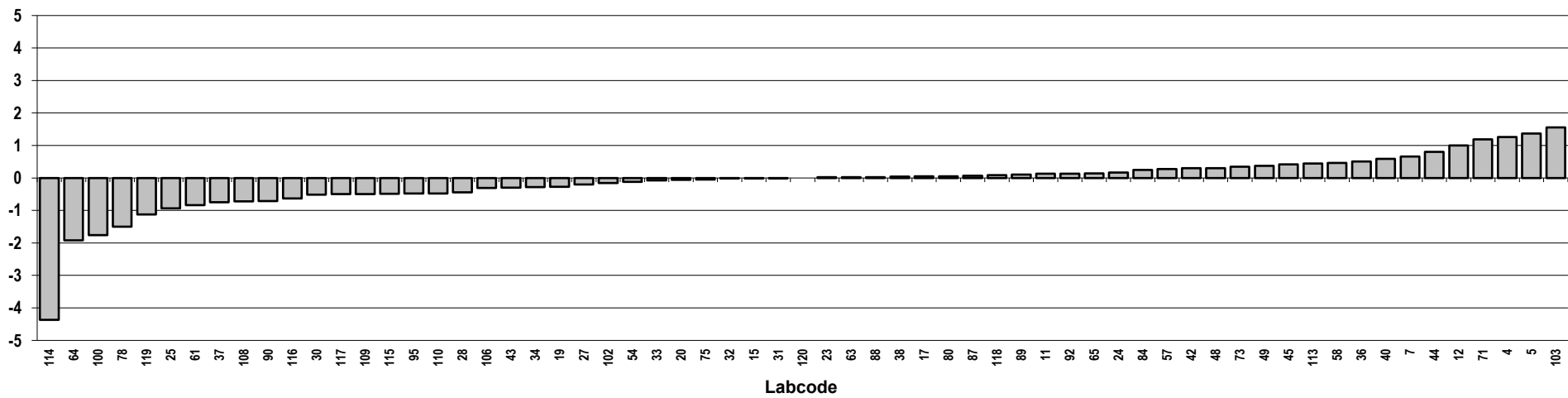
Herring
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,11	1,3		90	0,077		
5	0,067	-1,2		92	0,16		
7	0,091	0,20		95	0,082		
11	0,084	-0,20		100	0,069		
12	0,093	0,32		102	0,089		
15	0,088	0,031		103	0,14		
17	0,095	0,42		106	0,080		
19	0,028	-3,4	ND	108	0,077		
20	0,077	-0,60		109	0,081		
23	0,098	0,60		110	0,095		
24	0,087	-0,043		113	0,093		
25	0,071	-0,96		114	0,0047		
27	0,093	0,33		115	0,077		
28	0,24	8,7	Outlier	116	0,059		
30	0,084	-0,20		117	0,077		
31	0,084	-0,22		118	0,087		
32	0,088	0,048		119	0,072		
33	0,093	0,31		120	0,093		
34	0,085	-0,12					
36	0,093	0,32					
37	0,091	0,23					
38	0,10	0,72	ND				
40	0,12	1,9					
42	0,092	0,26					
43	0,080	-0,43					
44	0,088	0,054					
45	0,090	0,12					
48	0,086	-0,084					
49	0,092	0,26					
54	0,11	1,3					
57	0,085	-0,16					
58	0,082	-0,34					
61	0,047	-2,3					
63	0,091	0,20					
64	0,043	-2,5					
65	0,091	0,23					
71	0,058	-1,7					
73	0,098	0,61					
75	0,089	0,088					
78	0,080	-0,4	ND				
80	0,11	1,2					
84	0,10	0,77					
87	0,086	-0,084					
88	0,11	1,0					
89	0,079	-0,46					

Consensus statistics

Consensus median, pg/g	0,087
Median all values pg/g	0,088
Consensus mean, pg/g	0,086
Standard deviation, pg/g	0,022
Relative standard deviation, %	26
No. of values reported	63
No. of values removed	1
No. of reported non-detects	3

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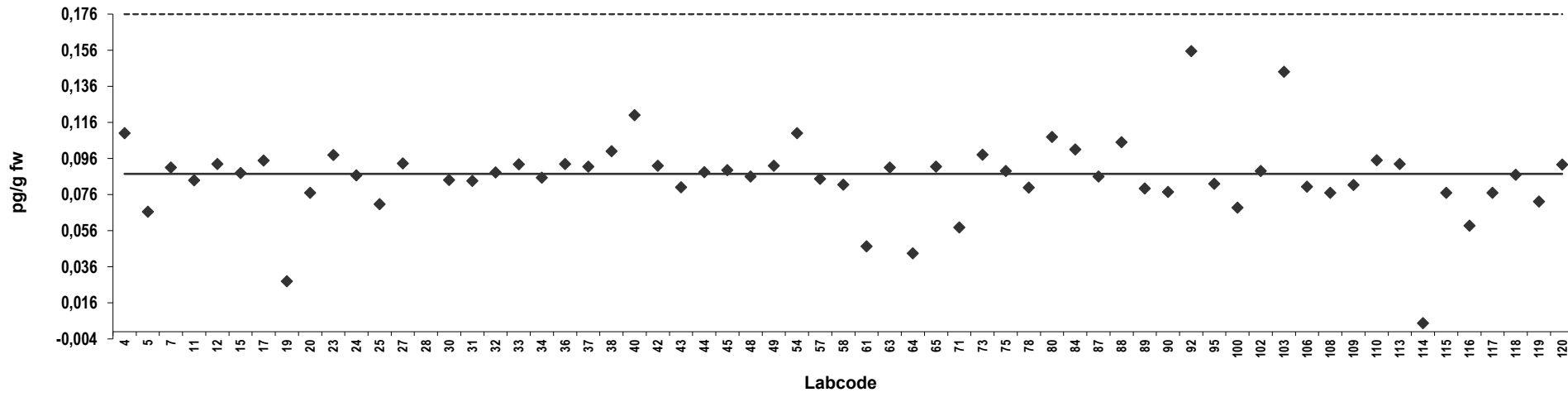
Z-score: 1,2,3,4,7,8 HxCDF
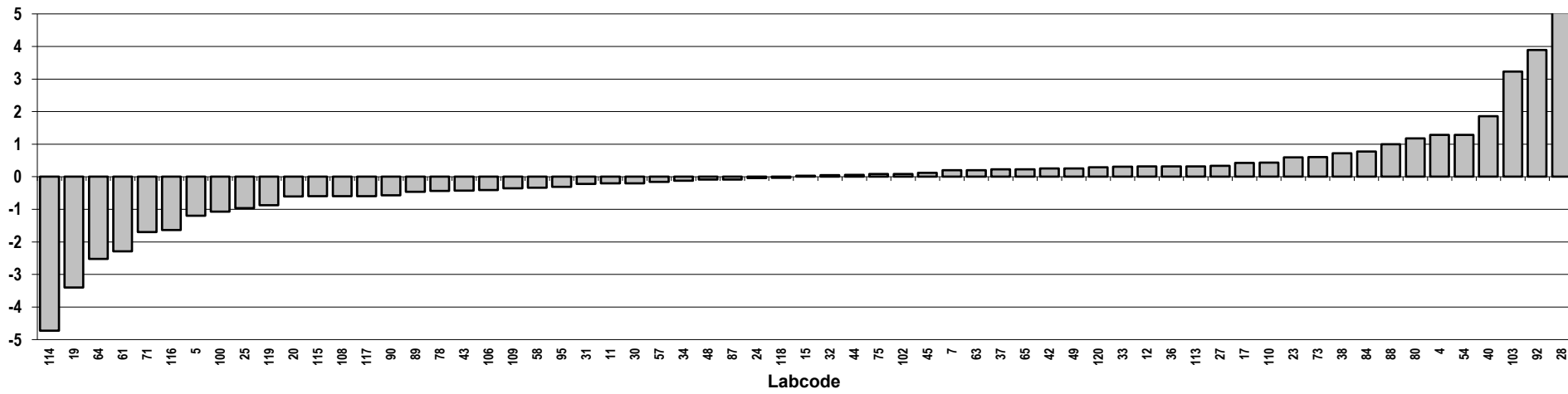
Herring

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,13	0,52		90	0,11	-0,53	
5	0,10	-0,65		92	0,18	2,7	
7	0,13	0,44		95	0,11	-0,54	
11	0,14	0,99		100	0,10	-0,75	
12	0,13	0,67		102	0,12	-0,071	
15	0,12	0,14		103	0,099	-0,79	
17	0,12	0,22		106	0,11	-0,19	
19	0,036	-3,5	ND	108	0,093	-1,0	
20	0,10	-0,58		109	0,10	-0,69	
23	0,13	0,31		110	0,060	-2,5	ND
24	0,11	-0,26		113	0,12	0,099	
25	0,084	-1,4		114	0,046	-3,0	
27	0,13	0,54		115	0,12	-0,014	
28	0,13	0,52	ND	116	0,10	-0,70	
30	0,095	-0,96		117	0,11	-0,20	
31	0,12	0,016		118	0,13	0,31	
32	0,24	5,2	Outlier	119	0,094	-0,99	
33	0,12	0,14		120	0,12	0,063	
34	0,11	-0,53					
36	0,13	0,64					
37	0,10	-0,67					
38	0,17	2,2					
40	0,097	-0,88					
42	0,12	0,099					
43	0,090	-1,2					
44	0,12	-0,097					
45	0,12	0,25					
48	0,12	0,099					
49	0,12	0,099					
54	0,13	0,52					
57	0,11	-0,14					
58	0,13	0,44					
61	0,081	-1,6					
63	0,13	0,35					
64	0,096	-0,94					
65	0,12	0,11					
71	0,11	-0,45					
73	0,14	0,96					
75	0,12	0,099					
78	0,081	-1,5	ND				
80	0,13	0,57					
84	0,12	0,15					
87	0,12	0,014					
88	0,15	1,3					
89	0,11	-0,40					

Consensus statistics

Consensus median, pg/g	0,12
Median all values pg/g	0,12
Consensus mean, pg/g	0,11
Standard deviation, pg/g	0,024
Relative standard deviation, %	21
No. of values reported	63
No. of values removed	1
No. of reported non-detects	4

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

Z-score: 1,2,3,6,7,8 HxCDF
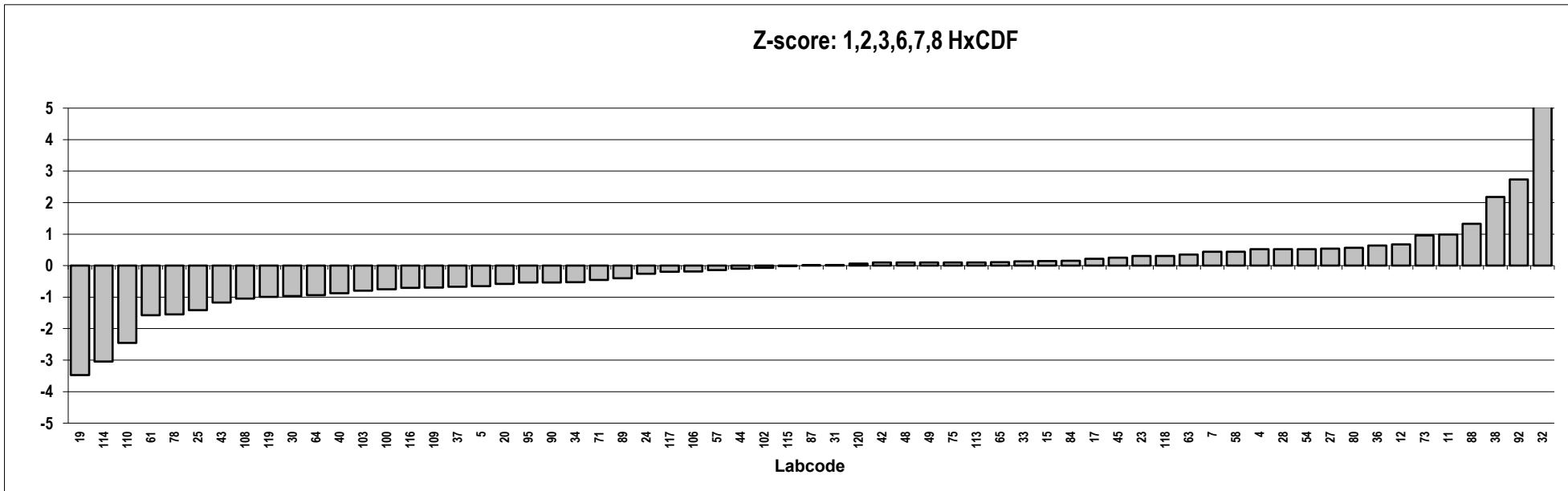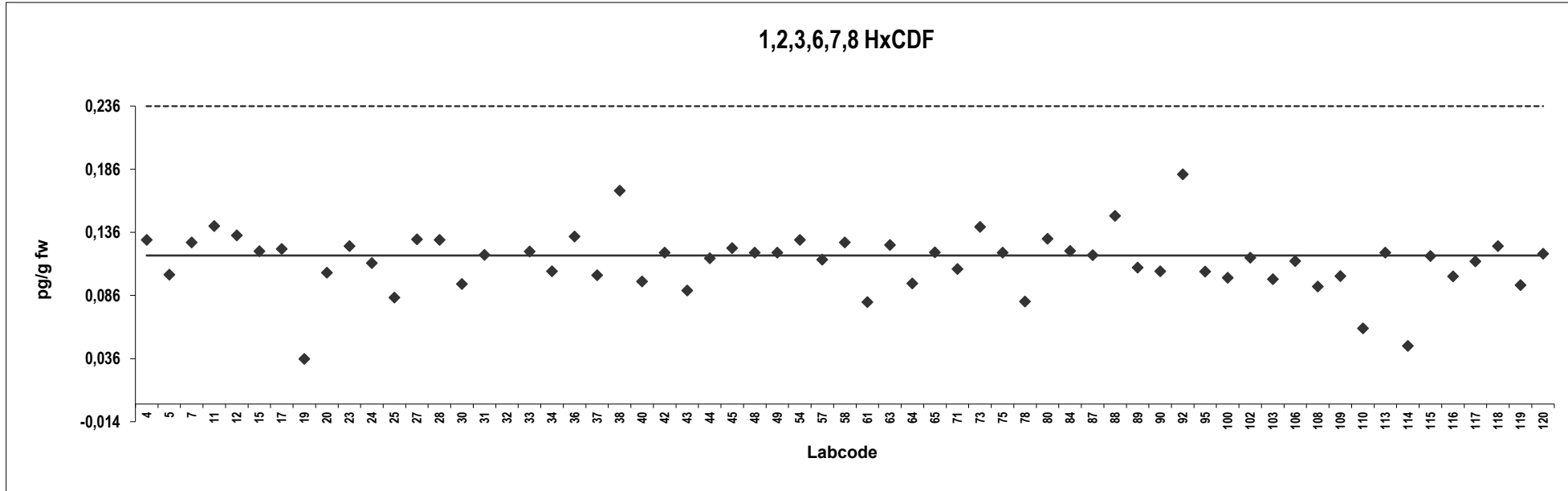
Herring
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,14	0,91		90	0,10	-0,64	
5	0,15	1,1		92	0,23	4,7	
7	0,12	0,068		95	0,096	-0,95	
11	0,086	-1,4		100	0,072	-2,0	
12	0,12	0,090		102	0,11	-0,23	
15	0,11	-0,27		103	0,13	0,62	
17	0,11	-0,23		106	0,11	-0,37	
19	0,033	-3,6	ND	108	0,095	-0,99	
20	0,13	0,31		109	0,10	-0,73	
23	0,087	-1,3		110	0,12	0,068	
24	0,11	-0,48		113	0,13	0,49	
25	0,027	-3,8		114	0,013	-4,5	
27	0,13	0,35		115	0,12	-0,019	
28	0,13	0,49	ND	116	0,11	-0,29	
30	0,12	0,11		117	0,11	-0,44	
31	0,11	-0,54		118	0,12	-0,058	
32	0,12	0,076		119	0,083	-1,5	
33	0,12	0,11		120	0,12	0,14	
34	0,087	-1,3					
36	0,14	0,71					
37	0,10	-0,69					
38	0,17	2,1					
40	0,16	1,6					
42	0,13	0,49					
43	0,11	-0,35					
44	0,14	0,70					
45	0,12	-0,057					
48	0,12	0,068					
49	0,11	-0,35					
54	0,12	0,068					
57	0,12	-0,093					
58	0,12	0,19					
61	0,15	1,3					
63	0,12	0,15					
64	0,091	-1,2					
65	0,12	-0,13					
71	0,12	0,19					
73	0,13	0,56					
75	0,11	-0,23					
78	0,12	0,00	ND				
80	0,13	0,41					
84	0,13	0,28					
87	0,13	0,32					
88	0,16	1,5					
89	0,12	-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	0,030
Relative standard deviation, %	26
No. of values reported	63
No. of values removed	0
No. of reported non-detects	3

2,3,4,6,7,8 HxCDF
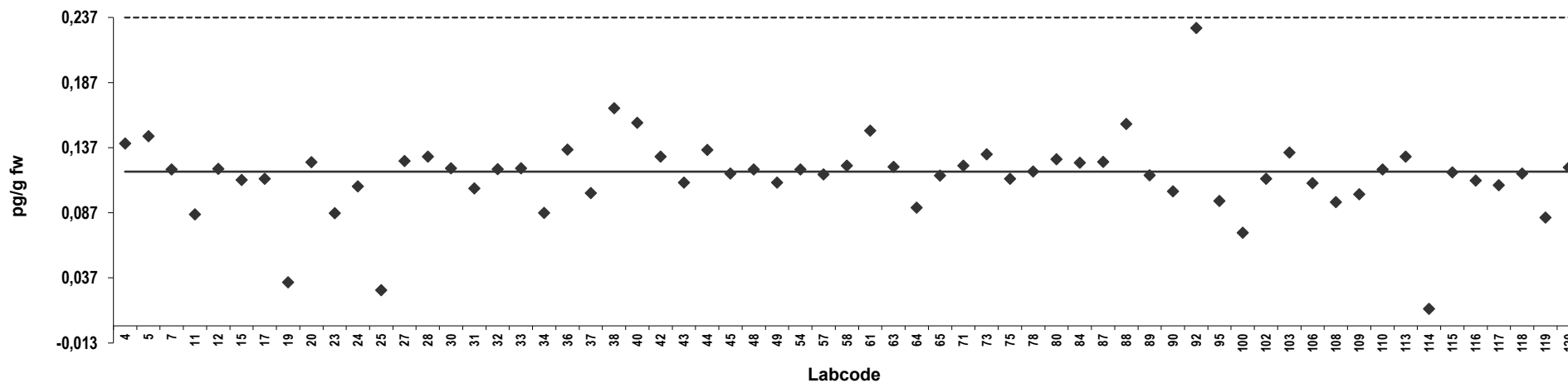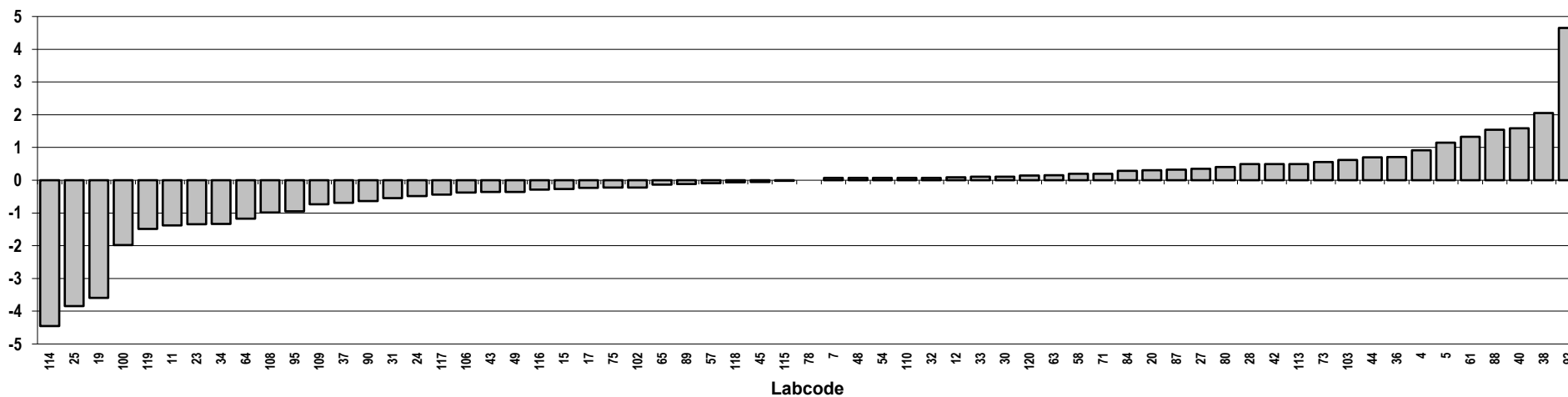
pg/g fw

Labcode

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

Labcode

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	35	Outlier,ND	90	0,0087	1,9	
5	0,014	6,4		92	0,18	135	Outlier
7	0,0010	-4,2		95	0,011	3,7	ND
11	0,0041	-1,8	ND	100	0,021	11	Outlier,ND
12	0,026	16	Outlier,ND	102	0,020	11	Outlier,ND
15	0,0050	-1,0		103	0,015	6,9	ND
17	0,0046	-1,3		106	0,0090	2,1	
19	0,012	4,3	ND	108	0,020	11	Outlier,ND
20	0,0032	-2,5		109	0,015	6,9	ND
23	0,025	15	Outlier,ND	110	0,060	43	Outlier,ND
24	0,0041	-1,8		113	0,012	4,5	
25	0,12	87	Outlier	114	0,0051	-0,95	ND
27	0,020	11	Outlier,ND	115	0,011	3,8	
28	0,18	138	Outlier,ND	116	0,0097	2,7	ND
30	0,0035	-2,2	ND	117	0,0080	1,3	
31	0,0040	-1,9	ND	118	0,0062	-0,095	
32	0,0065	0,16		119	0,0053	-0,79	
33	0,0063	0,00		120	0,0085	1,8	
34	0,0047	-1,3					
36	0,0020	-3,4	ND				
37	0,010	2,9	ND				
38	0,10	74	Outlier,ND				
40	0,018	9,3	Outlier,ND				
42	0,012	4,5	ND				
43	0,030	19	Outlier,ND				
44	0,0019	-3,5					
45	0,016	8,0					
48	0,0060	-0,24	ND				
49	0,0050	-1,0					
54	0,0078	1,2					
57	0,0073	0,79					
58	0,050	35	Outlier,ND				
61	0,0078	1,2	ND				
63	0,0050	-1,0	ND				
64	0,0080	1,3	ND				
65	0,0040	-1,8					
71	0,0024	-3,1	ND				
73	0,013	5,0					
75	0,0050	-1,0					
78	0,18	136	Outlier,ND				
80	0,025	15	Outlier,ND				
84	0,0071	0,66					
87	0,0040	-1,8					
88	0,019	10	Outlier				
89	0,0031	-2,5					

Consensus statistics

Consensus median, pg/g	0,0063
Median all values pg/g	0,0087
Consensus mean, pg/g	0,0072
Standard deviation, pg/g	0,0039
Relative standard deviation, %	54
No. of values reported	63
No. of values removed	18
No. of reported non-detects	32
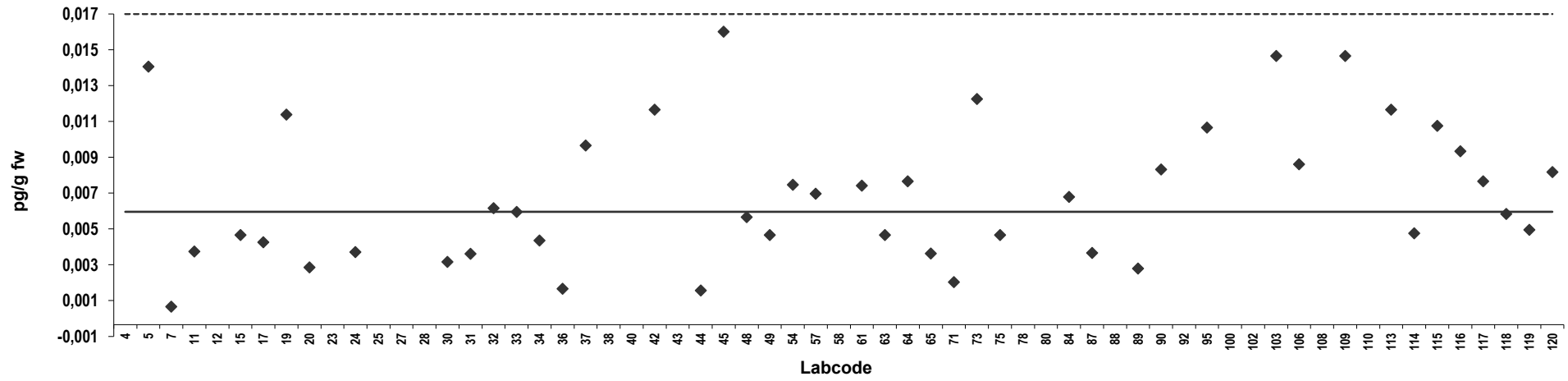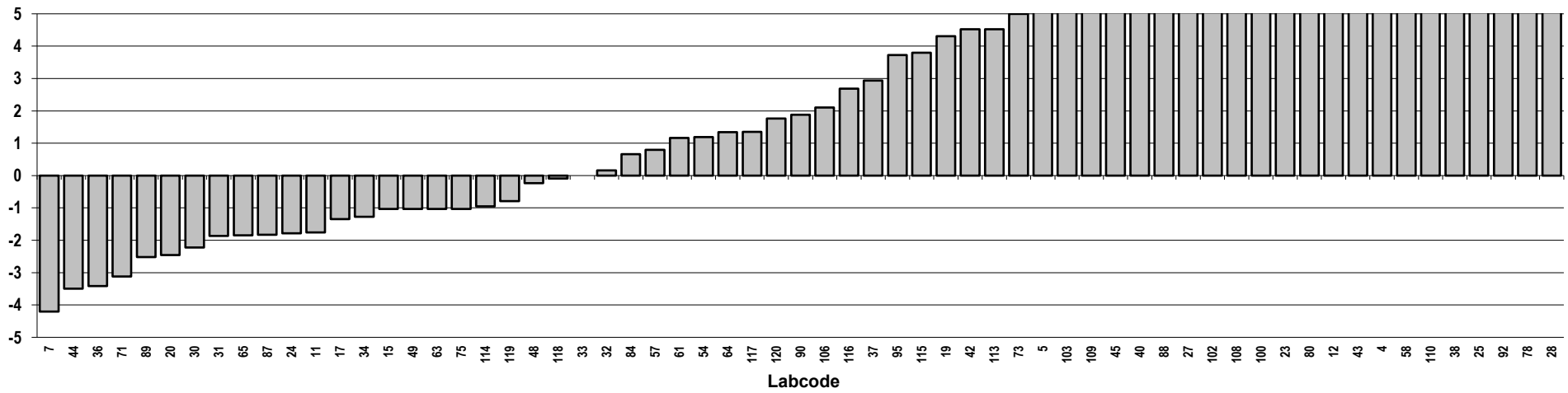
Herring
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	4,1		90	0,028	0,00	
5	0,034	1,1		92	0,14	19,6	Outlier
7	0,024	-0,65		95	0,031	0,62	
11	0,021	-1,2		100	0,041	2,5	
12	0,029	0,32		102	0,023	-0,83	
15	0,025	-0,47		103	0,039	2,1	
17	0,028	0,0061		106	0,051	4,2	
19	0,017	-1,8	ND	108	0,030	0,44	ND
20	0,025	-0,49		109	0,028	0,016	
23	0,026	-0,25		110	0,060	5,9	Outlier,ND
24	0,041	2,4		113	0,025	-0,47	
25	0,020	-1,4		114	0,0060	-3,9	ND
27	0,032	0,80		115	0,037	1,7	
28	0,12	17	Outlier,ND	116	0,018	-1,7	
30	0,018	-1,7	ND	117	0,027	-0,11	
31	0,026	-0,35		118	0,038	1,8	
32	0,023	-0,78		119	0,048	3,8	
33	0,023	-0,90		120	0,037	1,7	
34	0,022	-0,99					
36	0,026	-0,23					
37	0,025	-0,40					
38	0,10	13	Outlier,ND				
40	0,071	7,9	Outlier				
42	0,030	0,44					
43	0,030	0,44	ND				
44	0,026	-0,36					
45	0,024	-0,70					
48	0,026	-0,29					
49	0,021	-1,2					
54	0,036	1,5					
57	0,022	-1,0					
58	0,050	4,1	ND				
61	0,032	0,77					
63	0,024	-0,65					
64	0,041	2,4					
65	0,030	0,40					
71	0,042	2,6					
73	0,060	5,8	Outlier				
75	0,026	-0,29					
78	0,091	11	Outlier,ND				
80	0,050	4,1	ND				
84	0,025	-0,38					
87	0,039	2,1					
88	0,10	13	Outlier				
89	0,031	0,62					

Consenus statistics	
Consensus median, pg/g	0,028
Median all values pg/g	0,030
Consensus mean, pg/g	0,030
Standard deviation, pg/g	0,0094
Relative standard deviation, %	31
No. of values reported	63
No. of values removed	8
No. of reported non-detects	11

1,2,3,4,6,7,8 HpCDF
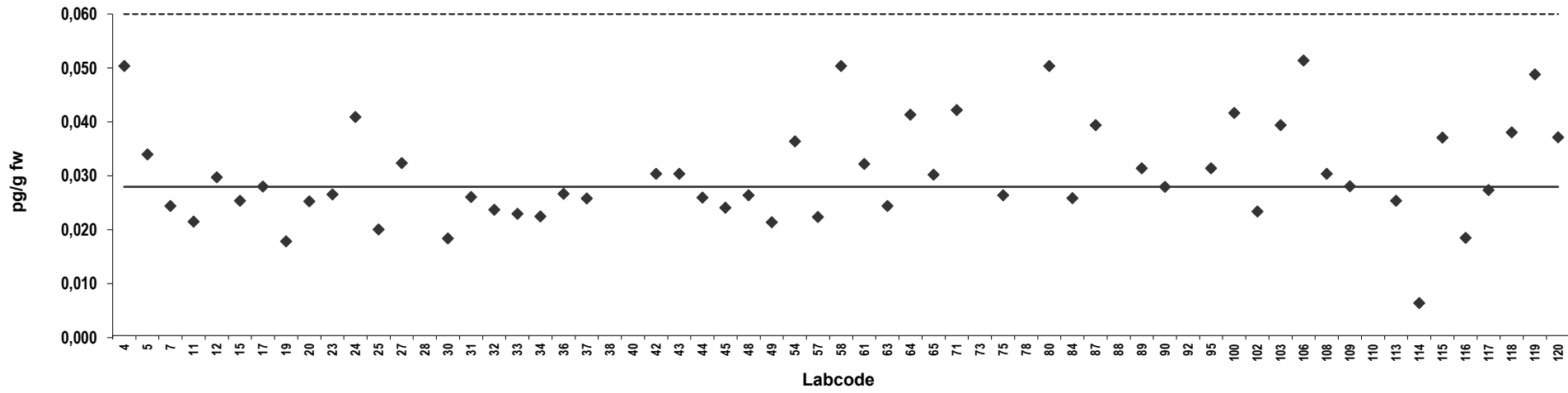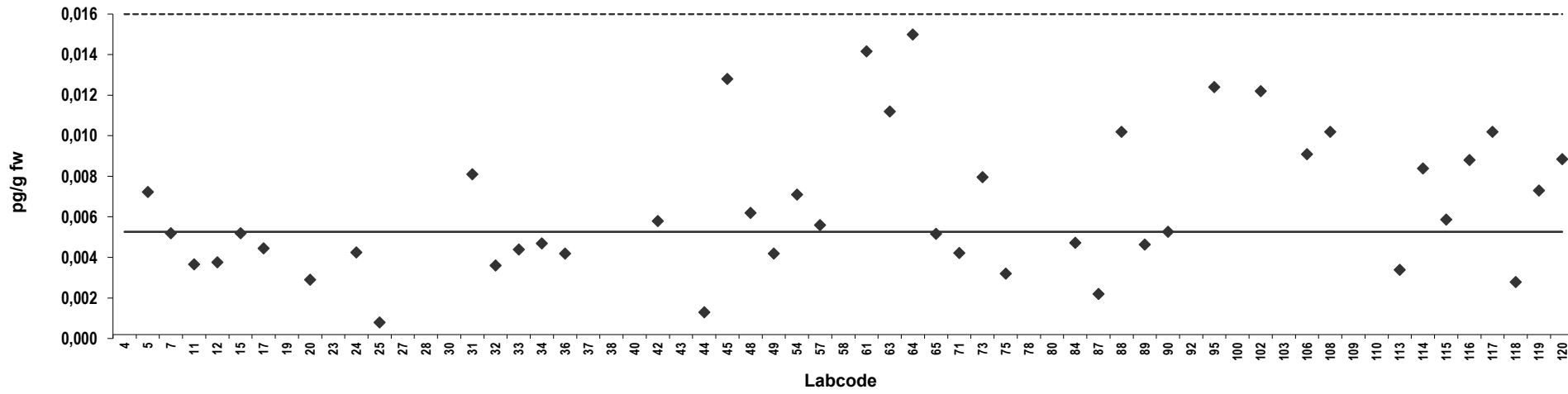
Z-score: 1,2,3,4,6,7,8 HpCDF
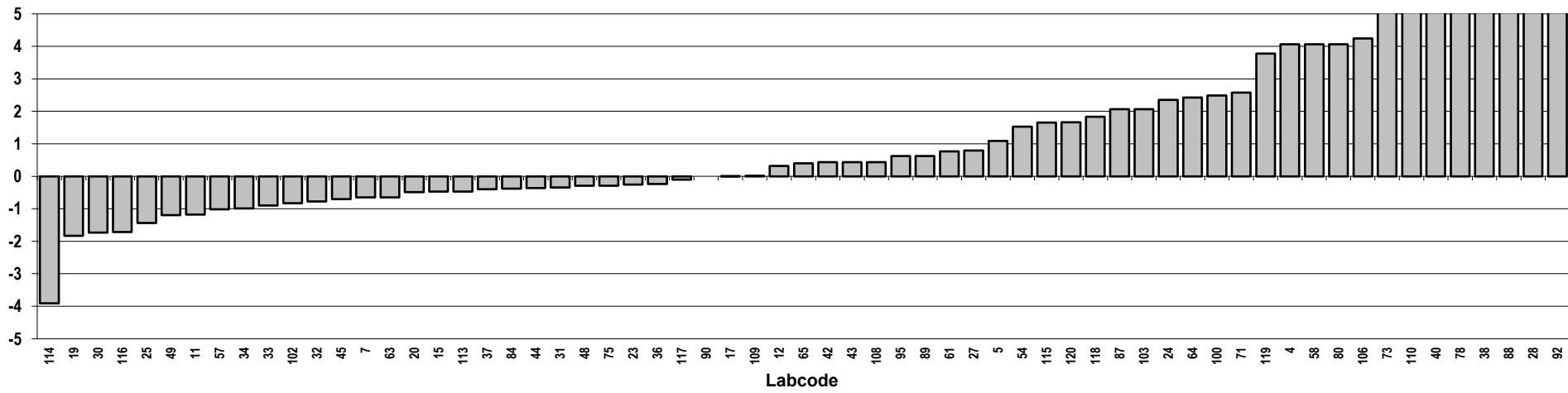
Herring
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	44	Outlier,ND	90	0,0051	0,00	
5	0,0070	1,9		92	0,062	56	Outlier
7	0,0050	-0,068		95	0,012	7,0	ND
11	0,0035	-1,6	ND	100	0,028	23	Outlier,ND
12	0,0036	-1,5		102	0,012	6,8	ND
15	0,0050	-0,068	ND	103	0,022	17	Outlier,ND
17	0,0042	-0,81		106	0,0089	3,8	ND
19	0,024	18	Outlier,ND	108	0,010	4,9	ND
20	0,0027	-2,3	ND	109	0,025	20	Outlier,ND
23	0,039	33	Outlier,ND	110	0,060	54	Outlier,ND
24	0,0041	-1,0		113	0,0032	-1,8	
25	0,00060	-4,4	ND	114	0,0082	3,1	ND
27	0,024	19	Outlier,ND	115	0,0057	0,59	
28	0,14	133	Outlier,ND	116	0,0086	3,5	ND
30	0,018	13	Outlier,ND	117	0,010	4,9	ND
31	0,0079	2,8	ND	118	0,0026	-2,4	
32	0,0034	-1,6	ND	119	0,0071	2,0	
33	0,0042	-0,86		120	0,0086	3,5	
34	0,0045	-0,56					
36	0,0040	-1,1	ND				
37	0,020	15	Outlier,ND				
38	0,10	94	Outlier,ND				
40	0,021	16	Outlier,ND				
42	0,0056	0,52	ND				
43	0,030	25	Outlier,ND				
44	0,0011	-3,9					
45	0,013	7,4	ND				
48	0,0060	0,92	ND				
49	0,0040	-1,1					
54	0,0069	1,8					
57	0,0054	0,33					
58	0,050	44	Outlier,ND				
61	0,014	8,8					
63	0,011	5,8	ND				
64	0,015	9,6					
65	0,0050	-0,10					
71	0,0040	-1,0	ND				
73	0,0078	2,7					
75	0,0030	-2,0					
78	0,16	148	Outlier,ND				
80	0,050	44	Outlier,ND				
84	0,0045	-0,5					
87	0,0020	-3,0					
88	0,010	4,9					
89	0,0044	-0,62					

Consensus statistics

|	
Consensus median, pg/g	0,0051
Median all values pg/g	0,0079
Consensus mean, pg/g	0,0063
Standard deviation, pg/g	0,0035
Relative standard deviation, %	55
No. of values reported	63
No. of values removed	18
No. of reported non-detects	36

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

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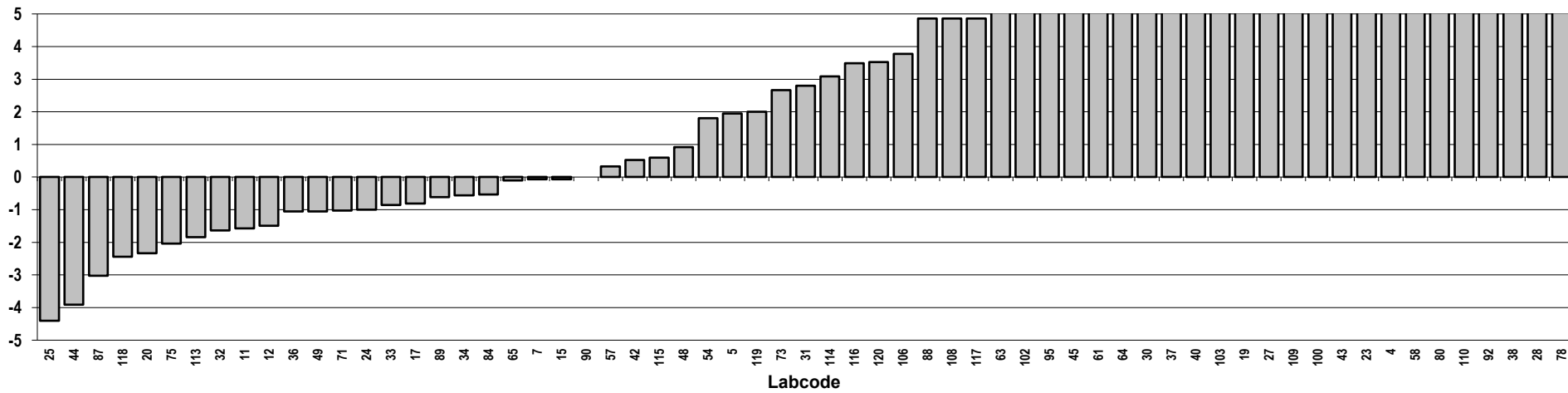
Herring

Congener: OCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,20	86	Outlier,ND	90	0,014	1,4	
5	0,0051	-2,7		92	0,30	132	Outlier
7	0,028	7,7		95	0,023	5,5	
11	0,0057	-2,4	ND	100	0,042	14	Outlier,ND
12	0,032	9,6	ND	102	0,037	12	Outlier,ND
15	0,011	0,00		103	0,011	0,00	
17	0,0028	-3,7		106	0,021	4,7	
19	0,018	3,3	ND	108	0,040	13	Outlier,ND
20	0,0089	-0,95	ND	109	0,012	0,45	
23	0,042	14	Outlier,ND	110	0,16	68	Outlier,ND
24	0,0087	-1,0		113	0,0025	-3,9	
25	0,033	10		114	0,0069	-1,9	ND
27	0,016	2,4	ND	115	0,033	10	
28	0,73	325	Outlier	116	0,014	1,2	ND
30	0,018	3,2	ND	117	0,019	3,6	
31	0,016	2,2	ND	118	0,0042	-3,1	
32	0,0081	-1,3		119	0,027	7,1	
33	0,0025	-3,9	ND	120	0,045	15	Outlier
34	0,0089	-0,95					
36	0,0062	-2,2					
37	0,040	13	Outlier,ND				
38	0,20	86	Outlier,ND				
40	0,045	15	Outlier,ND				
42	0,080	31	Outlier,ND				
43	0,050	18	Outlier,ND				
44	0,0021	-4,0					
45	0,032	9,3	ND				
48	0,010	-0,45	ND				
49	0,0050	-2,7					
54	0,012	0,45					
57	0,0070	-1,8					
58	0,050	18	Outlier,ND				
61	0,16	67	Outlier				
63	0,0080	-1,4	ND				
64	0,039	13	Outlier				
65	0,0099	-0,48					
71	0,0023	-4,0	ND				
73	0,025	6,2					
75	0,012	0,45					
78	0,47	208	Outlier,ND				
80	0,10	40	Outlier,ND				
84	0,0046	-2,9					
87	0,016	2,3					
88	0,020	4,1					
89	0,010	-0,27					

Consensus statistics

Consensus median, pg/g	0,011
Median all values pg/g	0,018
Consensus mean, pg/g	0,013
Standard deviation, pg/g	0,0091
Relative standard deviation, %	67
No. of values reported	63
No. of values removed	19
No. of reported non-detects	28

OCDF

pg/g fw

Labcode

Z-score: OCDF
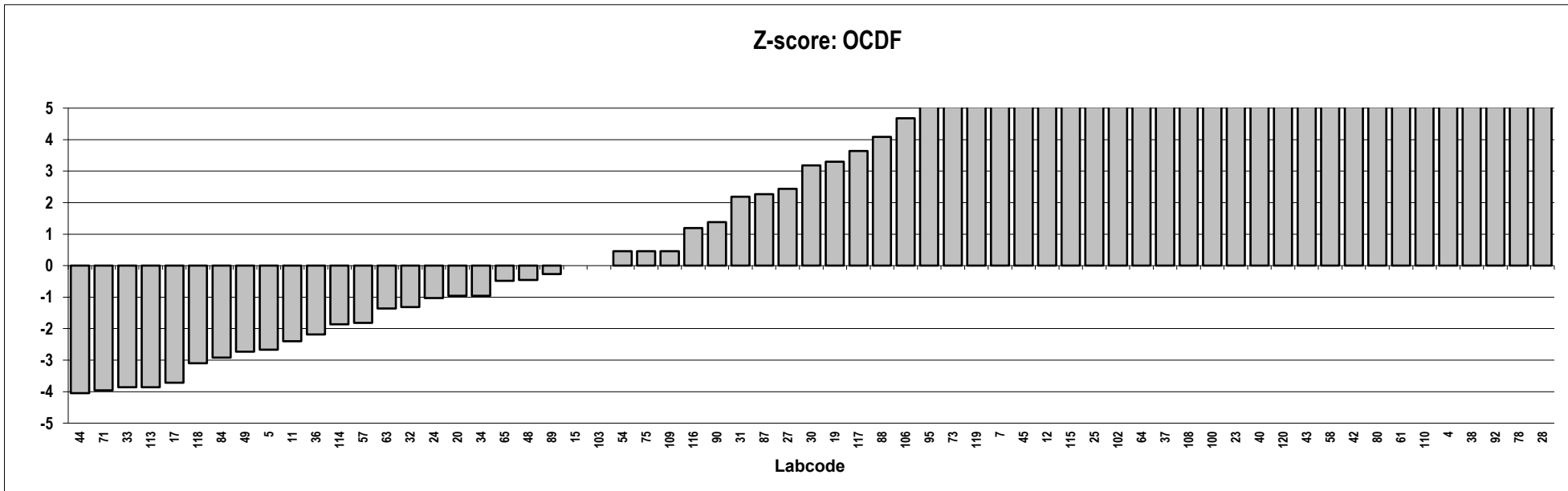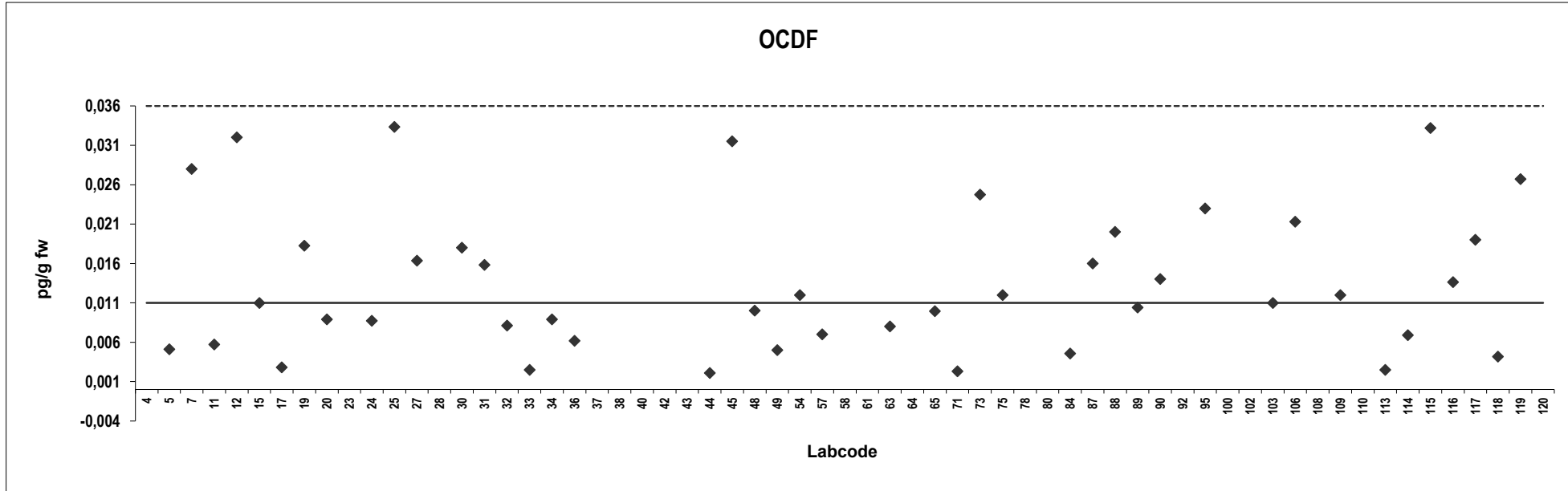
Labcode

Herring
Congener: PCB 77

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	27	1,1		90	26	0,93	
5	29	1,6		92	24	0,53	
7	23	0,18		95	22	0,068	
11	23	0,11		100	17	-1,1	
12	23	0,14		102	23	0,18	
15	25	0,61		103	20	-0,41	
17	24	0,41		106	18	-0,82	
19	17	-1,1		108	21	-0,27	
20	23	0,15		109	20	-0,43	
23	23	0,16		110	22	-0,11	
24	21	-0,17		113	24	0,39	
25	17	-1,3		114	3,0	-4,3	
27	20	-0,54		115	22	0,074	
28	32	2,4		116	21	-0,13	
30	23	0,32		117	19	-0,72	
31	22	-0,047		118	25	0,64	
32	18	-0,80		119	15	-1,7	
33	29	1,6		120	23	0,25	
34	21	-0,18					
36	19	-0,65					
37	20	-0,41					
38	23	0,18					
40	28	1,4					
42	25	0,68					
43	18	-1,0					
44	21	-0,12					
45	22	0,024					
48	22	0,00					
49	21	-0,34					
54	19	-0,66					
57	34	2,7					
58	25	0,65					
61	18	-0,91					
63	22	0,00					
64	27	1,1					
65	21	-0,28					
71	24	0,36					
73	24	0,44					
75	25	0,59					
78	17	-1,2					
80	21	-0,15					
84	23	0,33					
87	21	-0,17					
88	20	-0,49					
89	13	-2,1					

| Consenus statistics	
Consensus median, pg/g	22
Median all values pg/g	22
Consensus mean, pg/g	22
Standard deviation, pg/g	4,5
Relative standard deviation, %	20
No. of values reported	63
No. of values removed	0
No. of reported non-detects	0
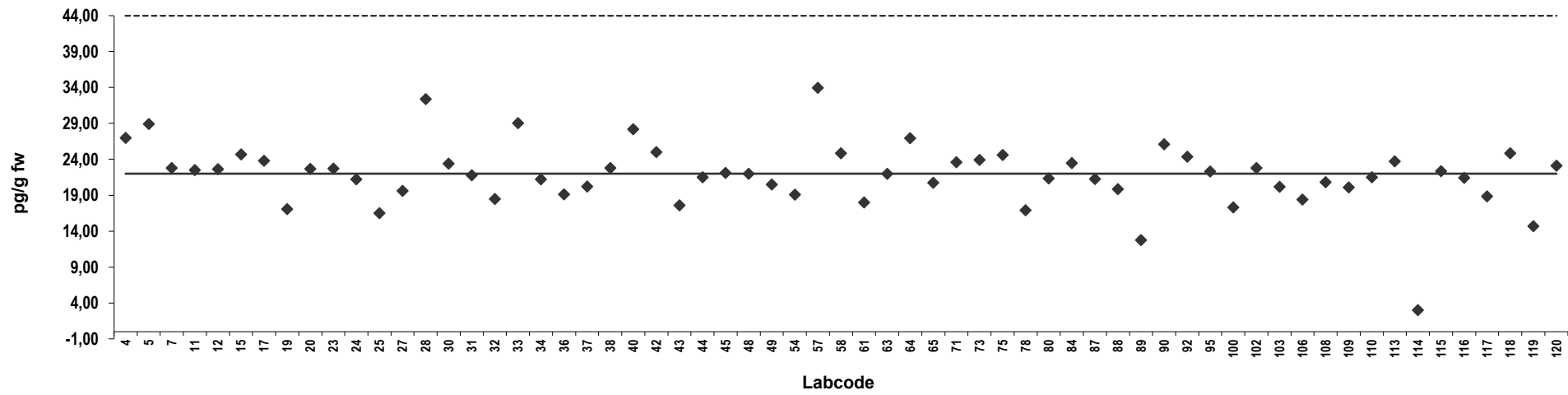
PCB 77

Z-score: PCB 77
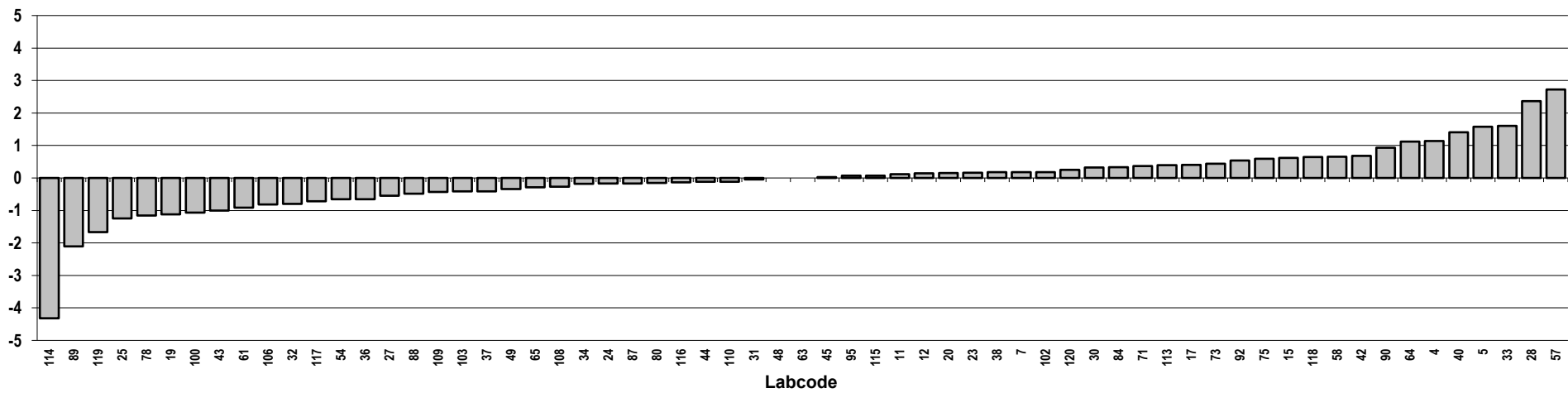
Herring
Congener: PCB 126

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	13	1,8		90	10	0,35	
5	13	1,7		92	10	0,30	
7	11	0,75		95	9,6	-0,021	
11	9,6	-0,026		100	7,4	-1,2	
12	9,9	0,12		102	9,0	-0,35	
15	9,4	-0,13		103	9,0	-0,32	
17	11	0,54		106	7,9	-0,93	
19	8,2	-0,74		108	9,0	-0,32	
20	10	0,30		109	8,2	-0,78	
23	11	0,43		110	10	0,26	
24	11	0,74		113	10	0,30	
25	14	2,4		114	1,0	-4,5	
27	7,9	-0,92		115	10	0,25	
28	11	0,49		116	11	0,59	
30	11	0,93		117	8,2	-0,77	
31	8,7	-0,47		118	11	0,78	
32	9,0	-0,35		119	6,4	-1,7	
33	12	1,1		120	10	0,20	
34	9,4	-0,16					
36	8,3	-0,71					
37	8,9	-0,39					
38	11	0,77					
40	14	2,1					
42	11	0,69					
43	8,1	-0,81					
44	10	0,27					
45	9,3	-0,18					
48	9,3	-0,19					
49	8,0	-0,85					
54	9,6	-0,021					
57	12	1,1					
58	10	0,31					
61	6,0	-1,9					
63	9,8	0,062					
64	11	0,67					
65	11	0,63					
71	9,6	-0,036					
73	11	0,71					
75	9,7	0,00					
78	7,2	-1,3					
80	8,2	-0,73					
84	9,1	-0,30					
87	9,3	-0,19					
88	9,2	-0,25					
89	11	0,48					

| Consenus statistics	
Consensus median, pg/g	9,7
Median all values pg/g	9,7
Consensus mean, pg/g	9,7
Standard deviation, pg/g	1,9
Relative standard deviation, %	20
No. of values reported	63
No. of values removed	0
No. of reported non-detects	0
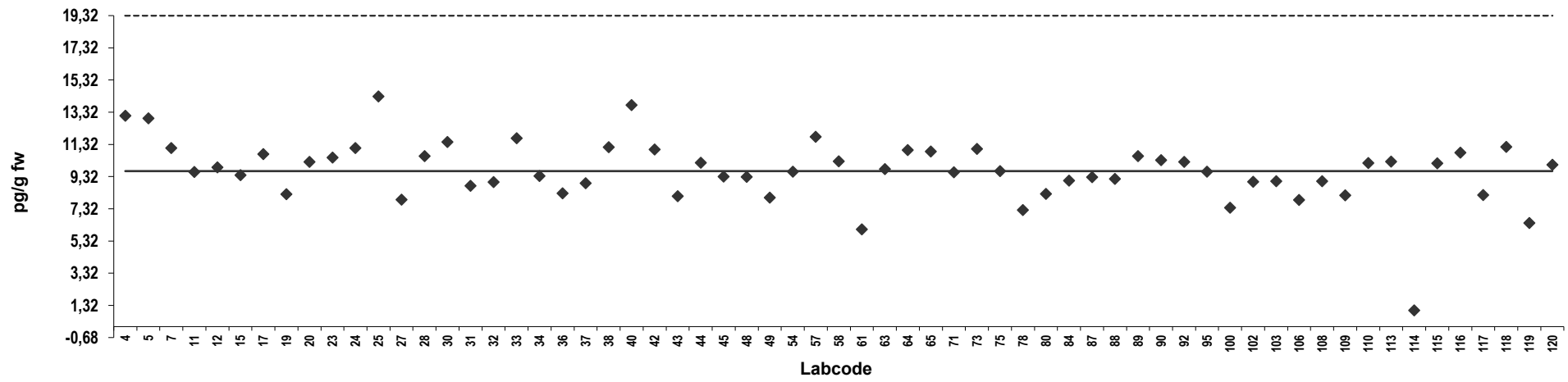
PCB 126

Z-score: PCB 126
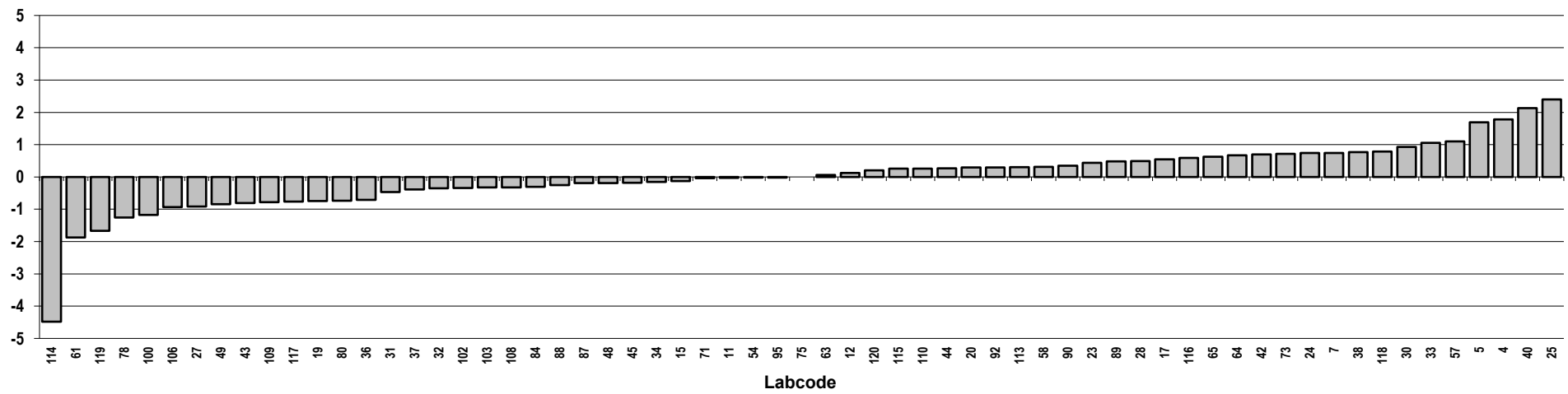
Herring
Congener: PCB 169

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	4,1	1,1		90	3,7	0,59	
5	3,0	-0,47		92	3,7	0,50	
7	4,0	0,92		95	3,2	-0,29	
11	3,3	-0,069		100	0,010	-5,0	ND
12	4,1	1,2		102	3,7	0,53	
15	3,9	0,81		103	3,0	-0,47	
17	3,7	0,55		106	3,2	-0,20	
19	3,3	-0,13		108	3,3	-0,099	
20	3,7	0,48		109	3,3	-0,11	
23	3,3	-0,099		110	2,6	-1,1	
24	3,3	-0,012		113	3,8	0,72	
25	2,6	-1,1		114	0,30	-4,6	
27	7,7	6,5	Outlier,ND	115	4,5	1,7	
28	2,6	-1,1		116	2,5	-1,3	
30	3,8	0,71		117	2,9	-0,67	
31	3,4	0,012		118	4,1	1,2	
32	3,1	-0,38		119	2,3	-1,5	
33	4,6	1,9		120	3,7	0,59	
34	3,4	0,086					
36	3,2	-0,16					
37	2,9	-0,74					
38	4,1	1,2					
40	4,6	1,9					
42	3,7	0,53					
43	2,9	-0,64					
44	3,1	-0,34					
45	3,5	0,24					
48	3,1	-0,37					
49	3,1	-0,32					
54	3,1	-0,38					
57	4,8	2,2					
58	4,2	1,2					
61	2,5	-1,3					
63	3,9	0,86					
64	3,7	0,57					
65	3,2	-0,16					
71	3,6	0,32					
73	4,0	0,98					
75	3,9	0,84					
78	2,5	-1,3					
80	2,5	-1,3					
84	3,5	0,16					
87	3,5	0,27					
88	3,6	0,40					
89	2,7	-1,0					

Consenus statistics	
Consensus median, pg/g	3,3
Median all values pg/g	3,4
Consensus mean, pg/g	3,3
Standard deviation, pg/g	0,82
Relative standard deviation, %	25
No. of values reported	63
No. of values removed	1
No. of reported non-detects	2

PCB 169

Z-score: PCB 169
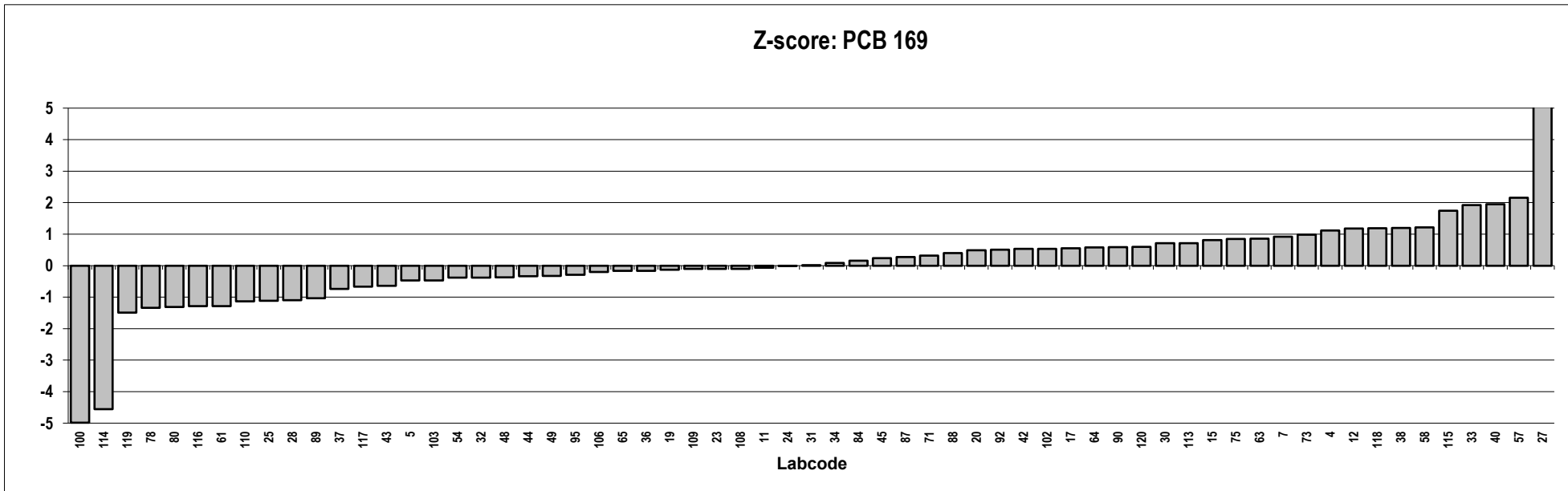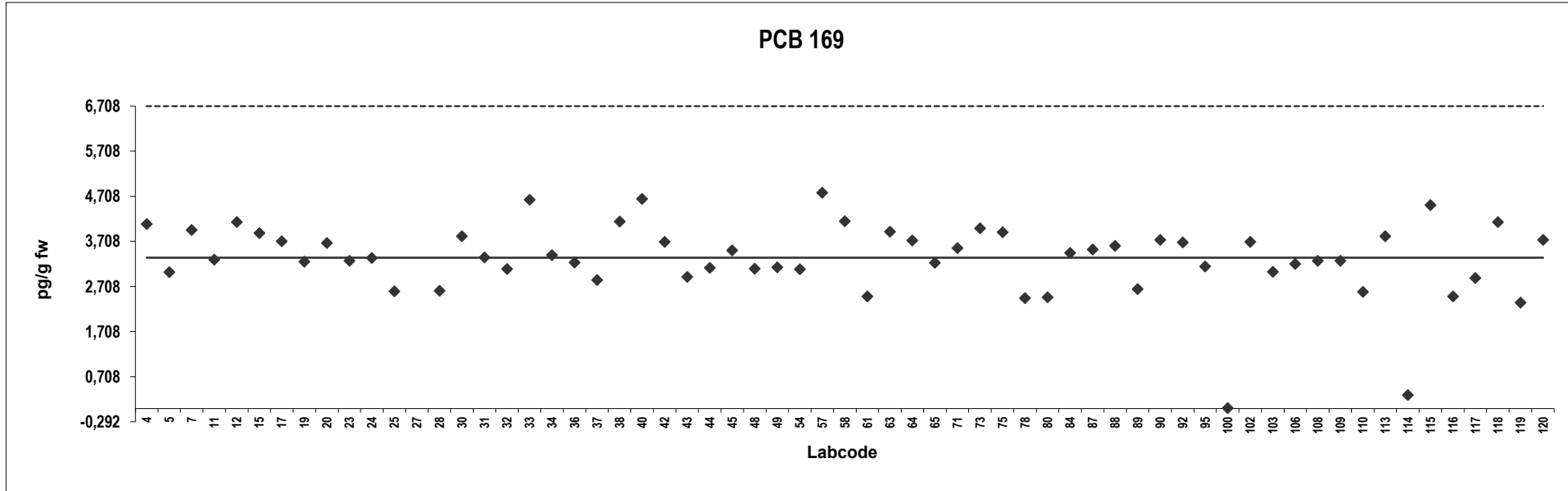
Herring

Congener: PCB 81

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	2,0	13	Outlier,ND	90	0,59	0,37	
5	0,43	-1,1		92	0,62	0,62	
7	0,57	0,17		95	0,44	-1,0	
11	0,45	-0,91		100	0,40	-1,4	
12	0,60	0,42		102	0,61	0,54	
15	0,58	0,26		103	1,0	4,1	
17	0,87	2,9		106	0,50	-0,44	
19	0,46	-0,83		108	0,56	0,039	
20	0,44	-1,0		109	0,49	-0,53	
23	0,57	0,20		110	0,13	-3,8	ND
24	7,5	63	Outlier	113	1,2	5,9	Outlier
25	0,22	-3,0		114	0,10	-4,1	
27	1,6	9,8	Outlier,ND	115	0,30	-2,3	
28	1,0	4,1	ND	116	2,9	22	Outlier
30	1,1	5,2		117	0,49	-0,52	
31	0,55	-0,041		118	0,53	-0,22	
32	0,35	-1,8		119	0,32	-2,1	
33	1,9	12	Outlier	120	0,22	-3,0	
34	0,51	-0,36					
36	0,51	-0,42					
37	0,30	-2,3					
38	0,55	-0,039					
40	0,86	2,8					
42	0,61	0,53					
43	0,67	1,1					
44	0,56	0,075					
45	0,46	-0,87					
48	0,57	0,17					
49	0,58	0,26					
54	0,62	0,62					
57	0,035	-4,7	ND				
58	0,67	1,1					
61	0,52	-0,31					
63	0,62	0,57					
64	0,72	1,6					
65	0,47	-0,77					
71	0,71	1,5					
73	4,8	38	Outlier				
75	0,60	0,44					
78	0,36	-1,7					
80	0,53	-0,20					
84	0,57	0,2					
87	0,95	3,6					
88	0,56	0,10					
89	0,59	0,33					

Consenus statistics

Consensus median, pg/g	0,55
Median all values pg/g	0,57
Consensus mean, pg/g	0,54
Standard deviation, pg/g	0,21
Relative standard deviation, %	39
No. of values reported	63
No. of values removed	7
No. of reported non-detects	5

PCB 81

pg/g fw

Labcode

Z-score: PCB 81
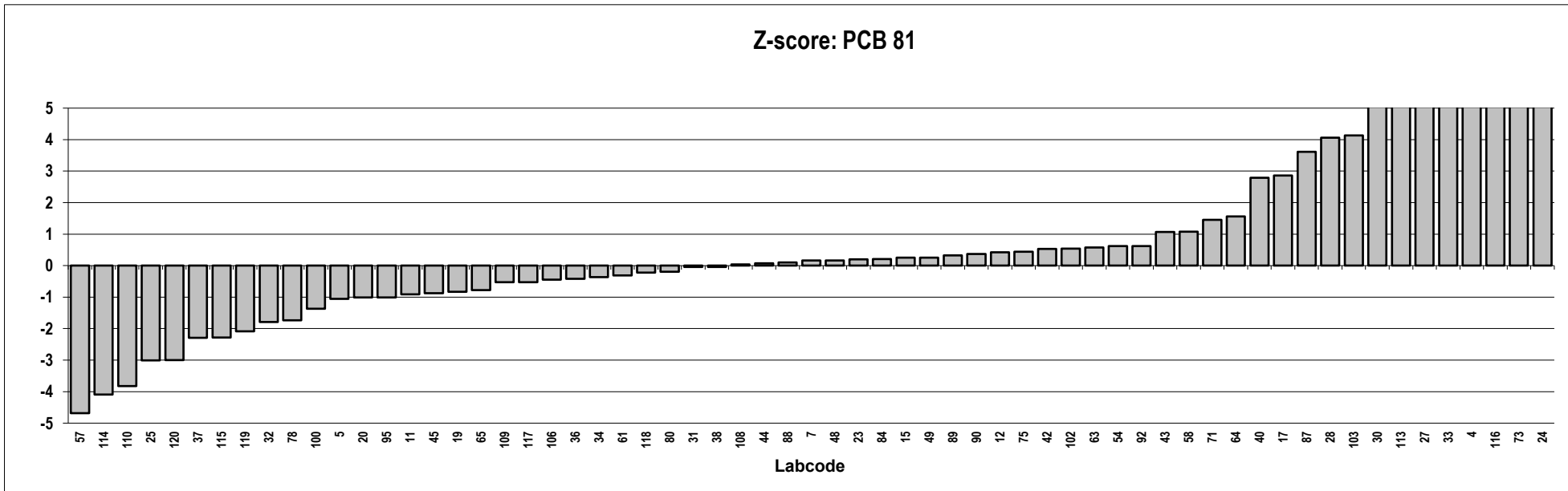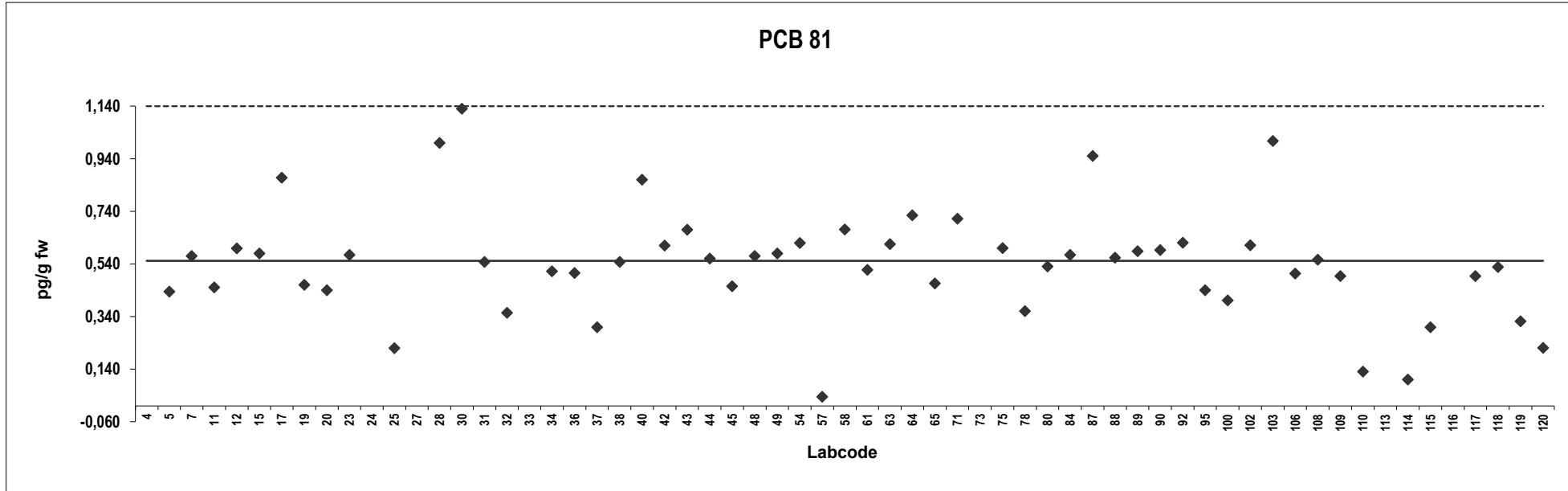
Labcode

Herring

Congener: PCB 105

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	519	1,2		90	470	0,61	
5	518	1,2		92	451	0,38	
7	499	0,95		95	357	-0,74	
11	398	-0,25		100	349	-0,84	
12	520	1,2		102	397	-0,26	
15	443	0,29		103	437	0,21	
17	438	0,22		106	373	-0,55	
19	375	-0,53		108	419	0,00	
20	358	-0,73		109	366	-0,63	
23	440	0,25		110	396	-0,27	
24	457	0,45		113	470	0,61	
25	401	-0,21		114	390	-0,35	
27	405	-0,16		115	409	-0,11	
28	404	-0,18		116	366	-0,63	
30	480	0,73		117	365	-0,65	
31	406	-0,15		118	430	0,14	
32	386	-0,39		119	279	-1,7	
33	556	1,6		120	476	0,68	
34	421	0,025					
36	392	-0,33					
37	362	-0,68					
38	473	0,65					
40	604	2,2					
42	424	0,060					
43	323	-1,1					
44	323	-1,1					
45	338	-0,97					
48	430	0,13					
49	392	-0,32					
54	577	1,9					
57	461	0,50					
58	477	0,69					
61	466	0,56					
63	419	0,00					
64	451	0,38					
65	465	0,55					
71	397	-0,26					
73	444	0,30					
75	438	0,23					
78	407	-0,14					
80	422	0,031					
84	406	-0,15					
87	404	-0,18					
88	393	-0,32					
89	332	-1,0					

| Consenus statistics	
Consensus median, pg/g	419
Median all values pg/g	419
Consensus mean, pg/g	423
Standard deviation, pg/g	61
Relative standard deviation, %	14
No. of values reported	63
No. of values removed	0
No. of reported non-detects	0
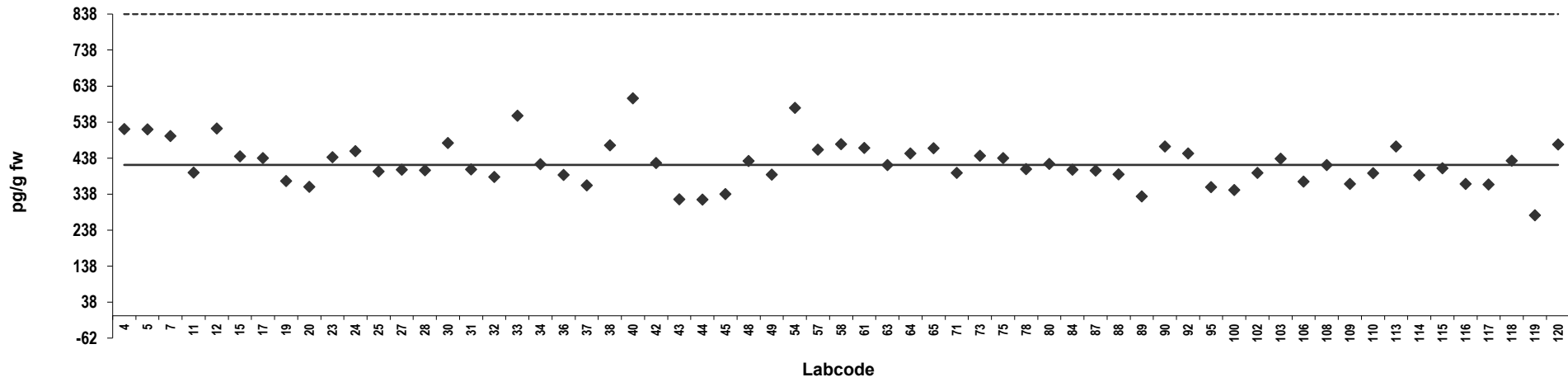
PCB 105

Z-score: PCB 105
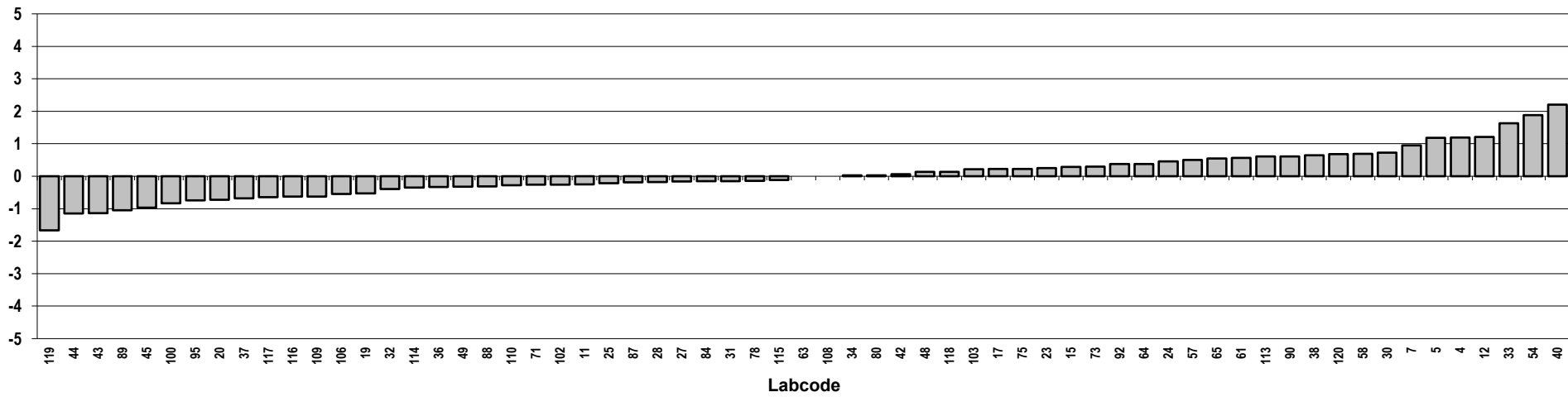
Herring
Congener: PCB 114

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	34	2,3		90	25	0,25	
5	29	1,1		92	24	0,18	
7	25	0,25		95	24	0,16	
11	25	0,31		100	18	-1,2	
12	33	2,0		102	21	-0,48	
15	25	0,25		103	17	-1,3	
17	22	-0,24		106	39	3,3	
19	18	-1,2		108	21	-0,52	
20	31	1,6		109	23	-0,035	
23	26	0,55		110	22	-0,23	
24	28	1,1		113	49	5,5	Outlier
25	18	-1,3		114	47	5,1	ND
27	10	-2,8		115	26	0,50	
28	26	0,65		116	21	-0,43	
30	28	1,0		117	23	-0,073	
31	18	-1,1		118	31	1,7	
32	20	-0,75		119	15	-1,7	
33	59	7,6	Outlier	120	26	0,62	
34	22	-0,20					
36	22	-0,37					
37	23	0,010					
38	19	-0,88					
40	33	2,1					
42	18	-1,1	ND				
43	23	-0,15					
44	26	0,47					
45	16	-1,5					
48	22	-0,29					
49	20	-0,65					
54	22	-0,21					
57	23	-0,010					
58	35	2,4					
61	27	0,87					
63	43	4,2					
64	23	-0,071					
65	24	0,18					
71	18	-1,3					
73	34	2,2					
75	24	0,18					
78	37	2,9					
80	23	-0,050					
84	27	0,74					
87	51	6,0	Outlier				
88	22	-0,24					
89	18	-1,09					

Consenus statistics

Consensus median, pg/g	23
Median all values pg/g	24
Consensus mean, pg/g	25
Standard deviation, pg/g	6,7
Relative standard deviation, %	27
No. of values reported	63
No. of values removed	3
No. of reported non-detects	2

PCB 114

Z-score: PCB 114
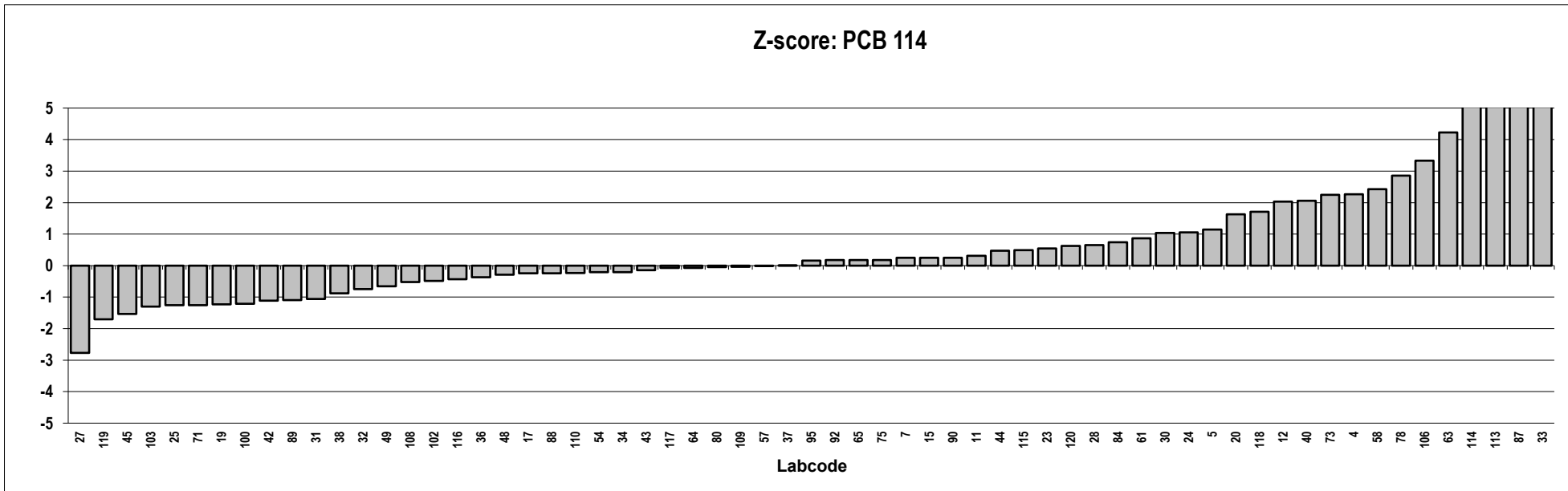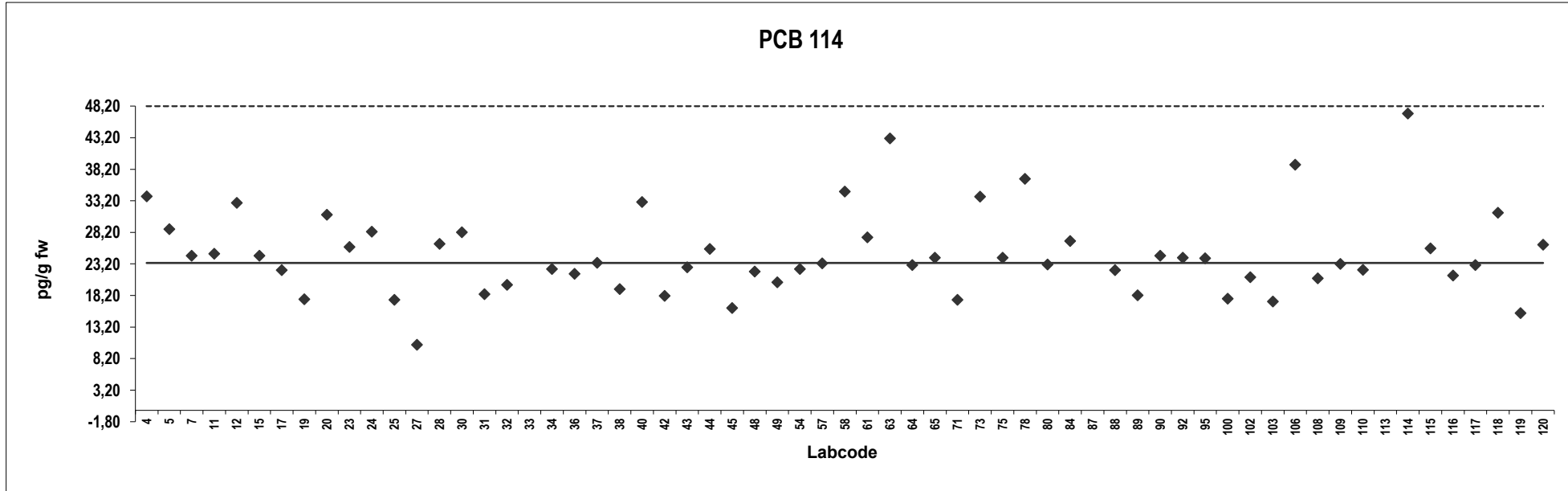
Herring
Congener: PCB 118

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	1948	1,8		90	1556	0,46	
5	1827	1,4		92	1594	0,59	
7	1730	1,1		95	1057	-1,3	
11	1350	-0,27		100	1220	-0,72	
12	1736	1,1		102	1290	-0,48	
15	1340	-0,30		103	118	-4,6	
17	1512	0,30		106	1187	-0,84	
19	1284	-0,50		108	1353	-0,26	
20	1497	0,25		109	1550	0,44	
23	1450	0,084		110	1336	-0,32	
24	1508	0,29		113	1794	1,3	
25	1290	-0,48		114	1500	0,26	
27	1349	-0,27		115	1507	0,28	
28	1310	-0,41		116	1454	0,097	
30	1637	0,74		117	1230	-0,69	
31	1367	-0,21		118	1397	-0,10	
32	1354	-0,25		119	970	-1,6	
33	1759	1,2		120	1625	0,70	
34	1319	-0,37					
36	1278	-0,52					
37	1210	-0,76					
38	1493	0,24					
40	1979	1,9					
42	1450	0,084					
43	1149	-0,97					
44	1484	0,20					
45	1176	-0,88					
48	1500	0,26					
49	1310	-0,41					
54	1524	0,34					
57	996	-1,5					
58	1544	0,41					
61	1454	0,097					
63	1426	0,00					
64	1575	0,52					
65	1475	0,17					
71	1500	0,26					
73	1743	1,1					
75	1370	-0,20					
78	1339	-0,31					
80	1479	0,19					
84	1397	-0,10					
87	1346	-0,28					
88	1357	-0,24					
89	935	-1,7					

Consenus statistics	
Consensus median, pg/g	1426
Median all values pg/g	1426
Consensus mean, pg/g	1409
Standard deviation, pg/g	269
Relative standard deviation, %	19
No. of values reported	63
No. of values removed	0
No. of reported non-detects	0

PCB 118

Z-score: PCB 118
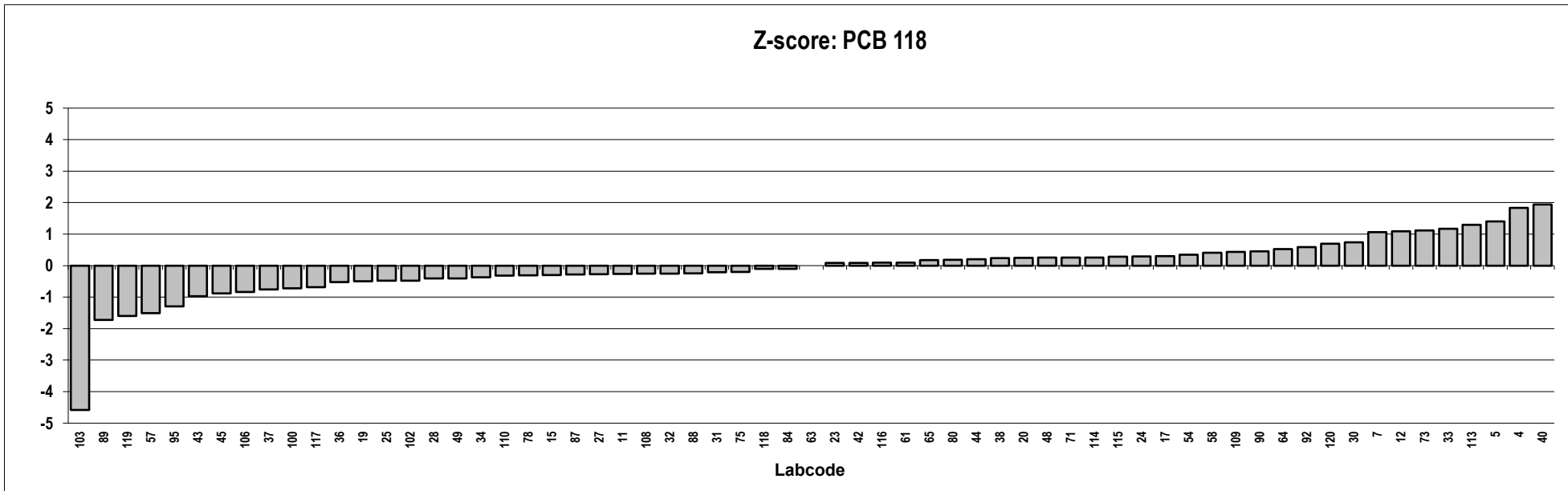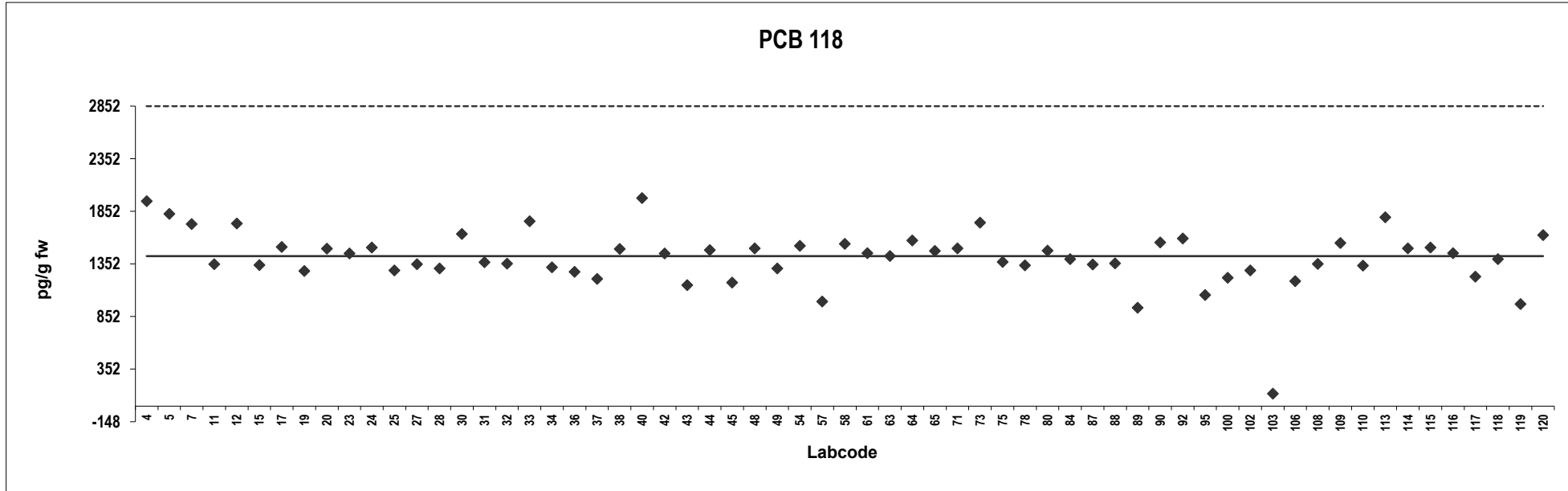
Herring

Congener: PCB 123

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	18	0,52		90	21	1,5	
5	14	-0,59		92	79	20	Outlier
7	20	1,4		95	16	-0,031	
11	18	0,53		100	11	-1,7	
12	0,49	-4,8	ND	102	13	-0,88	
15	18	0,53		103	31	4,8	
17	79	20	Outlier	106	26	3,1	ND
19	16	-0,12		108	12	-1,1	
20	25	3,0		109	6	-3,0	
23	32	5,0		110	23	2,3	
24	14	-0,68		113	19	1,1	
25	15	-0,25		114	240	70	Outlier,ND
27	21	1,5		115	67	16	Outlier
28	72	18	Outlier	116	12	-1,2	
30	15	-0,28		117	12	-1,2	
31	12	-1,3		118	16	-0,11	
32	23	2,3		119	6,8	-2,9	
33	19	0,94		120	42	8,1	Outlier
34	19	0,95					
36	14	-0,59					
37	30	4,4					
38	39	7,3	Outlier				
40	13	-0,85					
42	30	4,4					
43	38	7,0	Outlier				
44	19	0,94					
45	10	-1,8					
48	16	0,031					
49	11	-1,6					
54	19	0,85					
57	0,0075	-5,0	ND				
58	122	33	Outlier				
61	209	61	Outlier				
63	17	0,31					
64	13	-1,0					
65	8,0	-2,5					
71	17	0,35					
73	189	54	Outlier				
75	18	0,53					
78	32	5,0					
80	16	0,079					
84	14	-0,45					
87	11	-1,5					
88	22	2,0					
89	7,3	-2,7					

Consenus statistics	
Consensus median, pg/g	16
Median all values pg/g	18
Consensus mean, pg/g	17
Standard deviation, pg/g	7,1
Relative standard deviation, %	43
No. of values reported	63
No. of values removed	11
No. of reported non-detects	4

PCB 123

Z-score: PCB 123
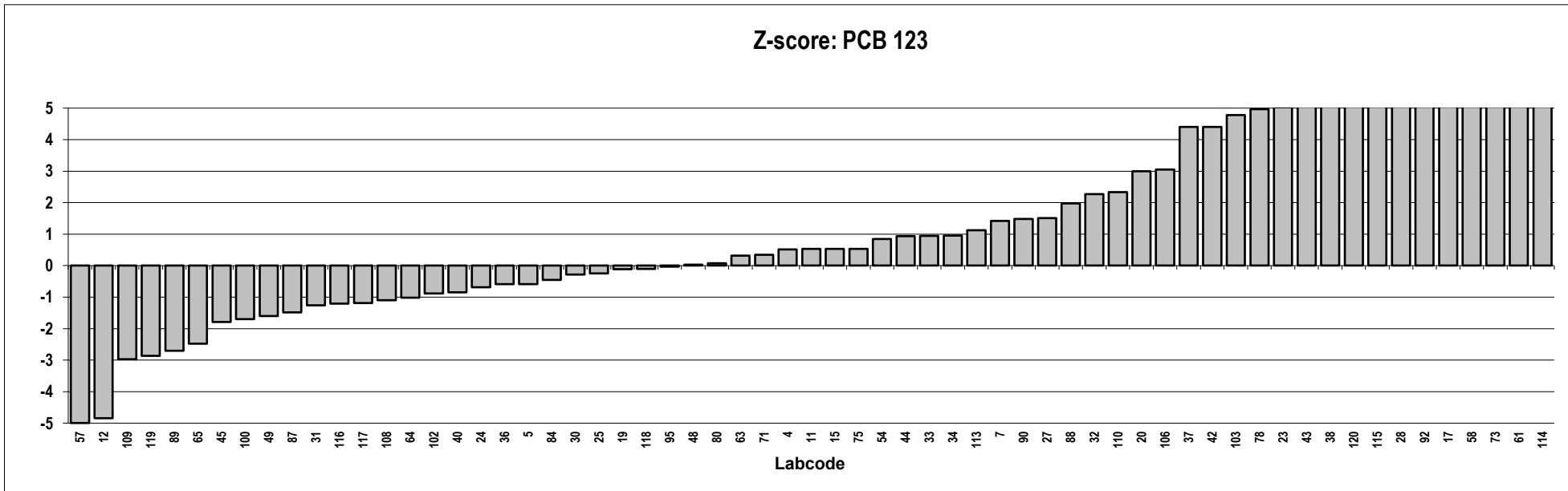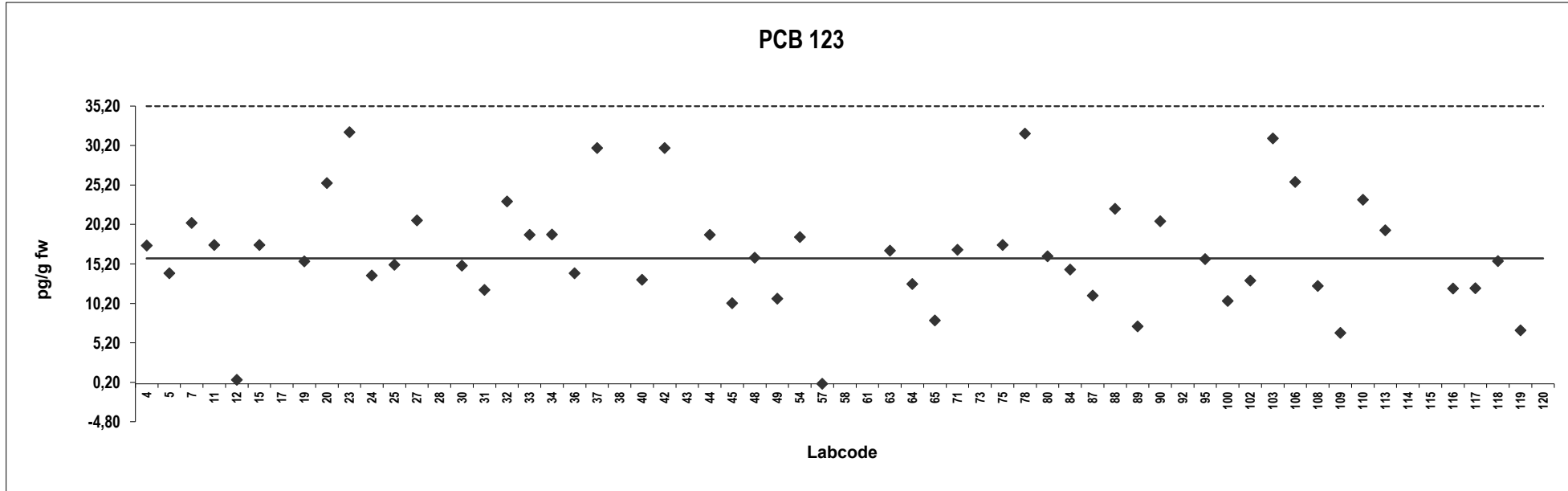
Herring

Congener: PCB 156

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	253	1,2		90	229	0,56	
5	259	1,3		92	230	0,58	
7	225	0,47		95	174	-0,77	
11	190	-0,38		100	166	-0,96	
12	220	0,35		102	213	0,18	
15	213	0,18		103	206	0,00	
17	233	0,67		106	186	-0,48	
19	193	-0,32		108	188	-0,43	
20	212	0,14		109	183	-0,54	
23	200	-0,14		110	190	-0,37	
24	212	0,17		113	219	0,33	
25	147	-1,4		114	190	-0,38	
27	203	-0,071		115	231	0,62	
28	193	-0,31		116	232	0,64	
30	225	0,47		117	172	-0,81	
31	200	-0,13		118	195	-0,26	
32	199	-0,15		119	137	-1,7	
33	243	0,91		120	232	0,64	
34	203	-0,074					
36	213	0,18					
37	191	-0,36					
38	211	0,12					
40	278	1,8					
42	223	0,42					
43	194	-0,29					
44	197	-0,21					
45	177	-0,69					
48	220	0,35					
49	201	-0,11					
54	196	-0,23					
57	221	0,38					
58	221	0,38					
61	218	0,30					
63	204	-0,040					
64	240	0,84					
65	195	-0,27					
71	230	0,59					
73	246	0,97					
75	212	0,15					
78	207	0,03					
80	221	0,37					
84	201	-0,11					
87	196	-0,25					
88	198	-0,18					
89	117	-2,2					

Consensus statistics

Consensus median, pg/g	206
Median all values pg/g	206
Consensus mean, pg/g	207
Standard deviation, pg/g	27
Relative standard deviation, %	13
No. of values reported	63
No. of values removed	0
No. of reported non-detects	0

PCB 156

Z-score: PCB 156
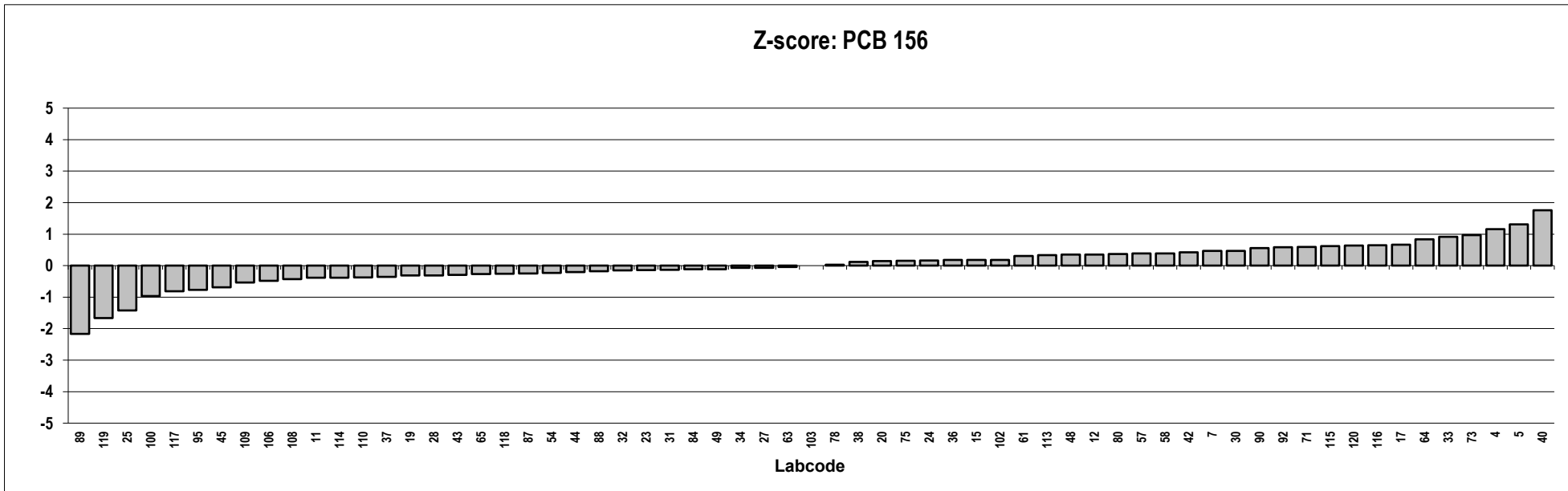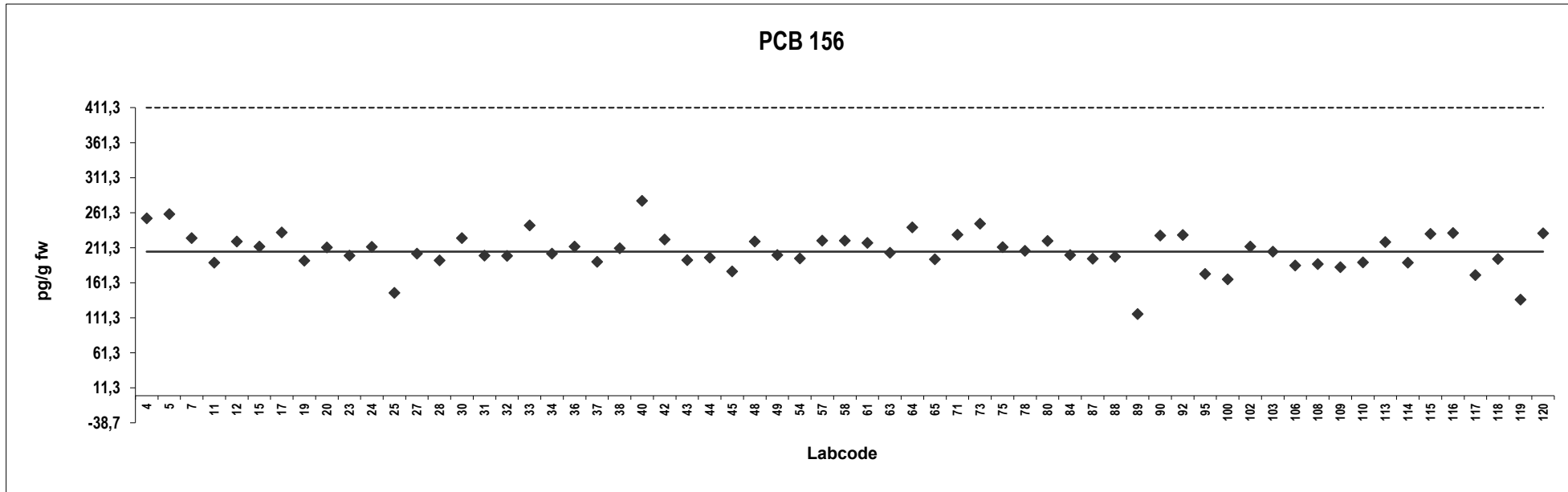
Herring
Congener: PCB 157

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	67	1,6		90	55	0,44	
5	66	1,5		92	53	0,23	
7	58	0,74		95	41	-0,91	
11	47	-0,33		100	40	-1,0	
12	65	1,4		102	43	-0,79	
15	48	-0,22		103	48	-0,24	
17	56	0,60		106	49	-0,11	
19	51	0,099		108	47	-0,34	
20	50	0,00		109	47	-0,36	
23	43	-0,72		110	45	-0,56	
24	52	0,15		113	58	0,71	
25	37	-1,3		114	55	0,45	
27	51	0,050		115	59	0,80	
28	48	-0,24		116	56	0,57	
30	55	0,48		117	46	-0,43	
31	48	-0,19		118	46	-0,41	
32	49	-0,16		119	33	-1,7	
33	67	1,6		120	52	0,18	
34	45	-0,57					
36	51	0,022					
37	47	-0,36					
38	52	0,17					
40	73	2,2					
42	47	-0,30					
43	47	-0,38					
44	49	-0,17					
45	47	-0,32					
48	53	0,26					
49	48	-0,28					
54	57	0,69					
57	52	0,12					
58	58	0,70					
61	48	-0,22					
63	51	0,048					
64	56	0,59					
65	51	0,063					
71	54	0,36					
73	57	0,68					
75	49	-0,10					
78	57	0,68					
80	56	0,50					
84	46	-0,48					
87	48	-0,23					
88	47	-0,37					
89	43	-0,71					

Consenus statistics	
Consensus median, pg/g	50
Median all values pg/g	50
Consensus mean, pg/g	51
Standard deviation, pg/g	7,1
Relative standard deviation, %	14
No. of values reported	63
No. of values removed	0
No. of reported non-detects	0

PCB 157

Z-score: PCB 157
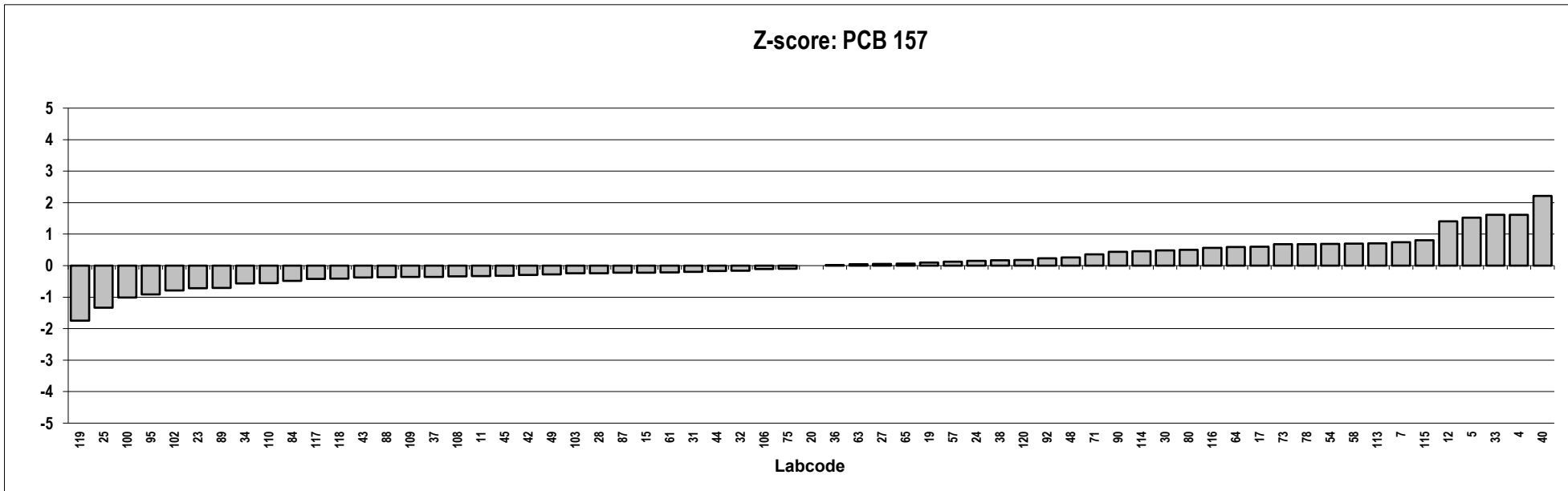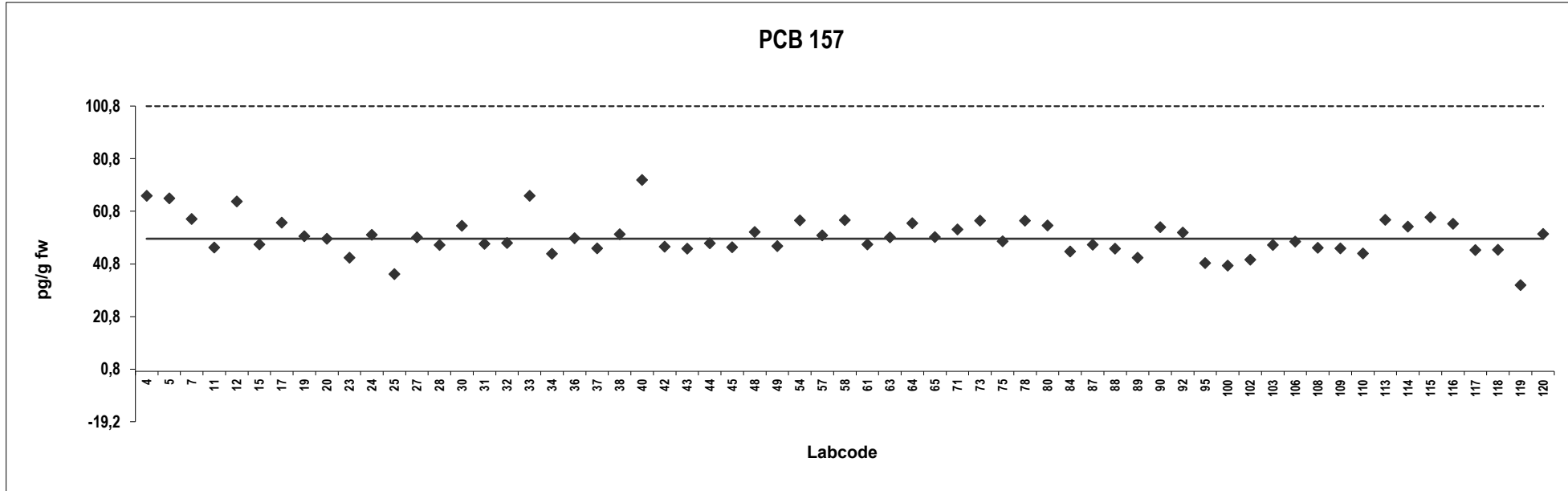
Herring

Congener: PCB 167

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	172	2,0		90	134	0,51	
5	153	1,3		92	134	0,48	
7	135	0,53		95	116	-0,25	
11	114	-0,33		100	106	-0,66	
12	142	0,82		102	121	-0,041	
15	122	0,00		103	118	-0,15	
17	128	0,25		106	124	0,082	
19	112	-0,42		108	136	0,57	
20	114	-0,35		109	103	-0,78	
23	158	1,5		110	122	0,00	
24	122	0,015		113	143	0,88	
25	87	-1,5		114	370	10	Outlier,ND
27	120	-0,091		115	112	-0,40	
28	48	-3,0		116	142	0,81	
30	130	0,33		117	94	-1,1	
31	123	0,050		118	132	0,42	
32	124	0,099		119	83	-1,6	
33	146	0,97		120	136	0,56	
34	118	-0,14					
36	114	-0,32					
37	100	-0,92					
38	409	12	Outlier				
40	111	-0,45					
42	119	-0,12					
43	124	0,072					
44	115	-0,28					
45	112	-0,43					
48	140	0,74					
49	127	0,20					
54	113	-0,37					
57	0,50	-5,0	ND				
58	122	0,0037					
61	125	0,12					
63	124	0,082					
64	132	0,42					
65	119	-0,13					
71	103	-0,78					
73	147	1,0					
75	125	0,12					
78	119	-0,12					
80	128	0,26					
84	118	-0,16					
87	126	0,16					
88	113	-0,37					
89	99	-0,95					

Consenus statistics	
Consensus median, pg/g	122
Median all values pg/g	122
Consensus mean, pg/g	120
Standard deviation, pg/g	24
Relative standard deviation, %	20
No. of values reported	63
No. of values removed	2
No. of reported non-detects	2

PCB 167

Z-score: PCB 167
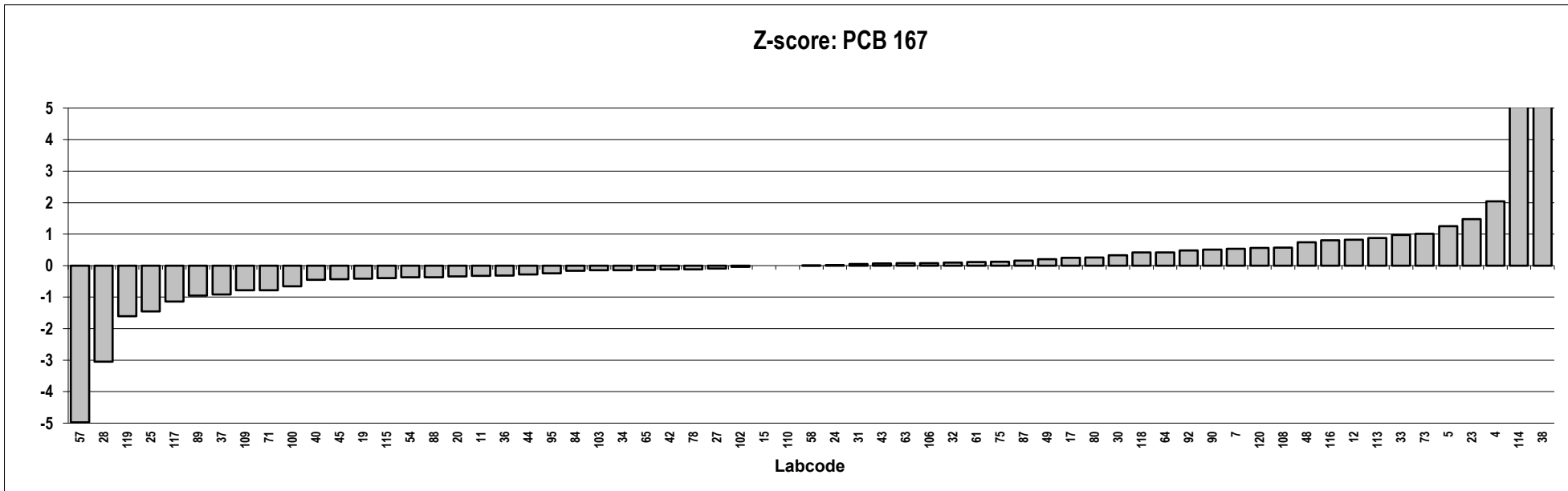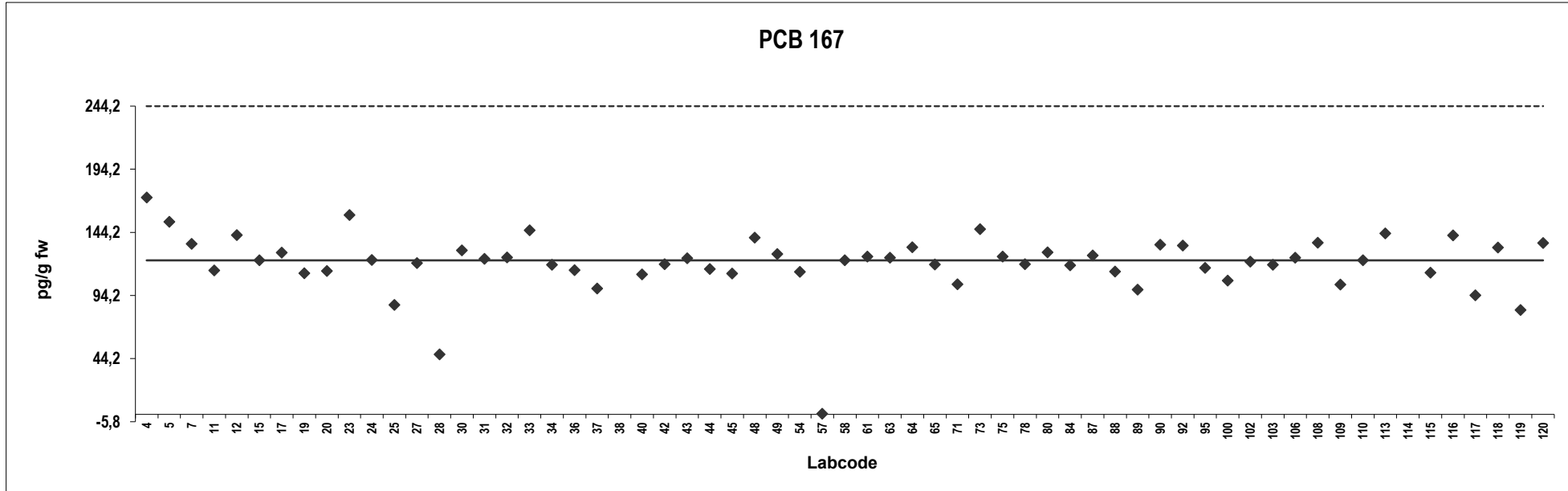
Herring

Congener: PCB 189

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	29	1,3		90	26	0,61	
5	30	1,5		92	26	0,50	
7	25	0,43		95	22	-0,28	
11	24	0,10		100	18	-1,2	
12	25	0,47		102	22	-0,20	
15	25	0,38		103	22	-0,18	
17	27	0,88		106	25	0,28	
19	19	-0,89		108	22	-0,33	
20	23	-0,043		109	22	-0,17	
23	24	0,060		110	23	-0,14	
24	25	0,32		113	27	0,73	
25	20	-0,80		114	21	-0,48	ND
27	21	-0,45		115	23	-0,056	
28	22	-0,26		116	25	0,29	
30	25	0,44		117	20	-0,76	
31	23	-0,055		118	26	0,65	
32	22	-0,20		119	15	-1,7	
33	30	1,4		120	24	0,23	
34	25	0,30					
36	23	-0,12					
37	21	-0,48					
38	24	0,23					
40	34	2,2					
42	20	-0,61					
43	23	0,00					
44	23	-0,073					
45	19	-0,80					
48	21	-0,48					
49	23	-0,16					
54	27	0,81					
57	27	0,74					
58	26	0,53					
61	23	-0,0123					
63	23	-0,026					
64	22	-0,19					
65	22	-0,25					
71	26	0,68					
73	28	1,0					
75	25	0,32					
78	23	0,017					
80	27	0,73					
84	24	0,083					
87	24	0,060					
88	22	-0,36					
89	19	-0,99					

Consenus statistics	
Consensus median, pg/g	23
Median all values pg/g	23
Consensus mean, pg/g	24
Standard deviation, pg/g	3,1
Relative standard deviation, %	13
No. of values reported	63
No. of values removed	0
No. of reported non-detects	1

PCB 189

Z-score: PCB 189
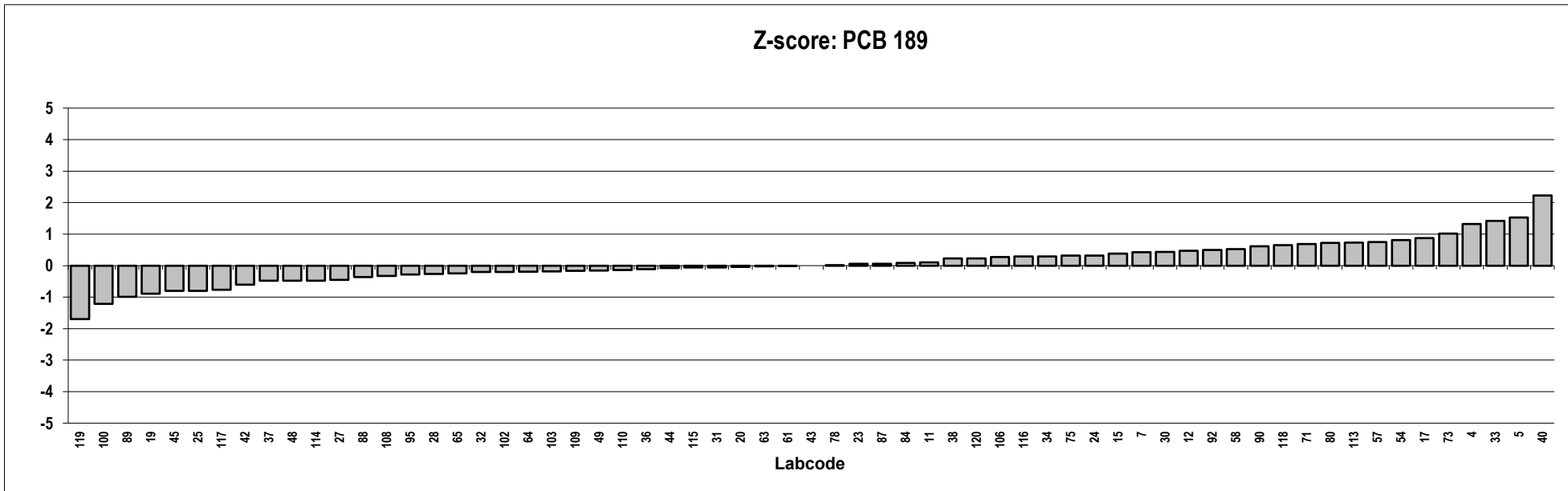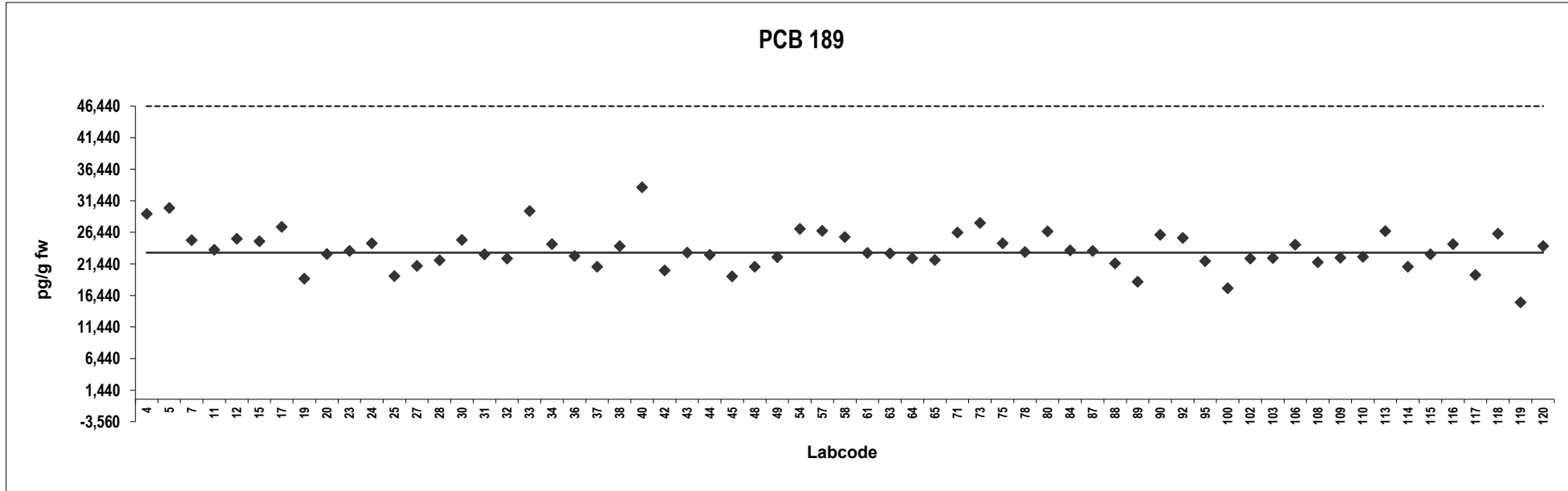
Herring
Congener: PCB 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	300	1,4		105	230	-0,085	
5	300	1,4		106	191	-0,92	
7	327	2,0		108	257	0,49	
11	0,25	-5,0		109	205	-0,61	
12	265	0,67		110	395	3,4	
15	284	1,1		113	313	1,7	
17	259	0,54		114	245	0,24	
19	172	-1,3		115	596	7,7	Outlier
23	223	-0,24		117	312	1,7	
24	292	1,2		118	355	2,6	
25	219	-0,32		120	185	-1,1	
27	160	-1,6					
28	231	-0,064					
30	254	0,43					
31	205	-0,62					
32	155	-1,7					
34	249	0,31					
37	231	-0,064					
38	222	-0,26					
40	354	2,6					
42	232	-0,043					
43	27	-4,4					
44	195	-0,83					
45	207	-0,58					
48	240	0,13					
49	212	-0,47					
54	203	-0,66					
57	246	0,26					
58	284	1,1					
61	1290	23	Outlier				
63	254	0,43					
64	332	2,1					
65	306	1,5					
71	319	1,8					
75	292	1,2					
78	290	1,2					
80	236	0,043					
81	210	-0,51					
84	264	0,63					
87	188	-0,98					
90	0,20	-5,0					
95	200	-0,73					
100	199	-0,75					
102	215	-0,41					
103	109	-2,7					

Consensus statistics	
Consensus median, pg/g	234
Median all values pg/g	238
Consensus mean, pg/g	234
Standard deviation, pg/g	78
Relative standard deviation, %	33
No. of values reported	56
No. of values removed	2
No. of reported non-detects	0

PCB 28

Z-score: PCB 28
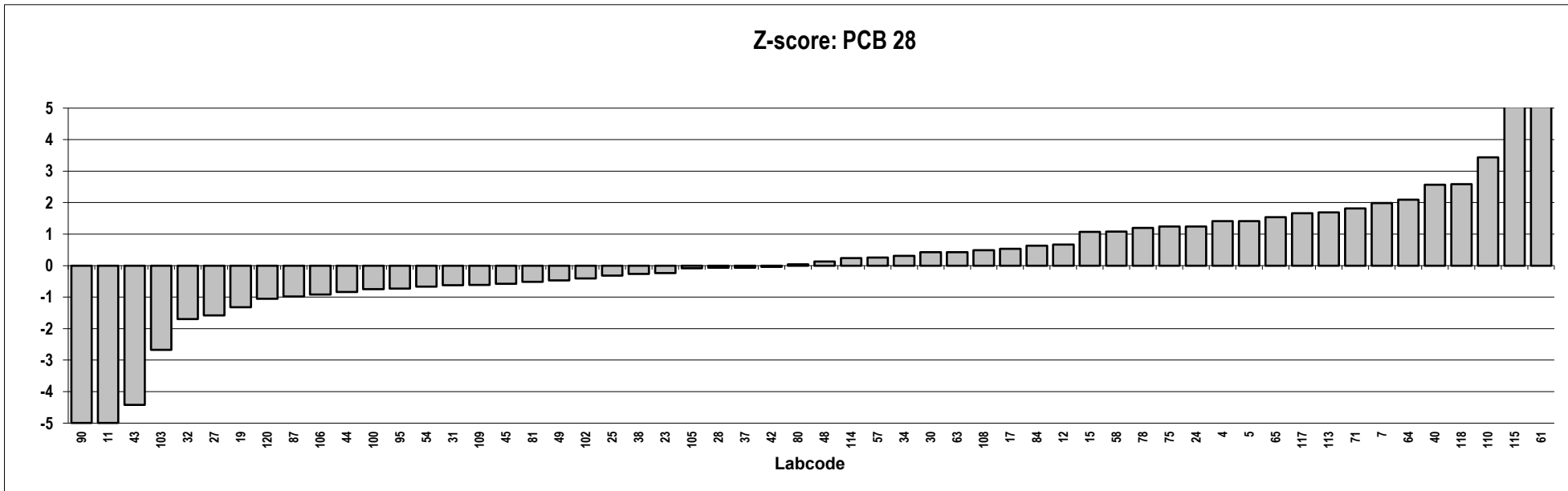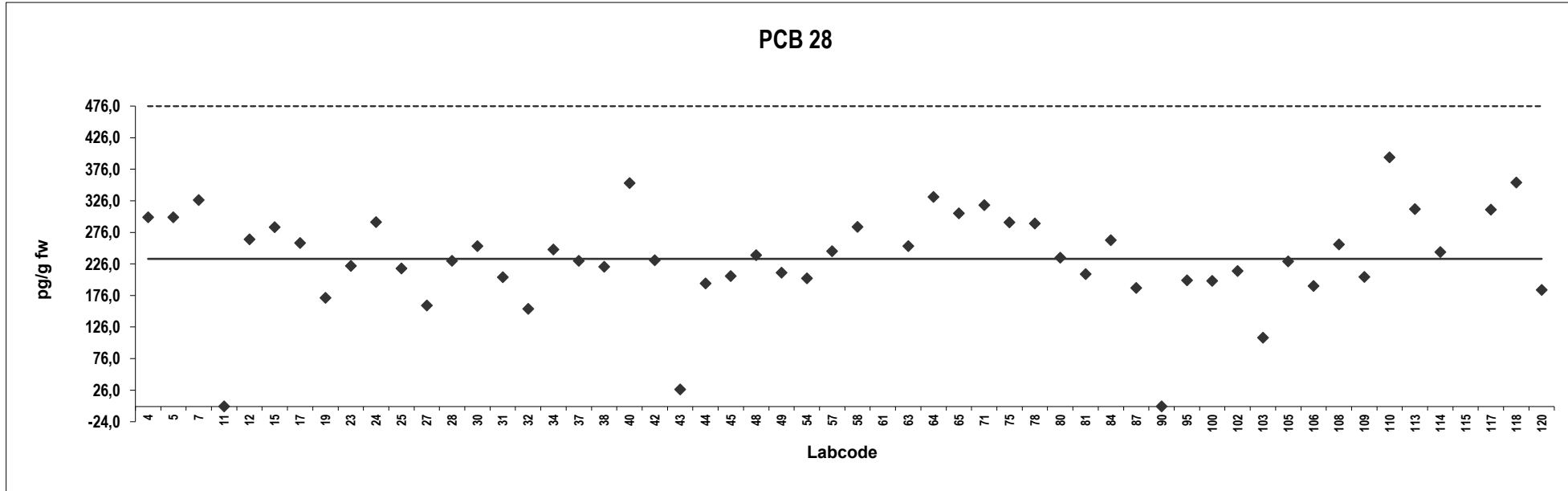
Herring

Congener: PCB 52

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	700	1,8		105	410	-1,0	
5	700	1,8		106	486	-0,29	
7	619	1,0		108	563	0,46	
11	0,55	-5,0		109	476	-0,39	
12	652	1,3		110	712	1,9	
15	560	0,43		113	698	1,8	
17	569	0,51		114	640	1,2	
19	423	-0,91		115	598	0,80	
23	519	0,029		117	533	0,17	
24	471	-0,44		118	565	0,47	
25	374	-1,4		120	661	1,4	
27	509	-0,068					
28	394	-1,2					
30	562	0,45					
31	500	-0,16					
32	455	-0,60					
34	435	-0,78					
37	511	-0,048					
38	474	-0,41					
40	724	2,0					
42	556	0,39					
43	69	-4,3					
44	612	0,93					
45	442	-0,71					
48	590	0,72					
49	494	-0,21					
54	519	0,029					
57	498	-0,18					
58	570	0,52					
61	692	1,7					
63	538	0,22					
64	531	0,14					
65	506	-0,10					
71	679	1,6					
75	566	0,48					
78	483	-0,32					
80	502	-0,14					
81	430	-0,83					
84	604	0,86					
87	465	-0,49					
90	0,51	-5,0					
95	465	-0,49					
100	404	-1,1					
102	513	-0,029					
103	317	-1,9					

Consenus statistics	
Consensus median, pg/g	516
Median all values pg/g	516
Consensus mean, pg/g	510
Standard deviation, pg/g	149
Relative standard deviation, %	29
No. of values reported	56
No. of values removed	0
No. of reported non-detects	0

PCB 52

Z-score: PCB 52
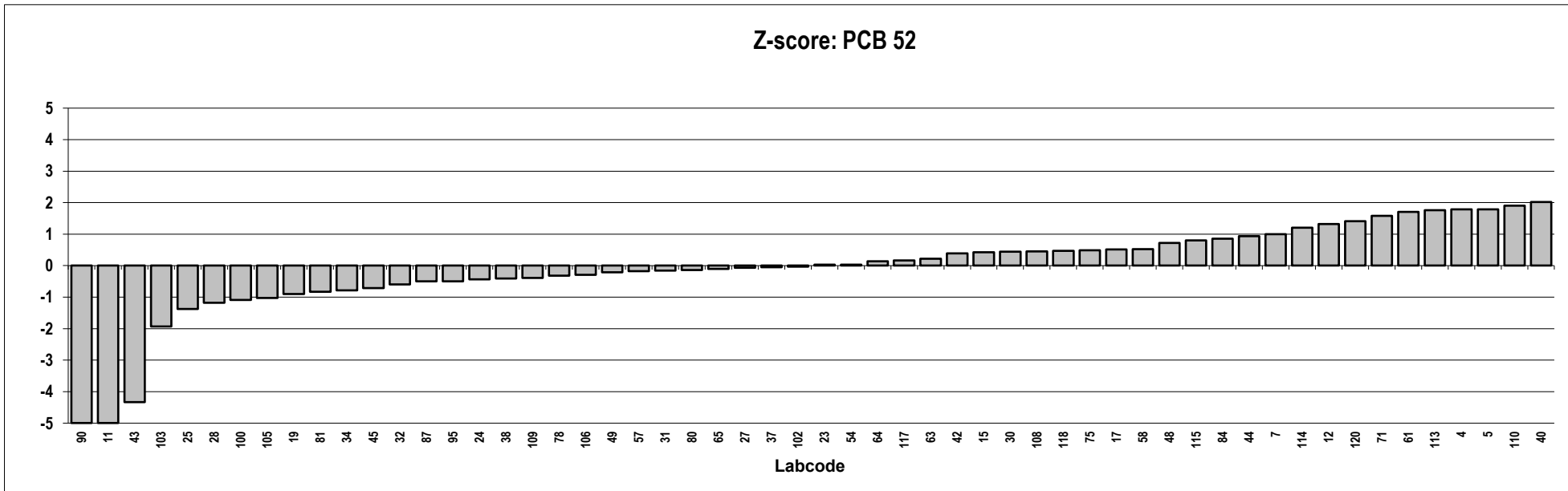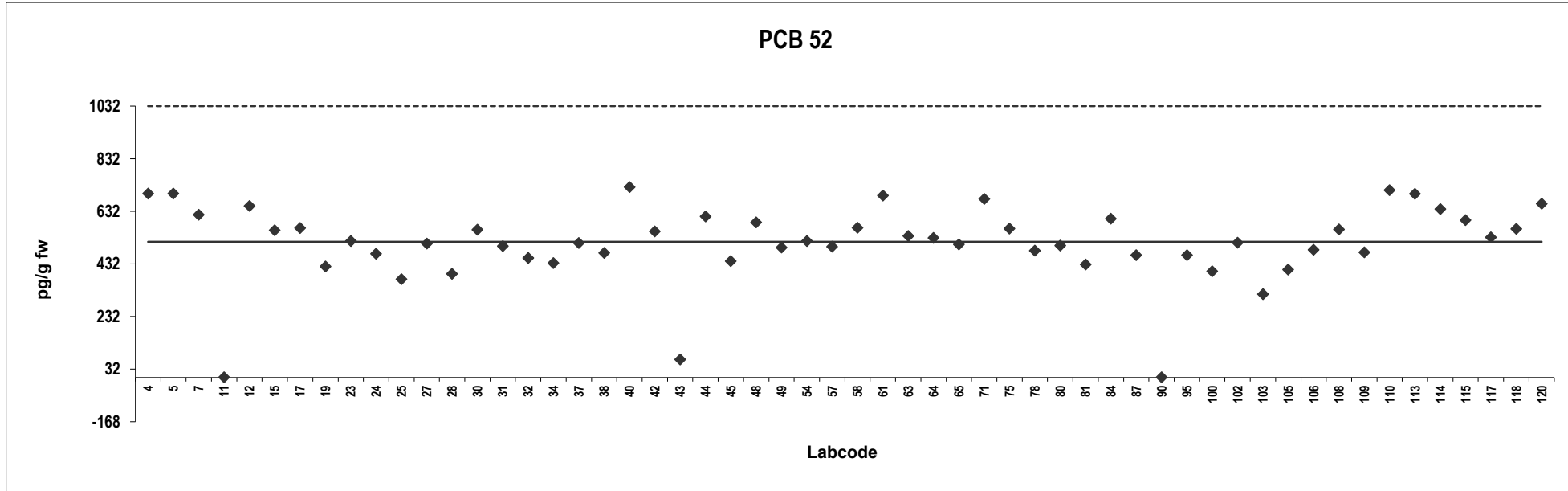
Herring

Congener: PCB 101

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	2680	2,0		105	1600	-0,84	
5	2680	2,0		106	1550	-0,97	
7	1597	-0,85		108	2120	0,51	
11	1,8	-5,0		109	1927	0,0087	
12	2545	1,6		110	1920	-0,0087	
15	2170	0,64		113	2421	1,3	
17	2150	0,59		114	2200	0,72	
19	1854	-0,18		115	2034	0,29	
23	2150	0,59		117	1961	0,098	
24	1859	-0,17		118	1751	-0,45	
25	1270	-1,7		120	2325	1,0	
27	1673	-0,65					
28	583	-3,5					
30	1962	0,10					
31	1919	-0,010					
32	1742	-0,47					
34	1855	-0,18					
37	1910	-0,035					
38	1867	-0,15					
40	2766	2,2					
42	2060	0,36					
43	971	-2,5					
44	1890	-0,086					
45	1695	-0,59					
48	2200	0,72					
49	1780	-0,37					
54	2321	1,0					
57	1460	-1,2					
58	2034	0,29					
61	3318	3,6					
63	1990	0,17					
64	2049	0,33					
65	2047	0,32					
71	2090	0,43					
75	2220	0,77					
78	1946	0,059					
80	1868	-0,14					
81	1640	-0,74					
84	2342	1,1					
87	1715	-0,54					
90	2,0	-5,0					
95	1660	-0,68					
100	1570	-0,92					
102	2000	0,20					
103	1707	-0,56					

Consenus statistics	
Consensus median, pg/g	1923
Median all values pg/g	1923
Consensus mean, pg/g	1886
Standard deviation, pg/g	557
Relative standard deviation, %	30
No. of values reported	56
No. of values removed	0
No. of reported non-detects	0

PCB 101

Z-score: PCB 101
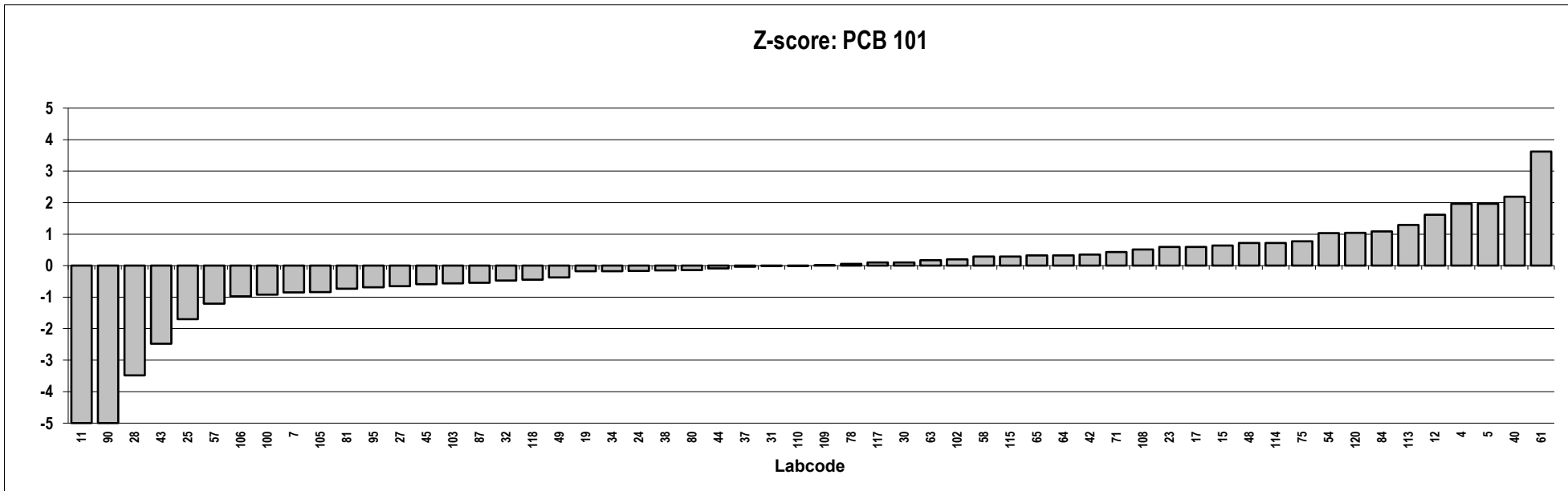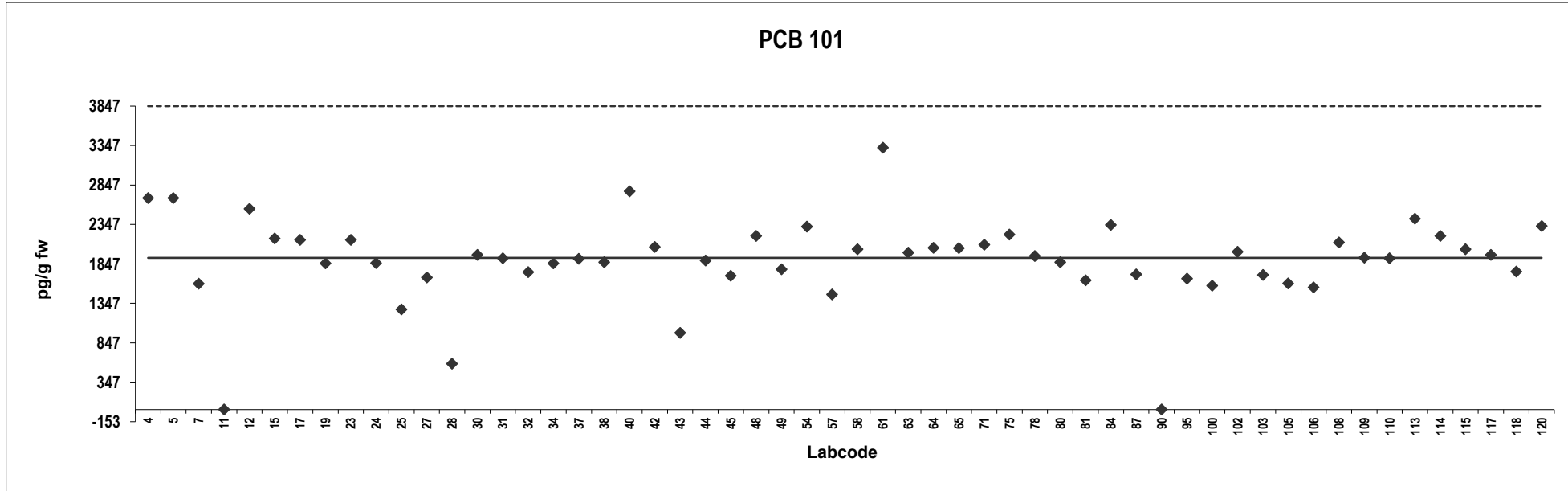
Herring

Congener: PCB 138

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	4350	1,7		105	2600	-1,0	
5	4350	1,7		106	3135	-0,19	
7	3283	0,033		108	3080	-0,28	
11	3,1	-5,0		109	3134	-0,20	
12	4105	1,3		110	2978	-0,43	
15	3670	0,63		113	3781	0,80	
17	6190	4,5		114	4400	1,7	
19	2855	-0,62		115	3698	0,67	
23	3160	-0,16		117	3010	-0,39	
24	2919	-0,53		118	1256	-3,1	
25	2310	-1,5		120	3106	-0,24	
27	3137	-0,19					
28	4000	1,1					
30	3064	-0,30					
31	2961	-0,46					
32	2505	-1,2					
34	3238	-0,036					
37	3400	0,21					
38	4188	1,4					
40	4444	1,8					
42	2860	-0,62					
43	4650	2,1					
44	4280	1,6					
45	2781	-0,74					
48	3400	0,21					
49	2660	-0,92					
54	3726	0,71					
57	4797	2,4					
58	3295	0,052					
61	3597	0,51					
63	3529	0,41					
64	3689	0,66					
65	2647	-0,94					
71	2940	-0,49					
75	3680	0,64					
78	4442	1,8					
80	3205	-0,087					
81	3240	-0,033					
84	3786	0,80					
87	3627	0,56					
90	3,1	-5,0					
95	2750	-0,78					
100	3950	1,1					
102	3150	-0,17					
103	3477	0,33					

Consenus statistics

Consensus median, pg/g	3262
Median all values pg/g	3262
Consensus mean, pg/g	3330
Standard deviation, pg/g	990
Relative standard deviation, %	30
No. of values reported	56
No. of values removed	0
No. of reported non-detects	0

PCB 138

Z-score: PCB 138
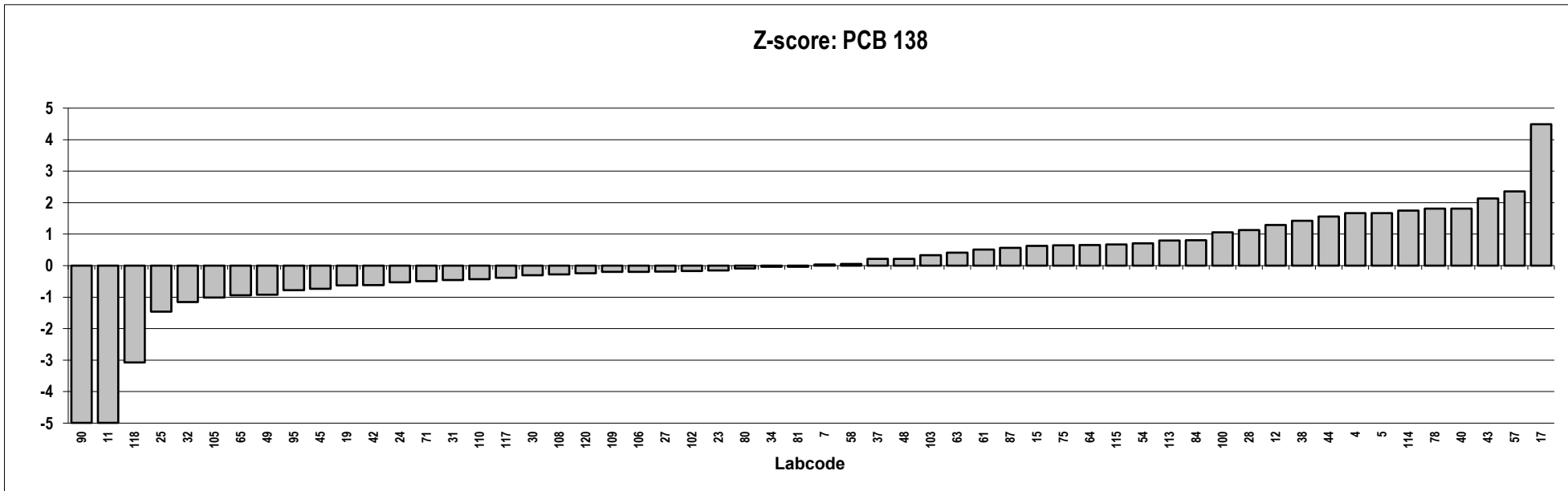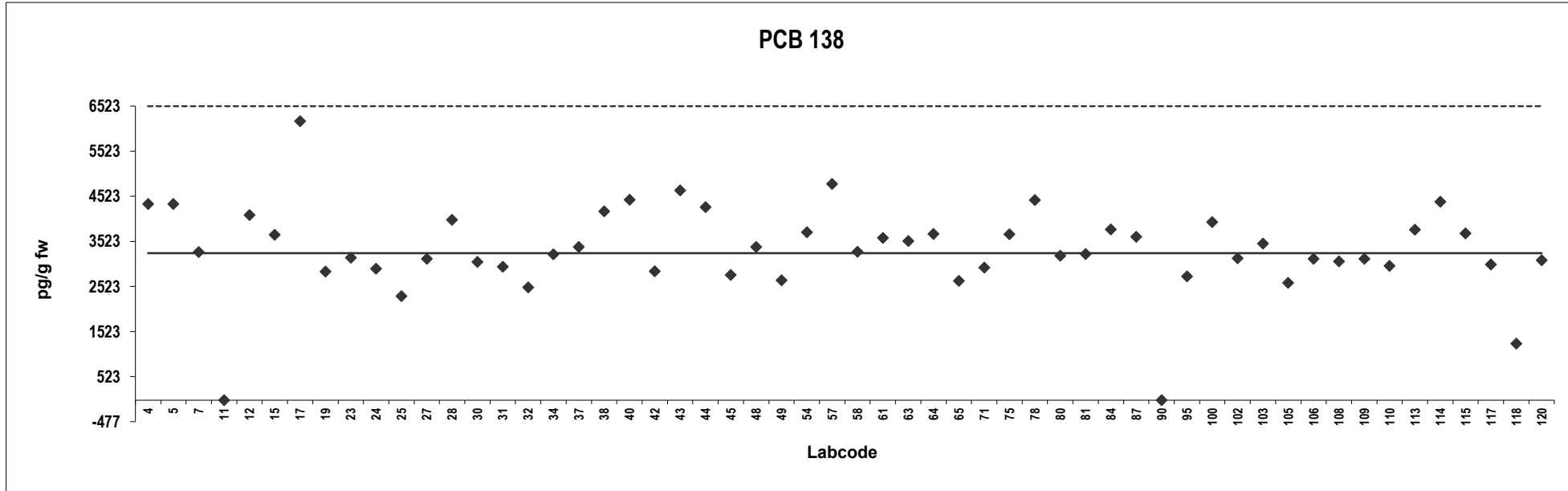
Herring

Congener: PCB 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	701	-4,3		105	4400	-0,72	
5	701	-4,3		106	4720	-0,40	
7	5215	0,077		108	5620	0,47	
11	4,9	-5,0		109	5570	0,42	
12	7044	1,9		110	5170	0,033	
15	5820	0,67		113	6167	1,0	
17	5715	0,56		114	5500	0,35	
19	12602	7,3	Outlier	115	5125	-0,011	
23	4780	-0,35		117	4878	-0,25	
24	5300	0,16		118	4130	-0,98	
25	3580	-1,5		120	5517	0,37	
27	5285	0,14					
28	5030	-0,10					
30	5485	0,34					
31	4998	-0,13					
32	4656	-0,47					
34	5138	0,0023					
37	5140	0,0039					
38	4708	-0,42					
40	7010	1,8					
42	5850	0,70					
43	3991	-1,1					
44	4900	-0,23					
45	4142	-0,97					
48	5700	0,55					
49	4330	-0,78					
54	6222	1,1					
57	5830	0,68					
58	5285	0,15					
61	581	-4,4					
63	4988	-0,14					
64	6157	0,99					
65	4789	-0,34					
71	5230	0,092					
75	5830	0,68					
78	4539	-0,58					
80	4789	-0,34					
81	4220	-0,89					
84	6069	0,91					
87	5499	0,35					
90	4,9	-5,0					
95	4500	-0,62					
100	4630	-0,49					
102	5280	0,14					
103	5136	0,00					

Consenus statistics	
Consensus median, pg/g	5136
Median all values pg/g	5137
Consensus mean, pg/g	4756
Standard deviation, pg/g	1550
Relative standard deviation, %	33
No. of values reported	56
No. of values removed	1
No. of reported non-detects	0

PCB 153

pg/g fw

Labcode

Z-score: PCB 153
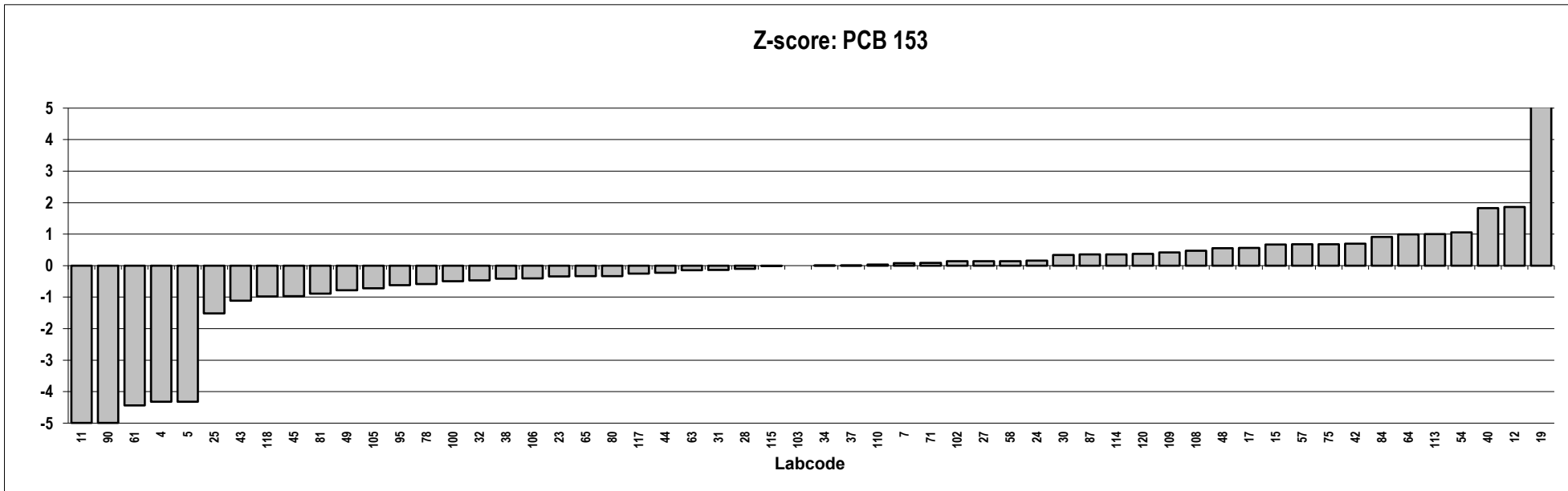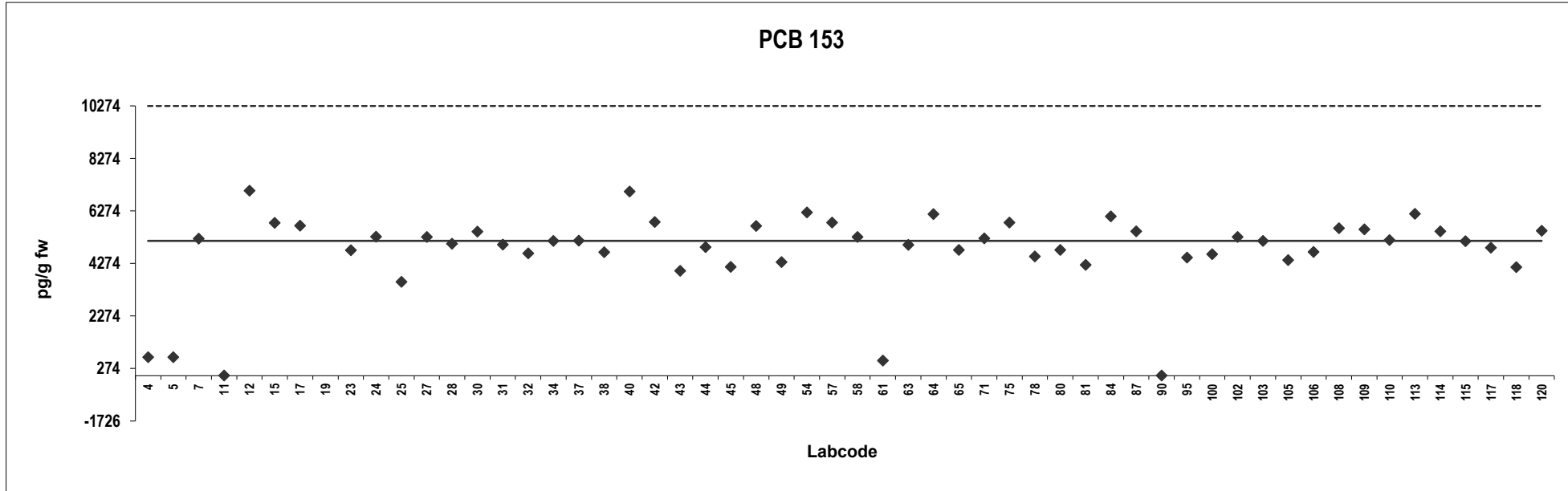
Labcode

Herring

Congener: PCB 180

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	141	-4,4		105	820	-1,4	
5	141	-4,4		106	917	-0,94	
7	1486	1,6		108	1190	0,26	
11	1,1	-5,0		109	1060	-0,31	
12	1415	1,3		110	1260	0,57	
15	1290	0,71		113	1267	0,60	
17	1231	0,45		114	1300	0,75	
19	1810	3,0		115	923	-0,92	
23	1350	0,97		117	1089	-0,19	
24	1211	0,36		118	1039	-0,41	
25	827	-1,3		120	1131	0,0023	
27	738	-1,7					
28	1170	0,17					
30	1353	0,98					
31	1013	-0,52					
32	1358	1,0					
34	1030	-0,44					
37	1150	0,086					
38	934	-0,87					
40	1630	2,2					
42	1220	0,40					
43	1136	0,024					
44	1110	-0,092					
45	959	-0,76					
48	1300	0,75					
49	1050	-0,36					
54	1363	1,0					
57	1098	-0,14					
58	1226	0,42					
61	675	-2,0					
63	1130	-0,0023					
64	1409	1,2					
65	1077	-0,24					
71	1360	1,0					
75	1260	0,57					
78	1177	0,21					
80	1056	-0,33					
81	950	-0,80					
84	1336	0,91					
87	1039	-0,40					
90	1,2	-5,0					
95	1000	-0,58					
100	964	-0,74					
102	1130	-0,0023					
103	1207	0,34					

Consenus statistics

Consensus median, pg/g	1131
Median all values pg/g	1131
Consensus mean, pg/g	1080
Standard deviation, pg/g	349
Relative standard deviation, %	32
No. of values reported	56
No. of values removed	0
No. of reported non-detects	0

PCB 180

Z-score: CB 180
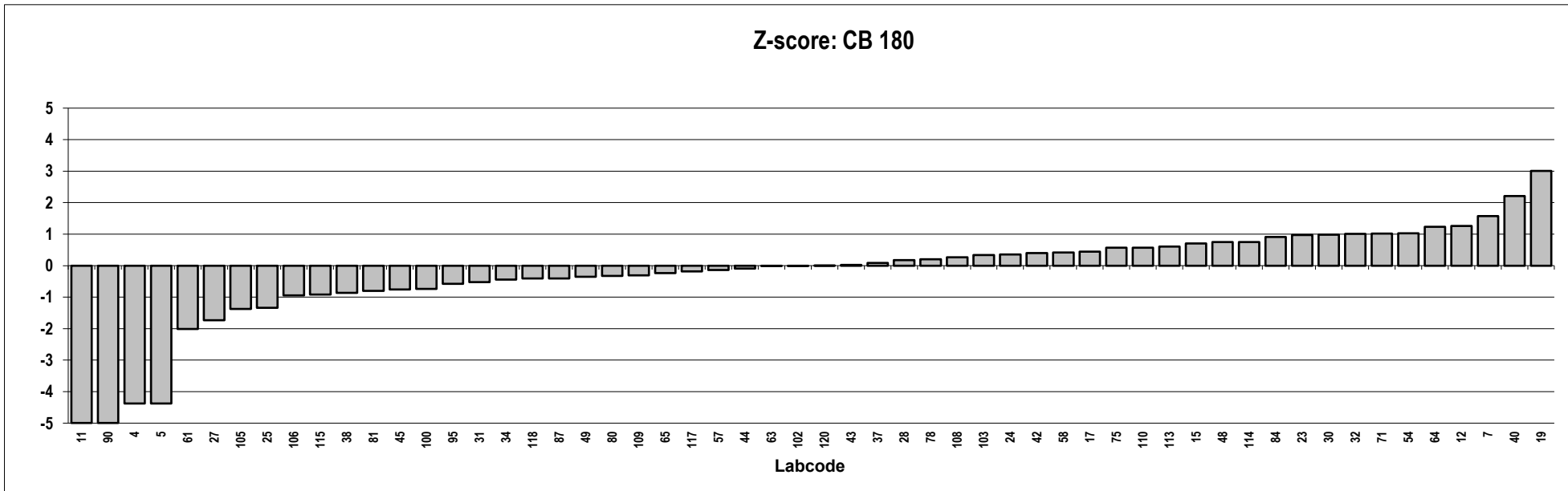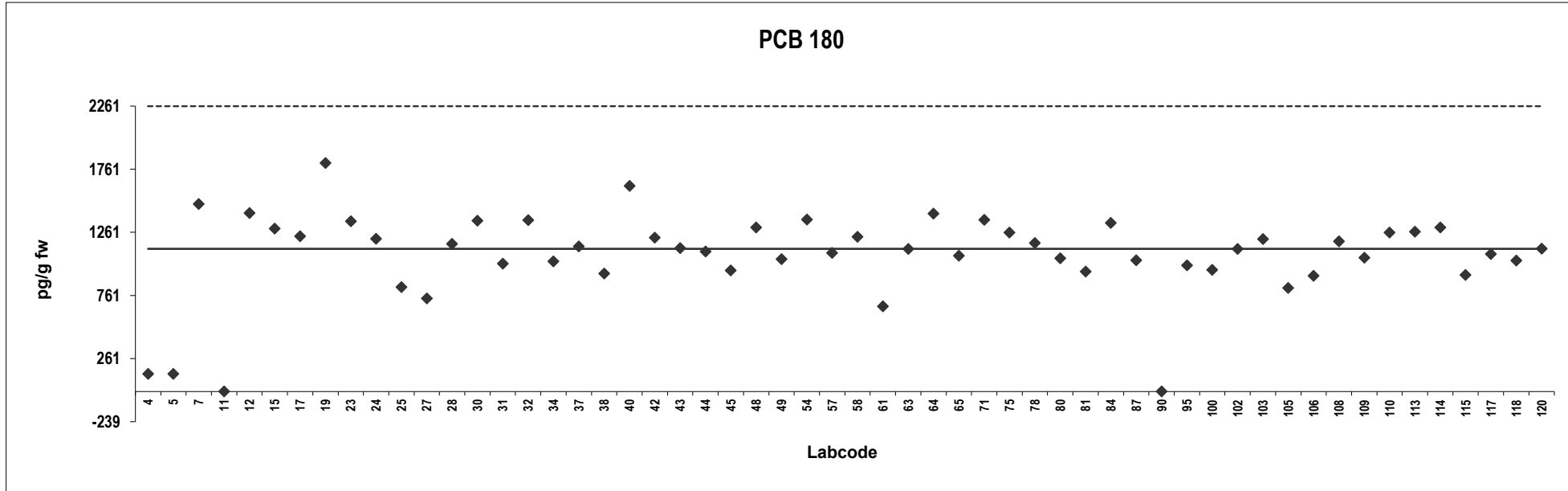
Herring
Congener: PBDE 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	10	0,54					
19	10	0,65					
23	14	2,9					
25	7,9	-0,62					
30	9,0	-0,042					
31	9,5	0,26					
36	9,8	0,41					
37	9,1	0,042					
40	13	2,2					
42	6,3	-1,5	ND				
43	3,8	-2,9					
49	6,7	-1,3					
54	8,7	-0,20					
57	8,2	-0,46					
63	9,8	0,41					
65	9,7	0,37					
71	2,1	-3,8					
78	11	0,98					
81	8,0	-0,57					
90	8,5	-0,32					
95	7,3	-0,96					
100	0,13	-4,9					
102	9,7	0,35					
108	24	8,4	Outlier				
113	13	2,1					
115	26	9,3	Outlier				
116	8,9	-0,096					

Consenus statistics

Consensus median, pg/g	9,0
Median all values pg/g	9,1
Consensus mean, pg/g	8,6
Standard deviation, pg/g	3,1
Relative standard deviation, %	36
No. of values reported	27
No. of values removed	2
No. of reported non-detects	1

PBDE 28

Z-score: PBDE 28
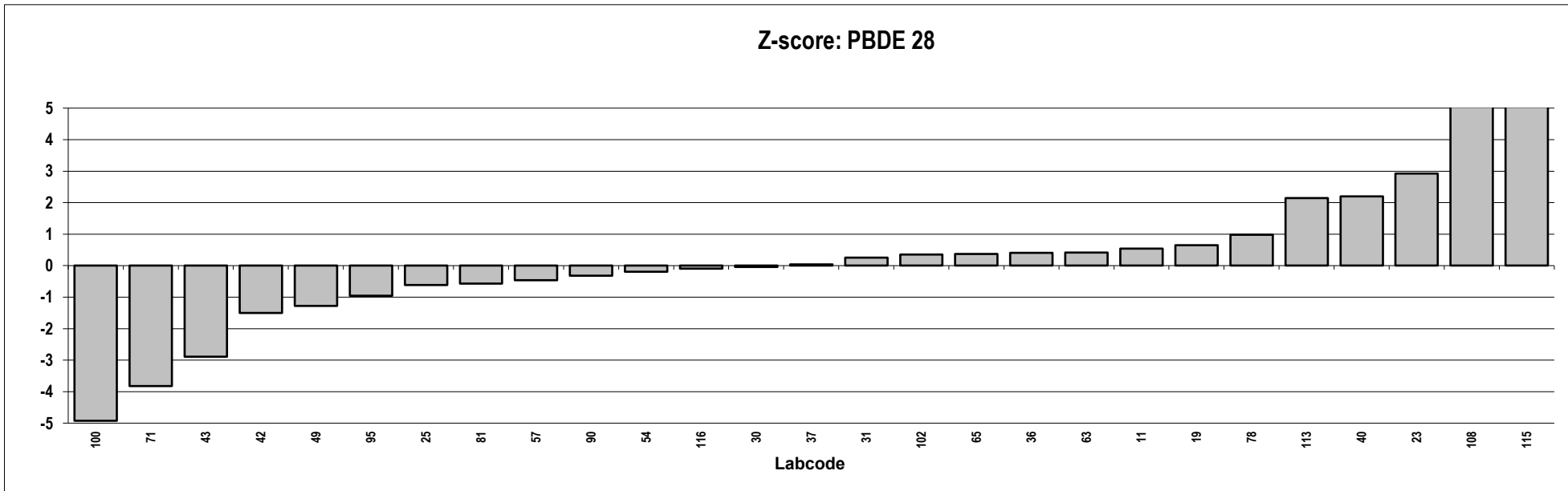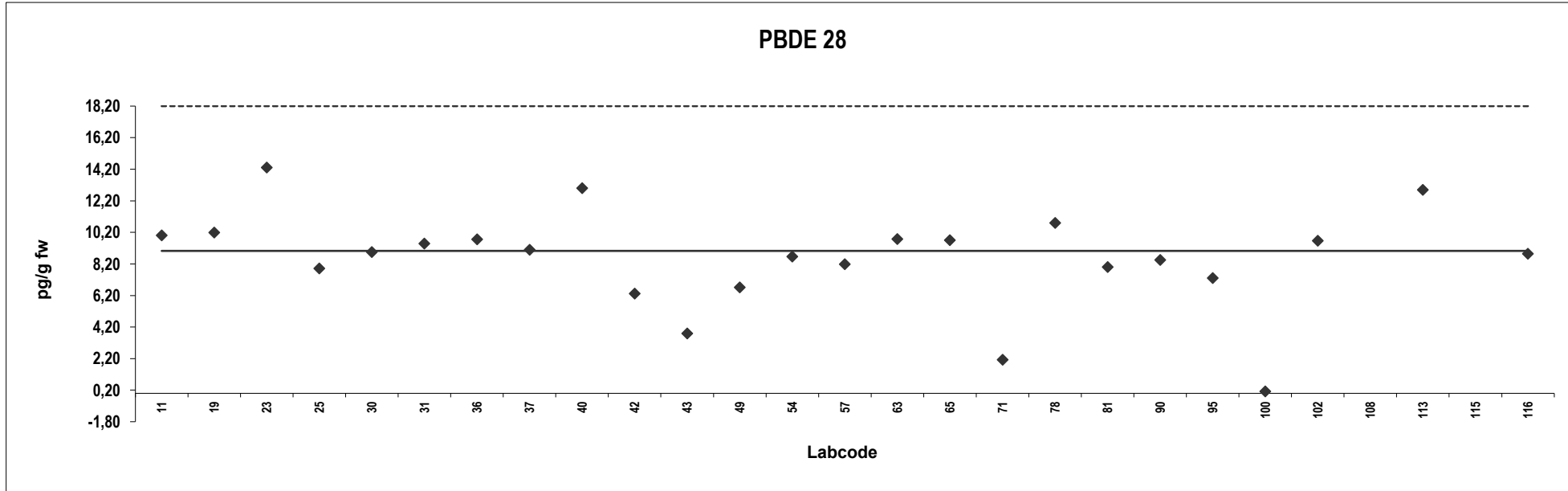
Herring

Congener: PBDE 47

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	331	0,50					
19	325	0,41					
23	301	0,00					
25	320	0,31					
30	320	0,32					
31	324	0,38					
36	295	-0,10					
37	254	-0,78					
40	469	2,8					
42	432	2,2					
43	273	-0,46					
49	254	-0,78					
54	289	-0,20					
57	295	-0,10					
63	301	0,0066					
65	305	0,059					
71	2,0	-5,0					
78	378	1,3					
81	292	-0,15					
90	262	-0,64					
95	287	-0,23					
100	248	-0,88					
102	285	-0,27					
108	501	3,3					
113	299	-0,033					
115	301	0,0058					
116	303	0,028					

Consenus statistics

Consensus median, pg/g	301
Median all values pg/g	301
Consensus mean, pg/g	305
Standard deviation, pg/g	86
Relative standard deviation, %	28
No. of values reported	27
No. of values removed	0
No. of reported non-detects	0

PBDE 47

Z-score: PBDE 47
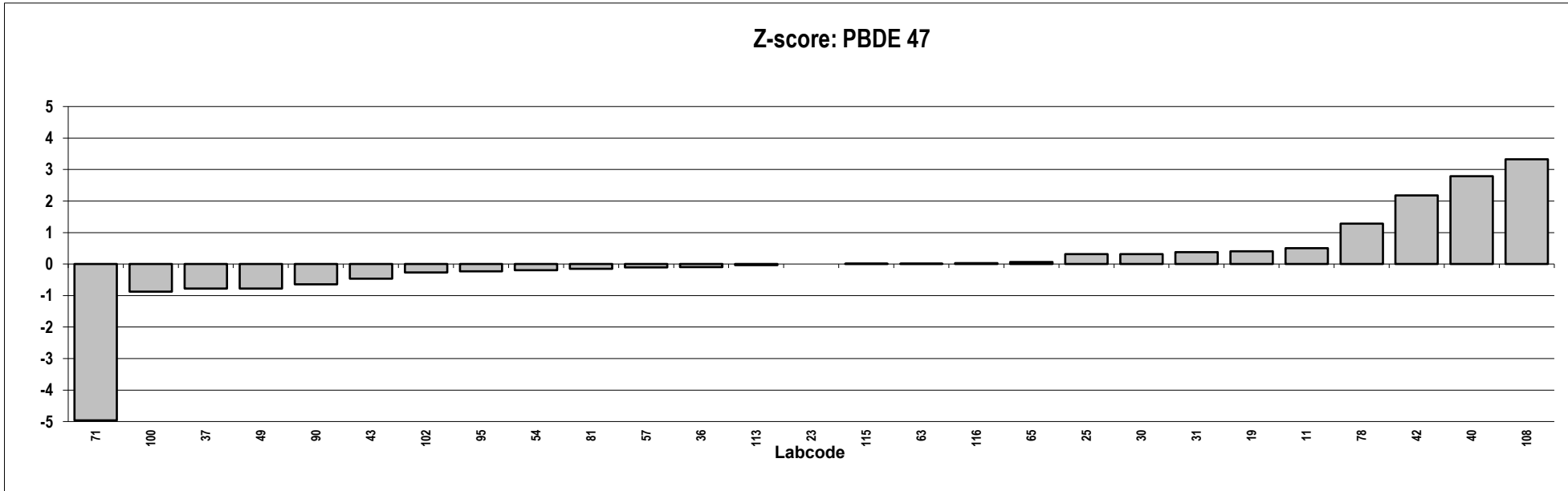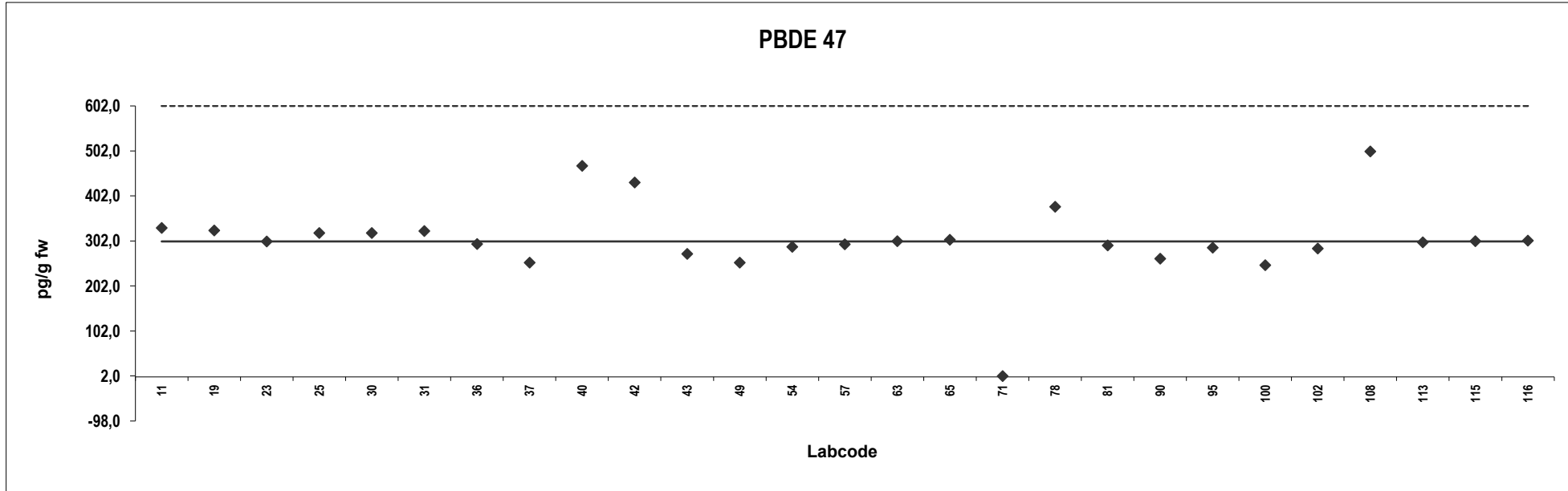
Herring

Congener: PBDE 99

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	69	0,13					
19	72	0,39					
23	70	0,23					
25	68	0,045					
30	65	-0,16					
31	70	0,20					
36	65	-0,16					
37	58	-0,70					
40	96	2,2					
42	132	4,8					
43	65	-0,18					
49	51	-1,2					
54	79	0,91					
57	67	-0,039					
63	67	0,00					
65	67	0,016					
71	2,0	-4,8					
78	71	0,28					
81	56	-0,83					
90	52	-1,2					
95	60	-0,56					
100	50	-1,3					
102	53	-1,1					
108	93	1,9					
113	74	0,47					
115	68	0,084					
116	64	-0,22					

Consenus statistics

Consensus median, pg/g	67
Median all values pg/g	67
Consensus mean, pg/g	67
Standard deviation, pg/g	21
Relative standard deviation, %	31
No. of values reported	27
No. of values removed	0
No. of reported non-detects	0

PBDE 99

Z-score: PBDE 99
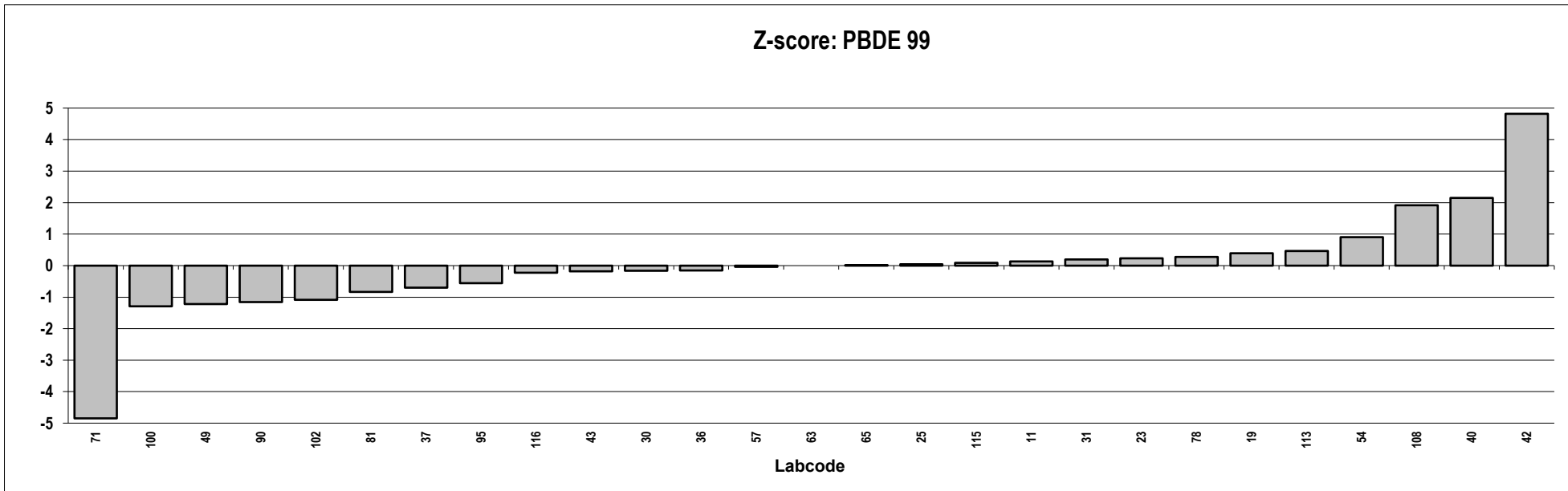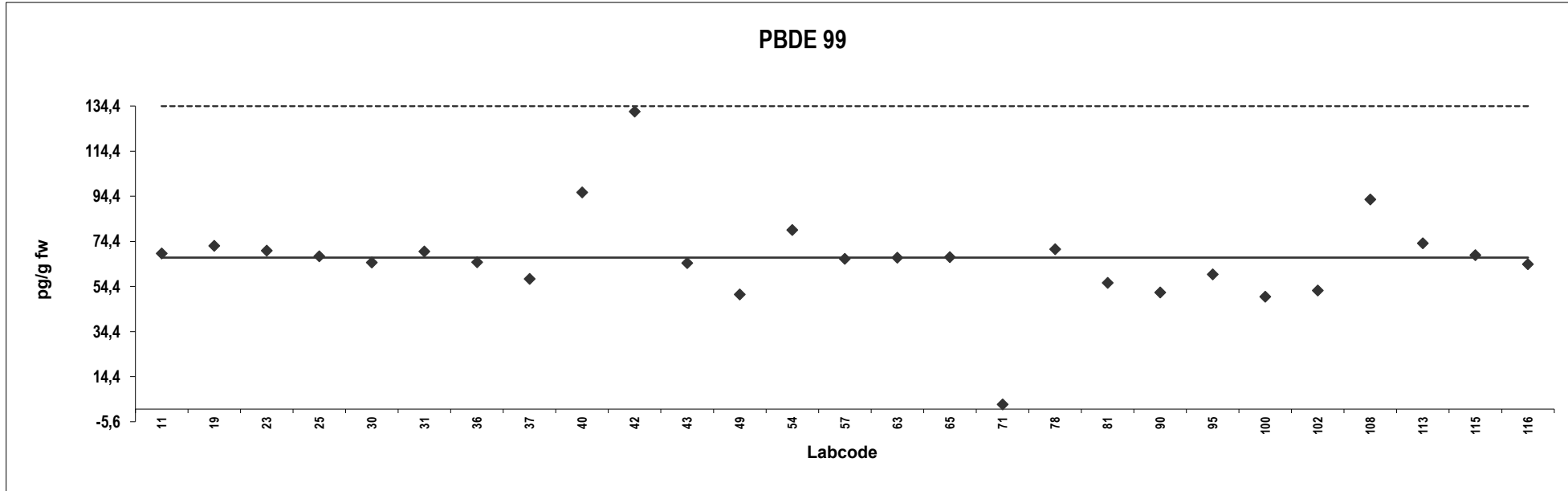
Herring

Congener: PBDE 100

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	88	0,24					
19	83	-0,057					
23	84	0,00					
25	84	-0,021					
30	86	0,11					
31	83	-0,051					
36	86	0,11					
37	73	-0,67					
40	127	2,6					
42	110	1,5					
43	81	-0,18					
49	72	-0,71					
54	85	0,042					
57	83	-0,052					
63	90	0,36					
65	84	0,022					
71	2,0	-4,9					
78	89	0,30					
81	77	-0,42					
90	77	-0,40					
95	74	-0,60					
100	70	-0,81					
102	71	-0,75					
108	115	1,8					
113	90	0,36					
115	91	0,43					
116	88	0,24					

Consenus statistics

Consensus median, pg/g	84
Median all values pg/g	84
Consensus mean, pg/g	83
Standard deviation, pg/g	21
Relative standard deviation, %	25
No. of values reported	27
No. of values removed	0
No. of reported non-detects	0

PBDE 100

Z-score: PBDE 100
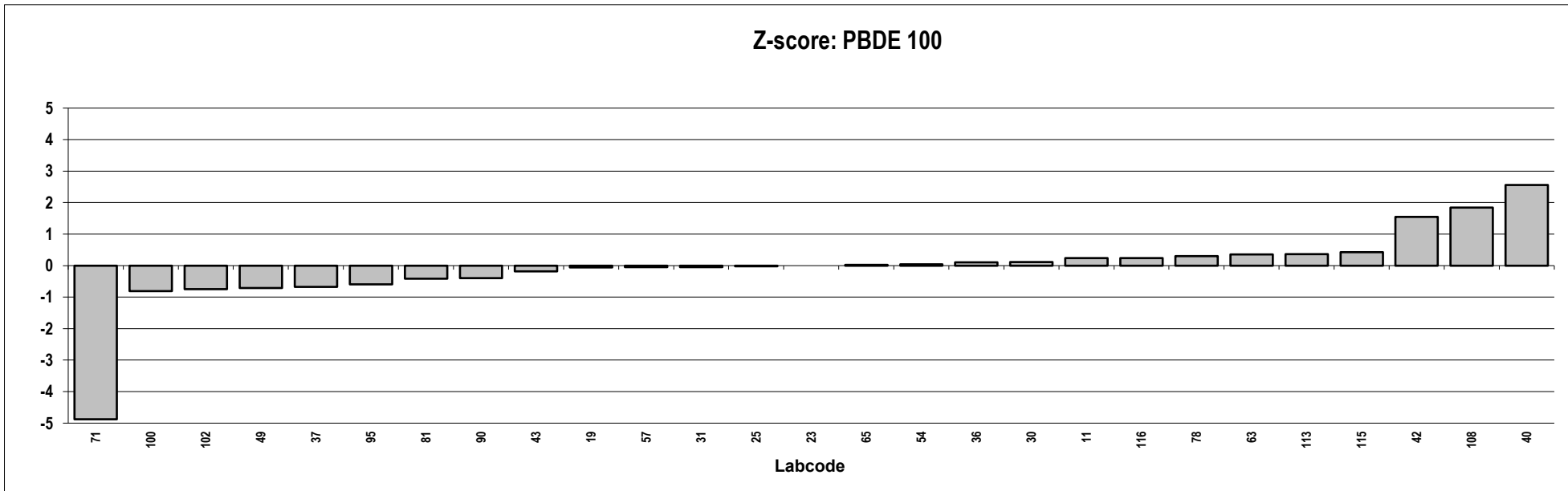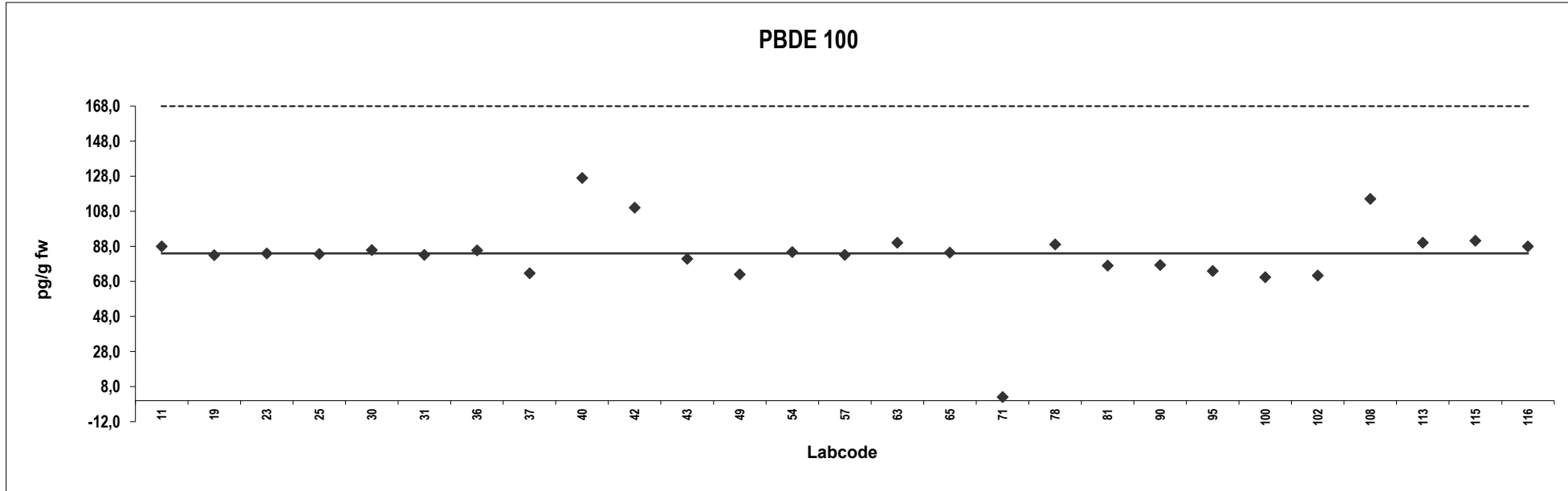
Herring

Congener: PBDE 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	14	0,92					
19	12	-0,018					
23	17	2,0					
25	11	-0,37					
30	14	0,88					
31	12	0,018					
36	11	-0,35					
37	11	-0,56					
40	18	2,6					
42	14	0,71	ND				
43	8,7	-1,3					
49	9,4	-1,0					
54	11	-0,18					
57	13	0,36					
63	13	0,33					
65	13	0,50					
71	4,0	-3,3					
78	14	1,1					
81	7,0	-2,0					
90	12	-0,047					
95	12	-0,13					
100	9,8	-0,86					
102	14	0,88					
108	16	1,8					
113	10	-0,73					
115	16	1,6					
116	14	0,97					

Consenus statistics

Consensus median, pg/g	12
Median all values pg/g	12
Consensus mean, pg/g	12
Standard deviation, pg/g	3,0
Relative standard deviation, %	24
No. of values reported	27
No. of values removed	0
No. of reported non-detects	1

PBDE 153
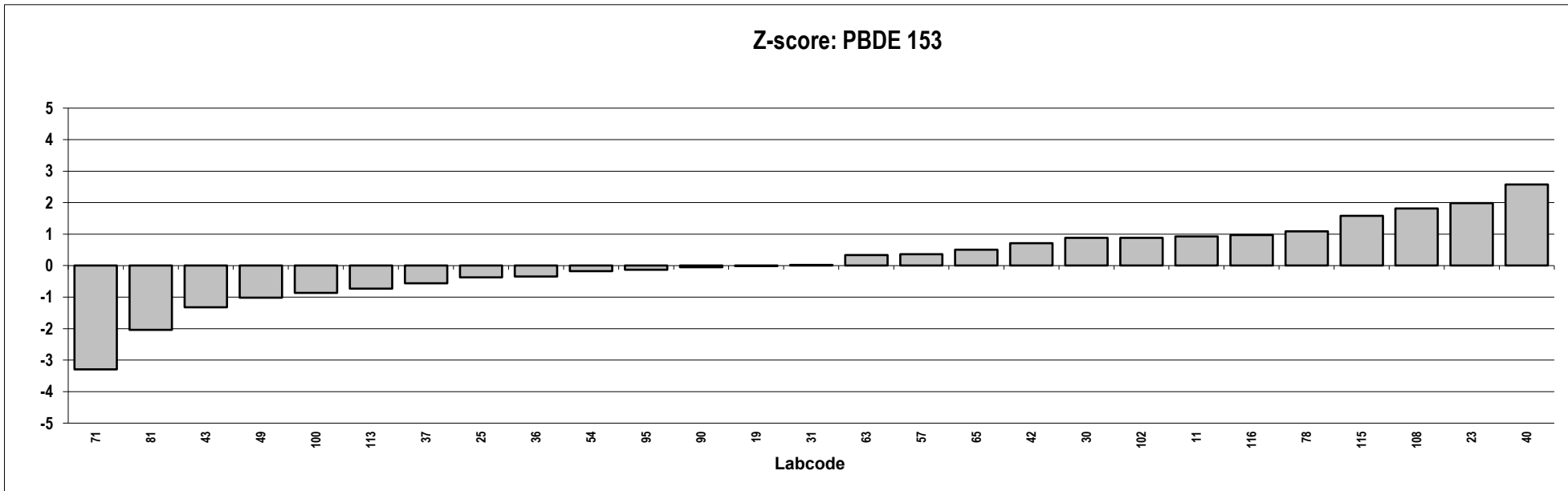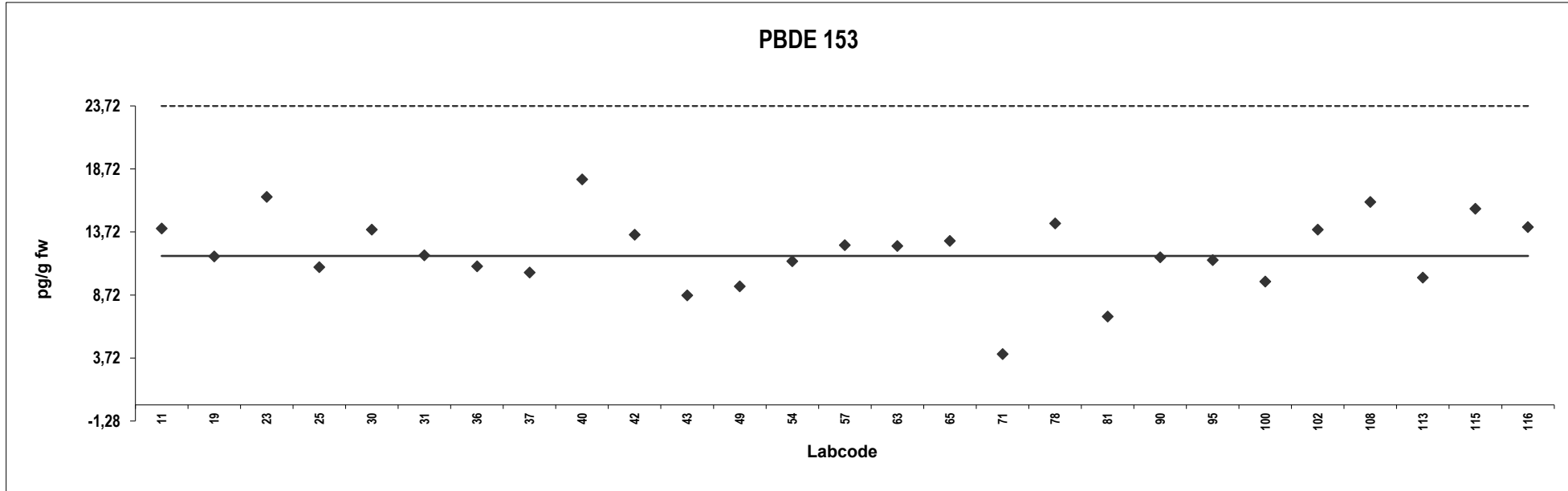
Z-score: PBDE 153

Herring

Congener: PBDE 154

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	34	-0,66					
19	38	-0,18					
23	54	1,9					
25	38	-0,11					
30	53	1,7					
31	22	-2,2					
36	20	-2,4	ND				
37	27	-1,6					
40	44	0,59					
42	43	0,51					
43	42	0,35					
49	48	1,2					
54	63	3,1					
57	65	3,3					
63	44	0,58					
65	37	-0,30					
71	4,1	-4,5					
78	35	-0,54					
81	24	-1,9					
90	40	0,11					
95	47	1,0					
100	37	-0,22					
102	32	-0,87					
108	24	-1,9					
113	1,1	-4,9					
115	64	3,2					
116	41	0,19					

Consenus statistics

Consensus median, pg/g	39
Median all values pg/g	38
Consensus mean, pg/g	38
Standard deviation, pg/g	16
Relative standard deviation, %	42
No. of values reported	27
No. of values removed	0
No. of reported non-detects	1

PBDE 154

Z-score: PBDE 154
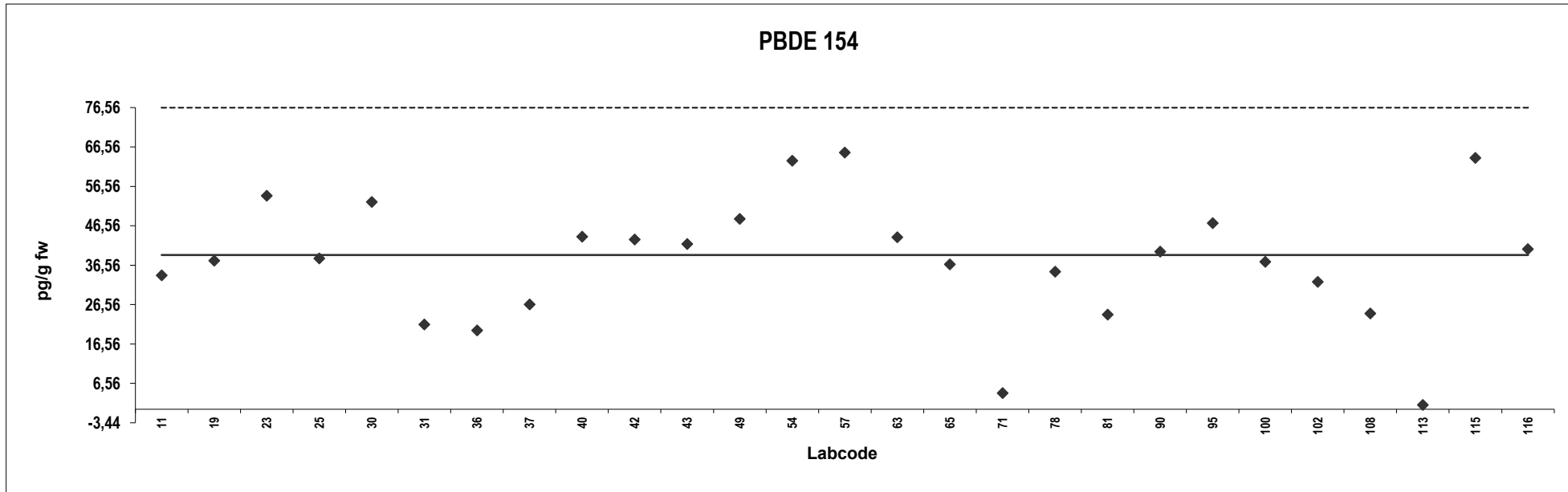
Herring
Congener: PBDE 183

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	4,9	17	Outlier,ND				
19	4,5	15	Outlier,ND				
23	1,2	0,27					
25	0,76	-1,5					
30	1,7	2,5					
31	0,86	-1,1	ND				
36	1,1	0,00					
37	0,62	-2,2					
40	2,8	7,7					
42	3,2	9,3	Outlier,ND				
43	1,0	-0,45	ND				
49	1,0	-0,27					
54	5,2	19	Outlier				
57	0,94	-0,74					
63	3,0	8,6	Outlier				
65	0,69	-1,9					
71	4,0	13	Outlier				
78	1,4	1,4					
81	2,0	4,1	ND				
90	0,97	-0,60					
95	1,8	3,4					
100	0,20	-4,1	ND				
102	1,4	1,2	ND				
108	2,5	6,4	ND				
113	2,3	5,3					
115	2,1	4,6					
116	0,82	-1,3					

Consenus statistics

Consensus median, pg/g	1,1
Median all values pg/g	1,4
Consensus mean, pg/g	1,3
Standard deviation, pg/g	0,68
Relative standard deviation, %	51
No. of values reported	27
No. of values removed	6
No. of reported non-detects	9

PBDE 183

Z-score: PBDE 183
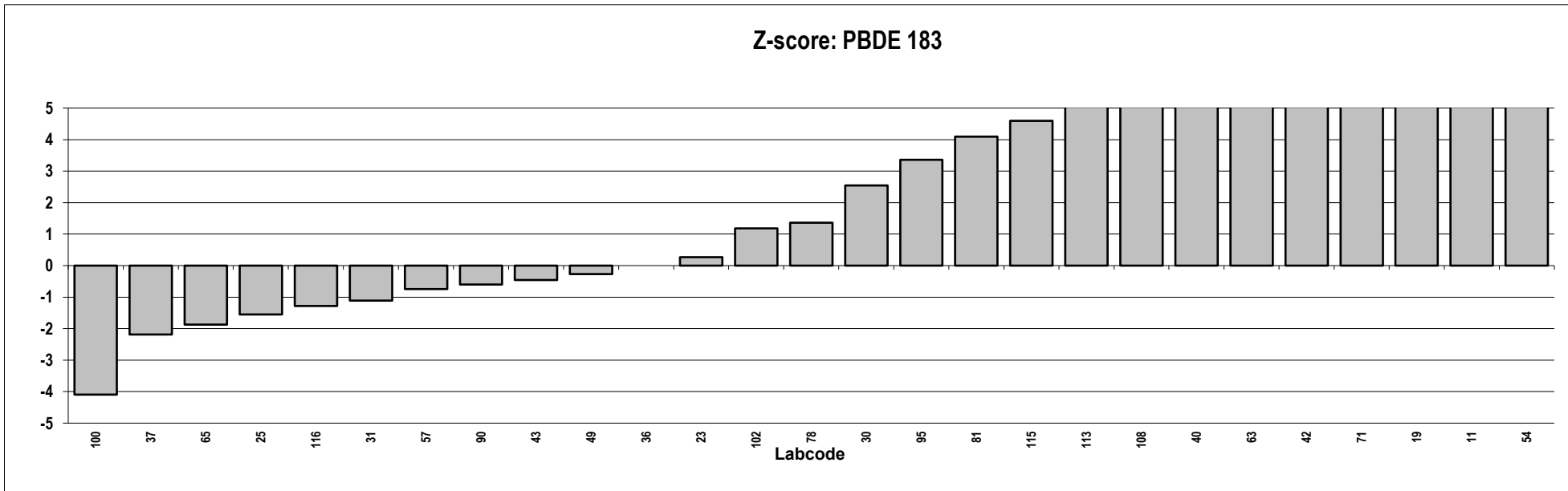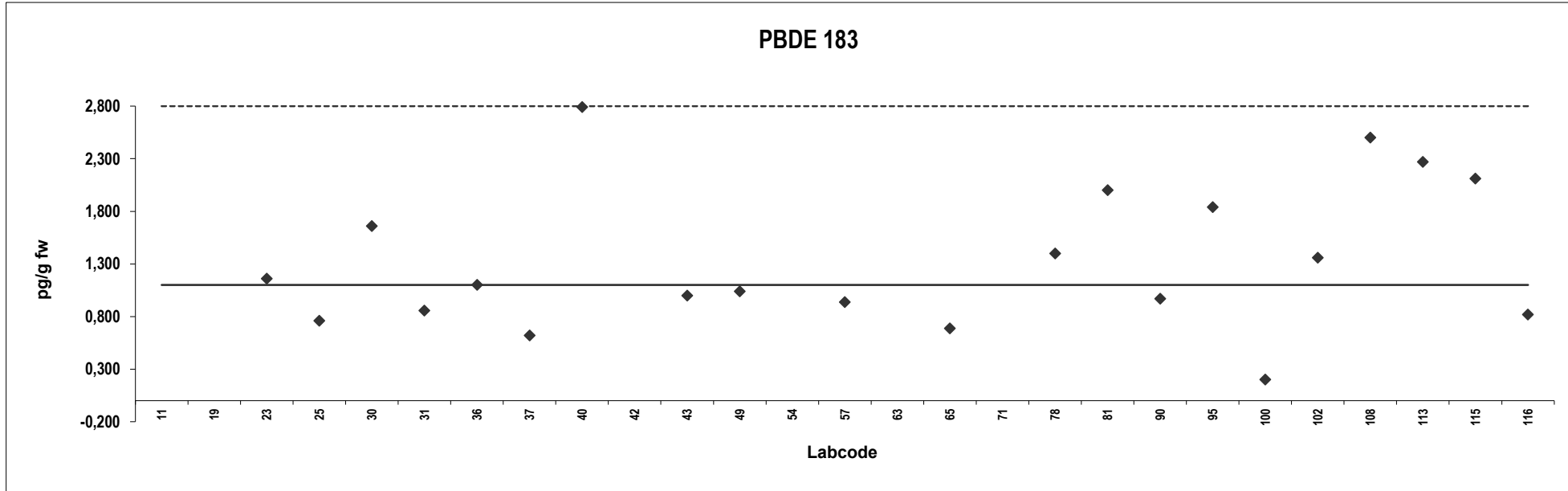
Herring

Congener: PBDE 209

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	200	88	Outlier				
23	58	22					
25	5,9	-2,3					
30	122	52	Outlier				
31	63	24	ND				
36	25	6,6	ND				
37	6,0	-2,2					
43	1,0	-4,5	ND				
57	2,5	-3,8					
63	115	48	Outlier,ND				
65	130	55	Outlier				
71	0,0	-5,0	ND				
81	130	55	Outlier,ND				
90	95	39	Outlier				
95	11	0,28					
100	3,9	-3,2	ND				
102	52	19	ND				
108	5,0	-2,7	ND				
113	35	11					
115	323	144	Outlier				
116	11	0,00					

Consenus statistics

|	
Consensus median, pg/g	11
Median all values pg/g	35
Consensus mean, pg/g	20
Standard deviation, pg/g	23
Relative standard deviation, %	114
No. of values reported	21
No. of values removed	7
No. of reported non-detects	9

PBDE 209
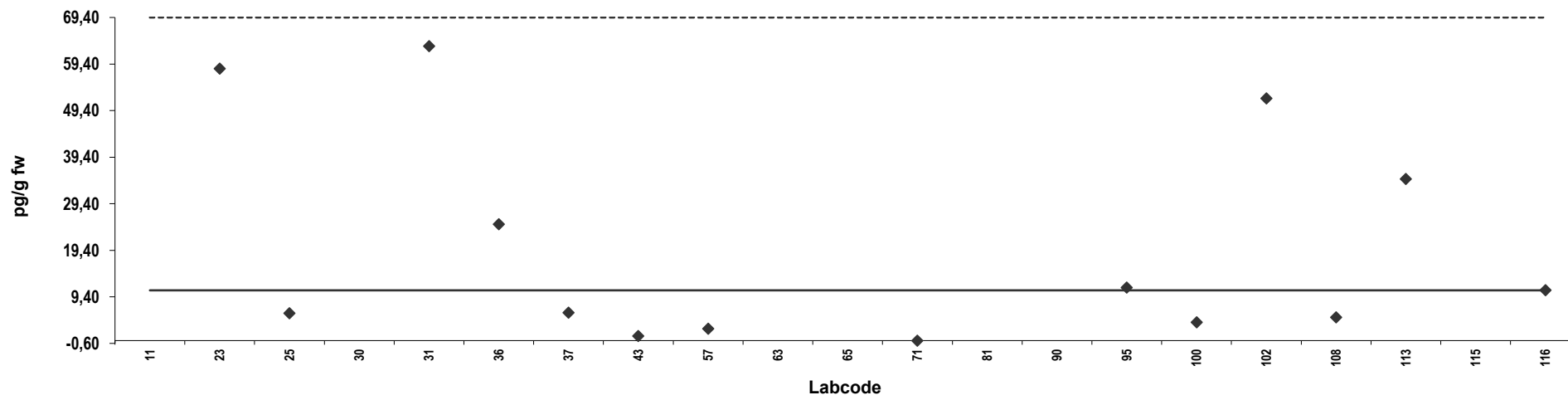
Z-score: PBDE 209
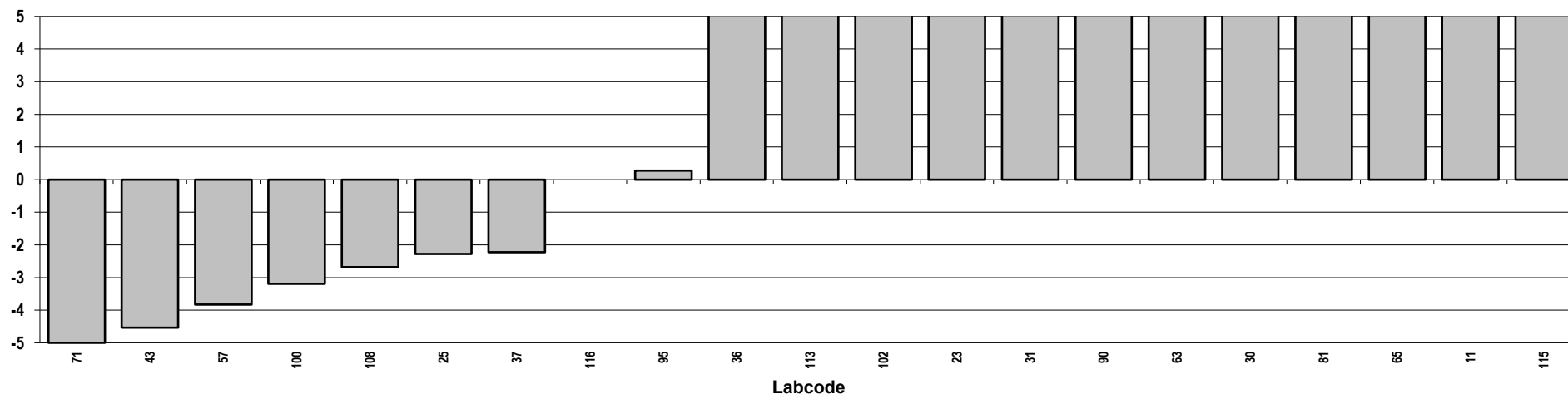
Herring

Congener: α-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	243	-1,1					
17	302	-0,12					
49	341	0,51					
65	317	0,12					
81	330	0,33					
95	288	-0,35					

Consenus statistics

Consensus median, pg/g	309
Median all values pg/g	309
Consensus mean, pg/g	303
Standard deviation, pg/g	35
Relative standard deviation, %	12
No. of values reported	6
No. of values removed	0
No. of reported non-detects	0
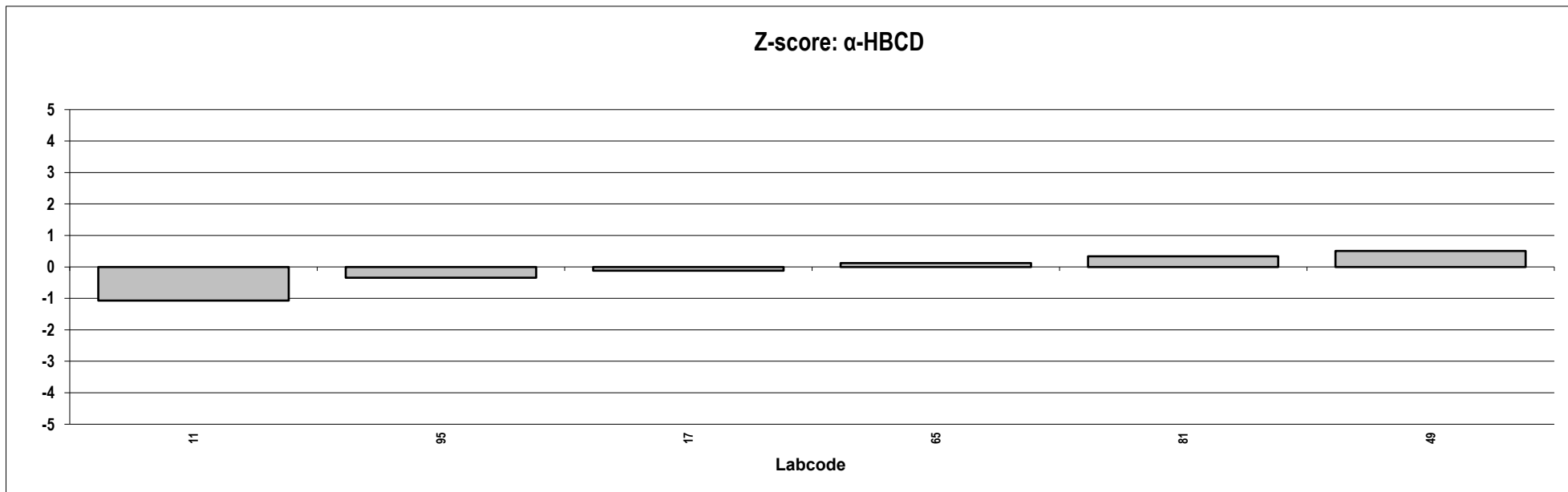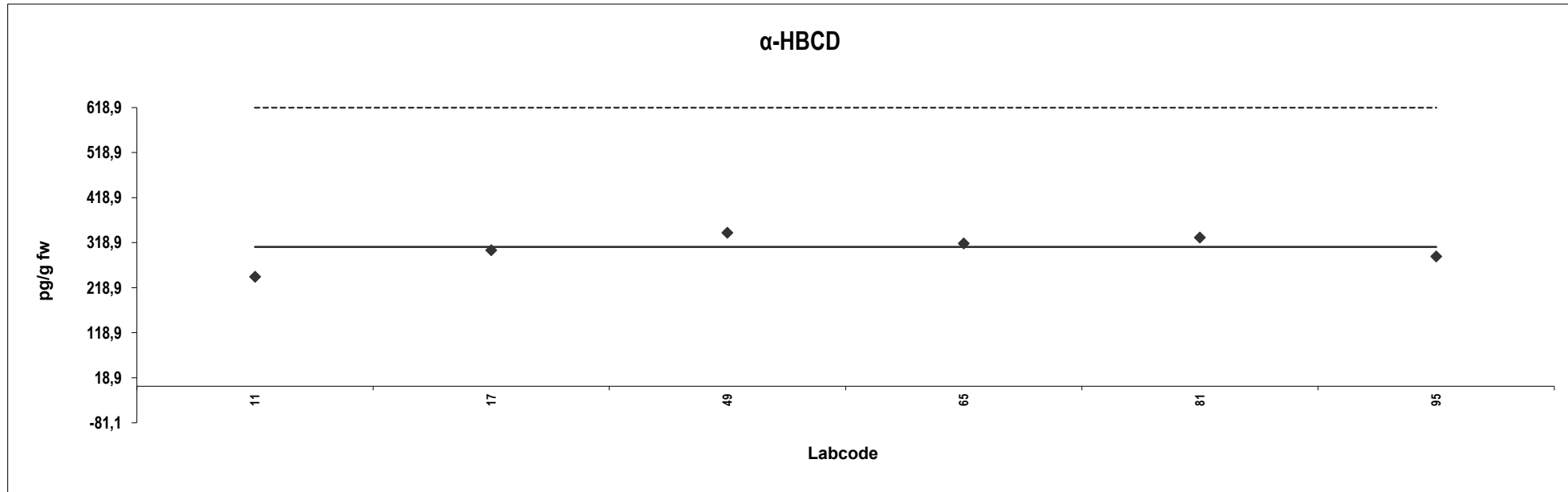
α-HBCD

Z-score: α-HBCD

Herring

Congener: β-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	6,0	0,56	ND				
17	4,8	-0,56					
49	14	8,0	Outlier,ND				
65	6,0	0,56					
81	10	4,3	ND				
95	5,0	-0,37	ND				

Consenus statistics

Consensus median, pg/g	5,4
Median all values pg/g	6,0
Consensus mean, pg/g	6,4
Standard deviation, pg/g	2,1
Relative standard deviation, %	33
No. of values reported	6
No. of values removed	1
No. of reported non-detects	4

β-HBCD

Z-score: β-HBCD
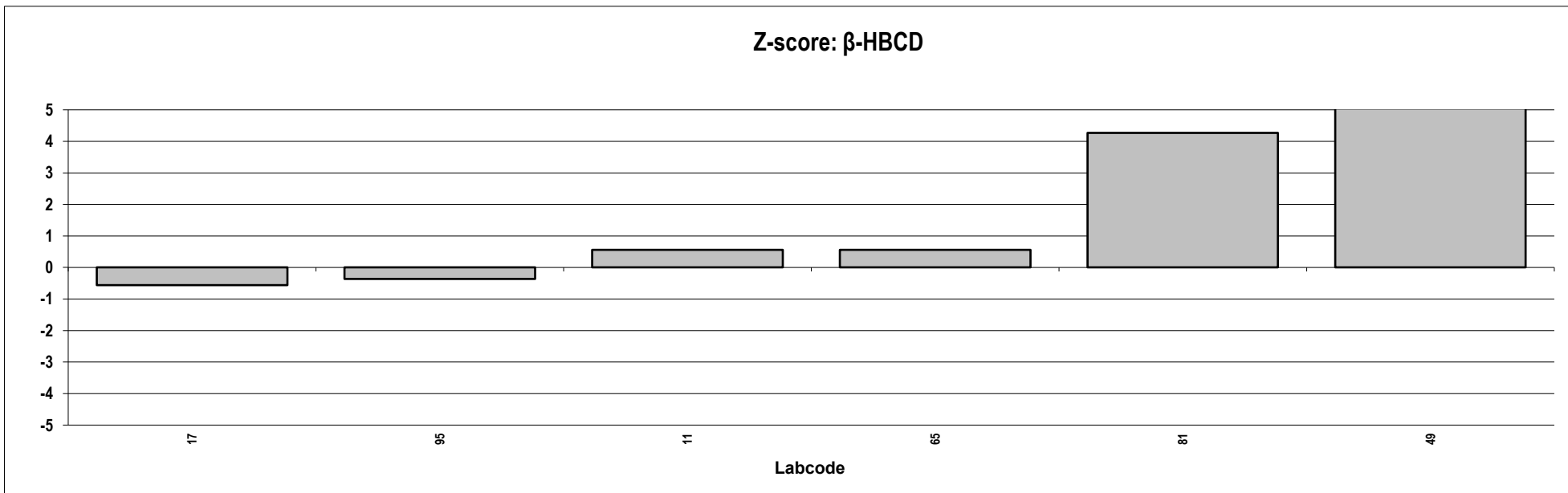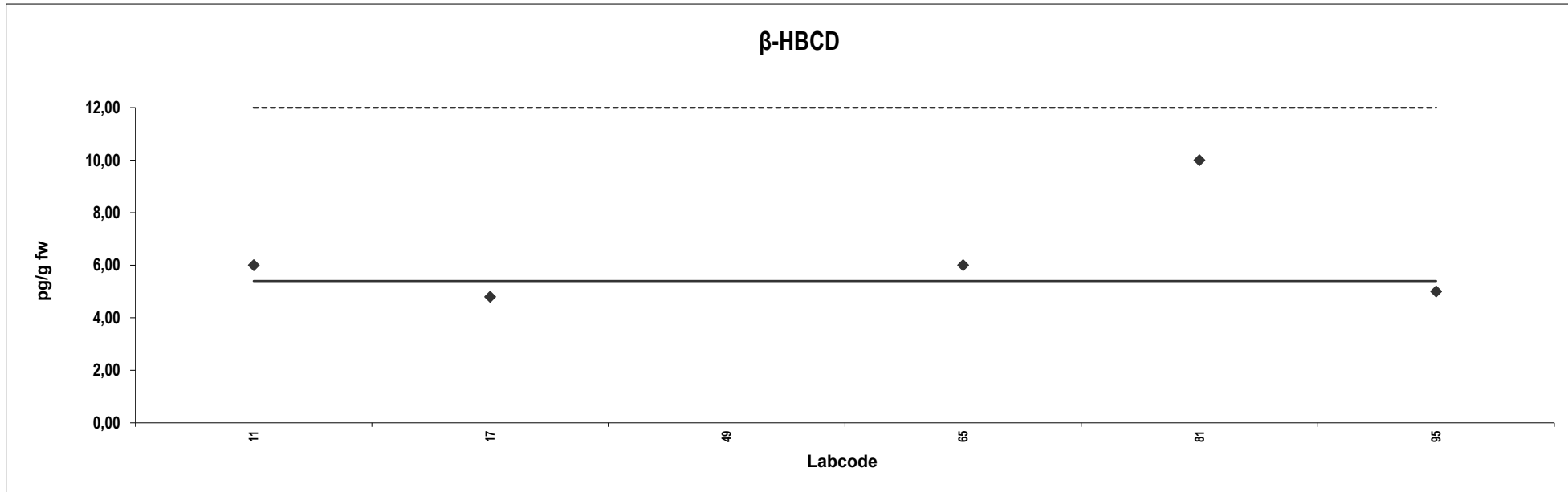
Herring
Congener: γ-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	6,1	-1,0					
17	9,4	1,0					
49	14	4,0	ND				
65	29	14	Outlier				
81	10	1,4	ND				
95	10	1,4	ND				

Consenus statistics

Consensus median, pg/g	7,8
Median all values pg/g	10
Consensus mean, pg/g	9,9
Standard deviation, pg/g	2,8
Relative standard deviation, %	28
No. of values reported	6
No. of values removed	1
No. of reported non-detects	3

γ-HBCD

Z-score: γ-HBCD
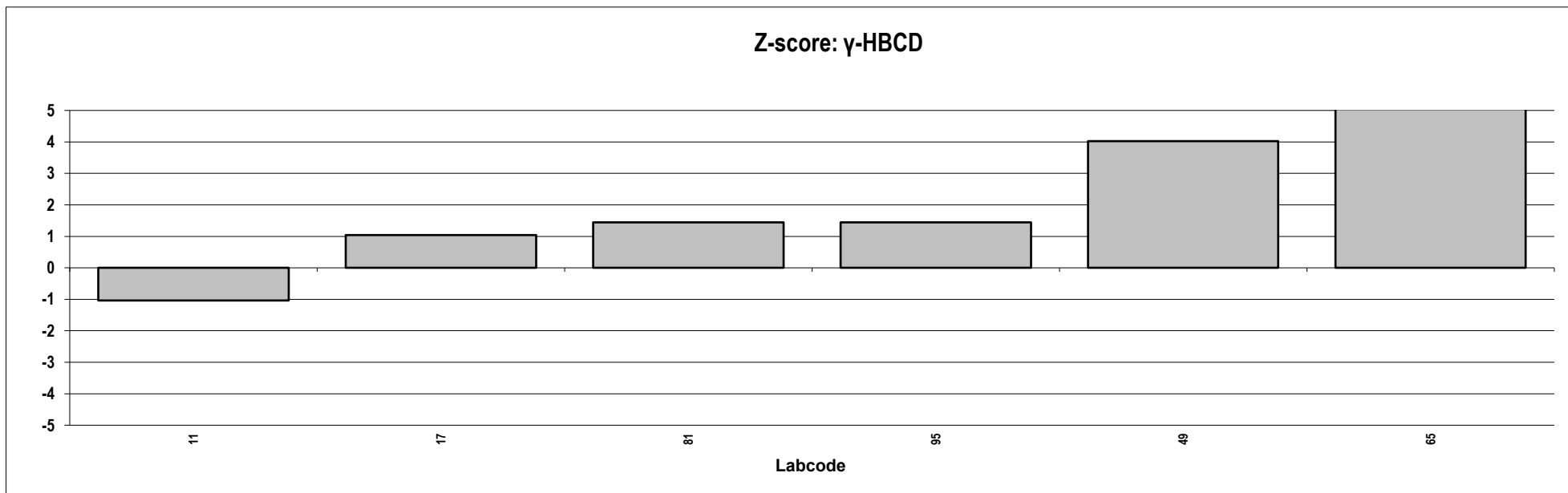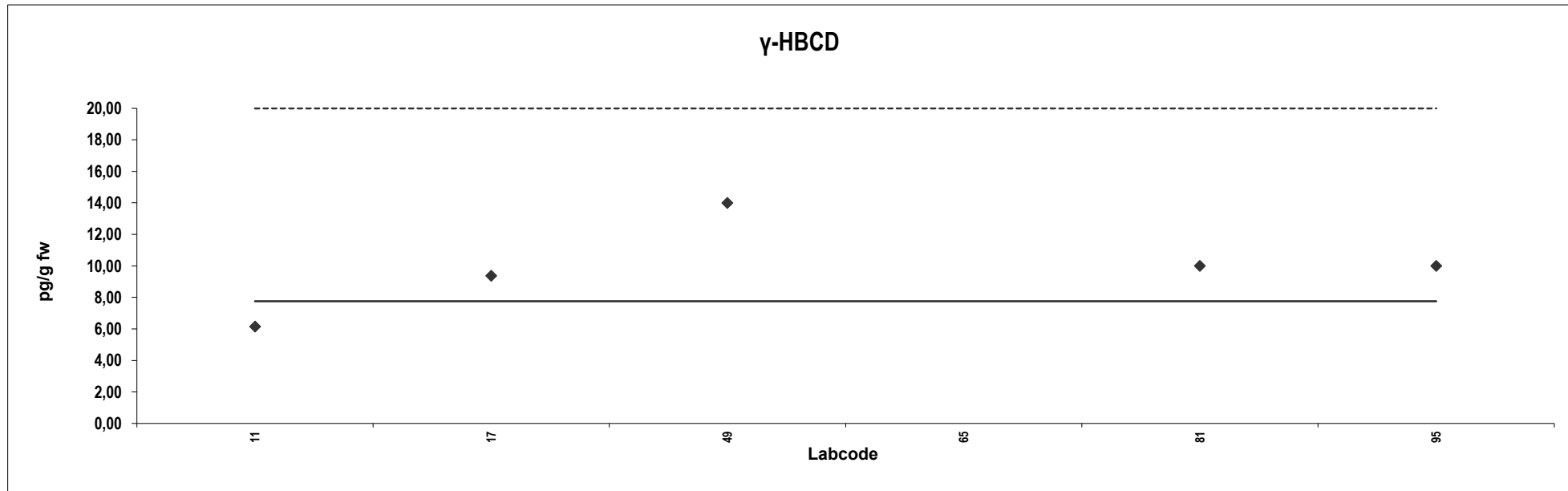
Herring

Congener: total HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	249	-1,2					
17	316	-0,19					
49	341	0,19					
65	352	0,36					
95	288	-0,62					
108	381	0,80					

Consenus statistics

Consensus median, pg/g	329
Median all values pg/g	329
Consensus mean, pg/g	321
Standard deviation, pg/g	47
Relative standard deviation, %	15
No. of values reported	6
No. of values removed	0
No. of reported non-detects	0

total HBCD

Z-score: total HBCD
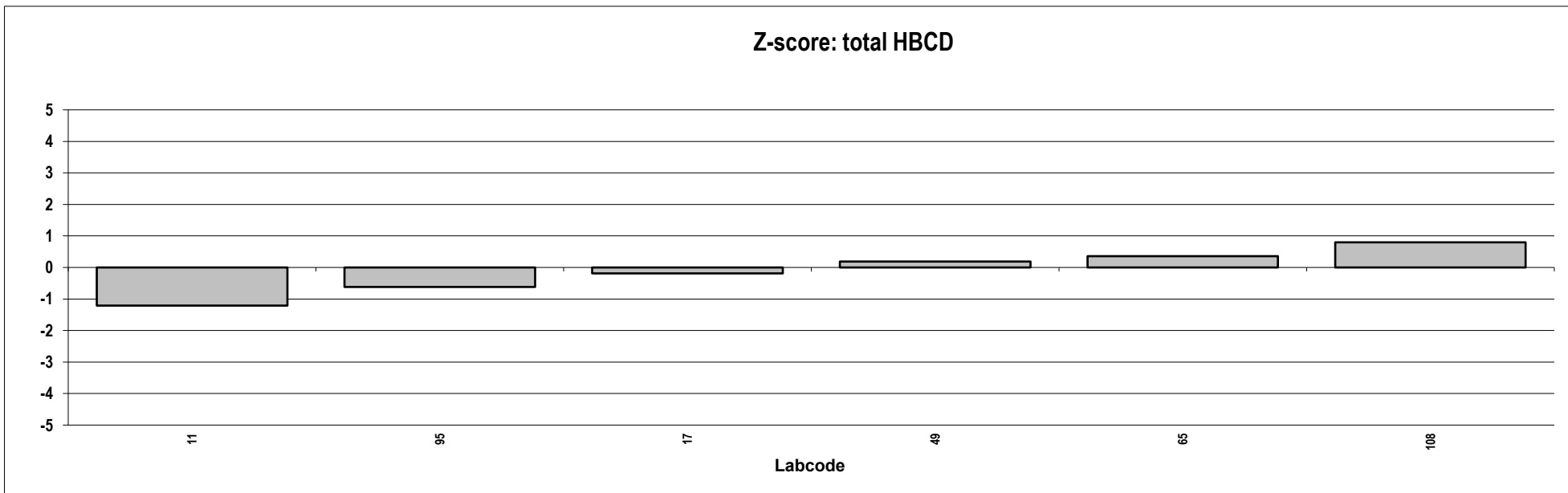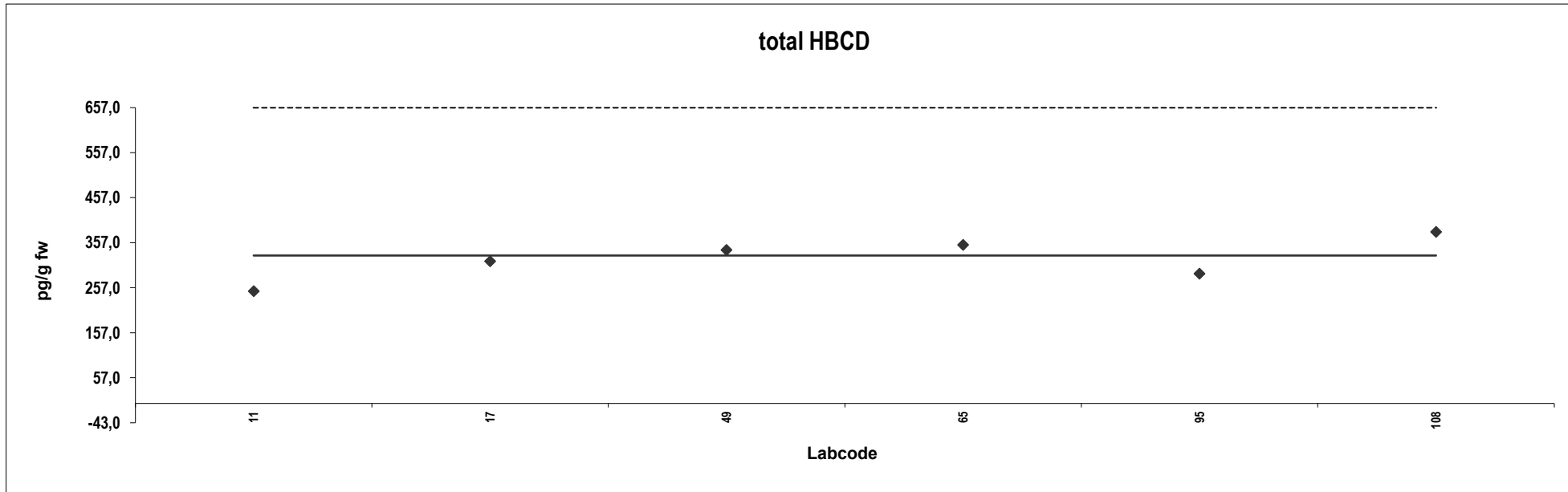
Appendix 4:

Presentation of results for
Brown meat-2019

Appendix 4: Presentation of results: Brown meat-2019

Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

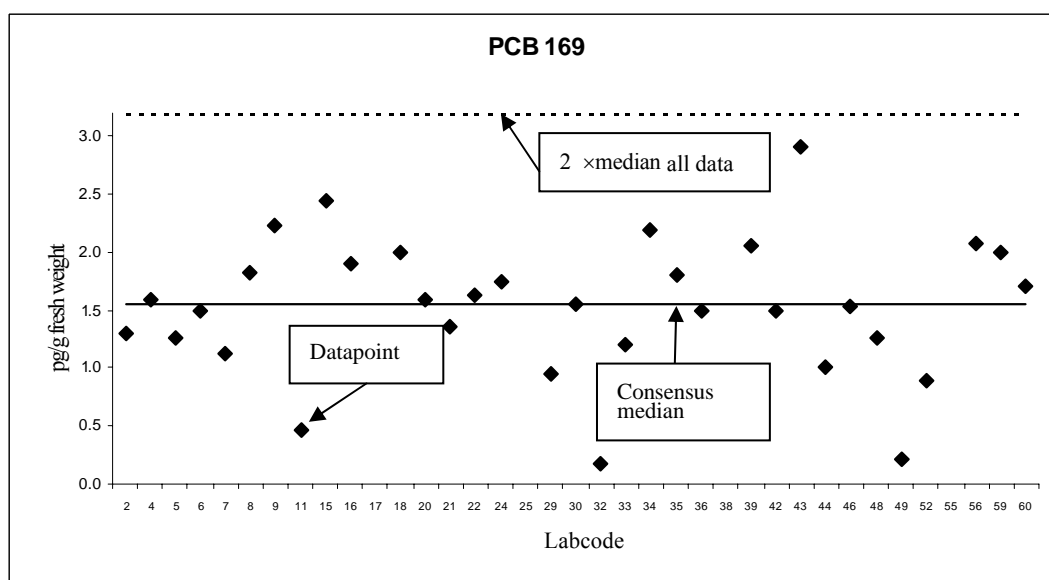For each congener, the outliers were removed and the consensus calculated according to the following procedure:
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding 2 × this median were defined as outliers 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 × 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 × 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 ± 20% from the consensus value.
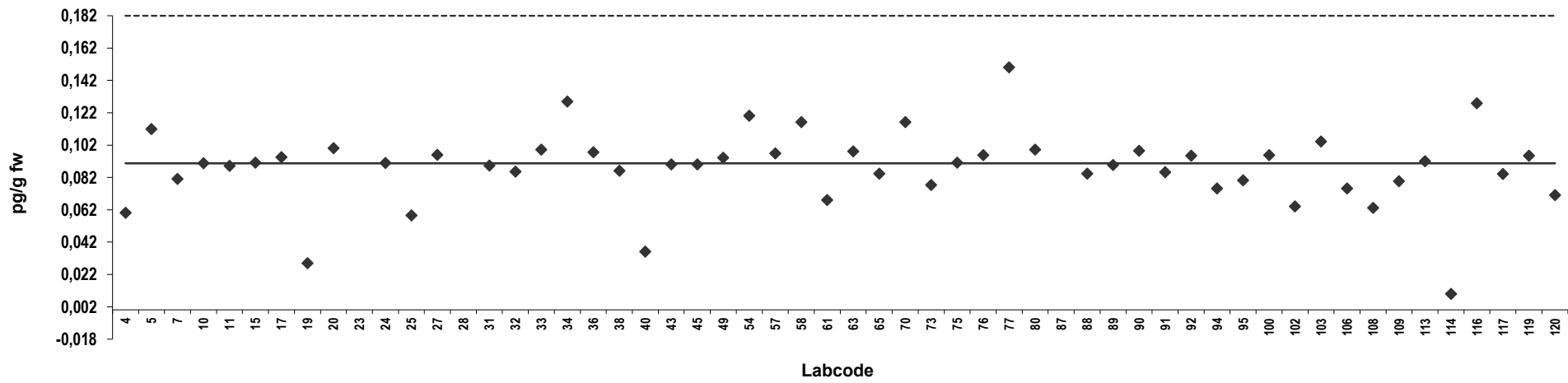
Brown meat
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,060	-1,7		102	0,064	-1,5	
5	0,11	1,2		103	0,10	0,74	
7	0,081	-0,53		106	0,075	-0,86	
10	0,091	0,00		108	0,063	-1,5	
11	0,089	-0,092		109	0,080	-0,61	
15	0,091	0,022		113	0,092	0,072	
17	0,094	0,21		114	0,0098	-4,5	
19	0,029	-3,4	ND	116	0,13	2,1	
20	0,10	0,52		117	0,084	-0,36	
23	0,18	5,2	Outlier	119	0,095	0,26	
24	0,091	0,015		120	0,071	-1,1	
25	0,058	-1,8					
27	0,096	0,28					
28	0,21	6,6	Outlier,ND				
31	0,089	-0,072					
32	0,085	-0,29					
33	0,099	0,47					
34	0,13	2,1					
36	0,098	0,38					
38	0,086	-0,26					
40	0,036	-3,0	ND				
43	0,090	-0,033					
45	0,090	-0,035					
49	0,094	0,19					
54	0,12	1,6					
57	0,097	0,34					
58	0,12	1,4					
61	0,068	-1,2					
63	0,098	0,41					
65	0,084	-0,35					
70	0,12	1,4					
73	0,077	-0,74					
75	0,091	0,022					
76	0,096	0,28					
77	0,15	3,3	ND				
80	0,099	0,46					
87	0,84	41	Outlier				
88	0,084	-0,36					
89	0,090	-0,060					
90	0,098	0,43					
91	0,085	-0,31					
92	0,095	0,26					
94	0,075	-0,86					
95	0,080	-0,58					
100	0,096	0,28					

Consensus statistics

Consensus median, pg/g	0,091
Median all values pg/g	0,091
Consensus mean, pg/g	0,088
Standard deviation, pg/g	0,023
Relative standard deviation, %	26
No. of values reported	56
No. of values removed	3
No. of reported non-detects	4

2,3,7,8 TCDD
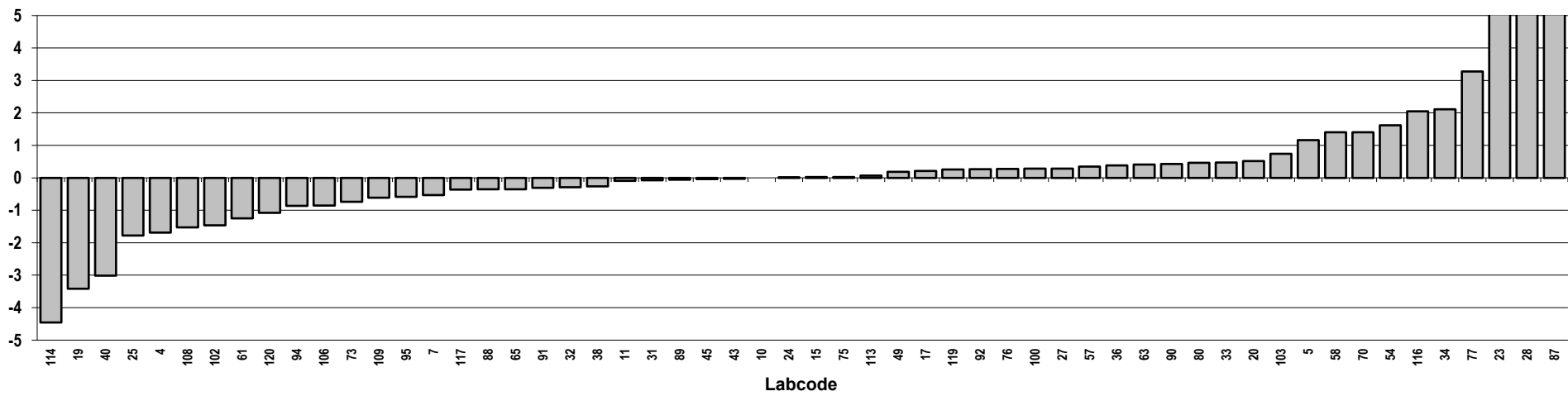
Labcode

pg/g fw

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

Labcode

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,26	-1,5		102	0,56	2,5	
5	0,48	1,4		103	0,36	-0,21	
7	0,33	-0,49		106	0,31	-0,81	
10	0,35	-0,25		108	0,43	0,83	
11	0,38	0,069		109	0,31	-0,85	
15	0,38	0,13		113	0,26	-1,5	
17	0,37	-0,052		114	0,029	-4,6	
19	0,29	-1,1		116	0,39	0,30	
20	0,050	-4,3	ND	117	0,37	-0,044	
23	0,51	1,8		119	0,40	0,37	
24	0,37	-0,056		120	0,40	0,36	
25	0,50	1,8					
27	0,37	0,00					
28	0,10	-3,6	ND				
31	0,33	-0,61					
32	0,36	-0,16					
33	0,46	1,2					
34	0,38	0,16					
36	0,40	0,42					
38	0,45	1,1					
40	0,39	0,27					
43	0,29	-1,1					
45	0,45	1,1					
49	0,37	-0,0034					
54	0,43	0,81					
57	0,49	1,7					
58	0,47	1,3					
61	0,20	-2,3					
63	0,39	0,24					
65	0,39	0,29					
70	0,36	-0,17					
73	0,40	0,44					
75	0,38	0,078					
76	0,33	-0,60					
77	0,33	-0,48					
80	0,55	2,4					
87	1,7	18	Outlier				
88	0,30	-0,94					
89	0,39	0,31					
90	0,33	-0,57					
91	0,35	-0,27					
92	0,33	-0,51					
94	0,32	-0,68					
95	0,39	0,20					
100	0,40	0,36					

Consensus statistics

Consensus median, pg/g	0,37
Median all values pg/g	0,37
Consensus mean, pg/g	0,36
Standard deviation, pg/g	0,10
Relative standard deviation, %	28
No. of values reported	56
No. of values removed	1
No. of reported non-detects	2

1,2,3,7,8 PeCDD
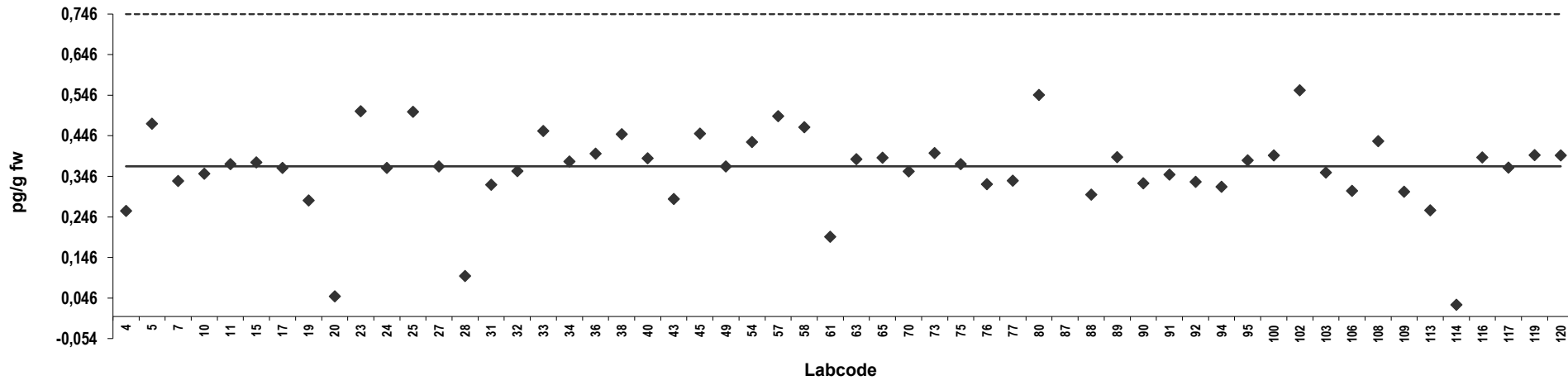
Z-score: 1,2,3,7,8 PeCDD
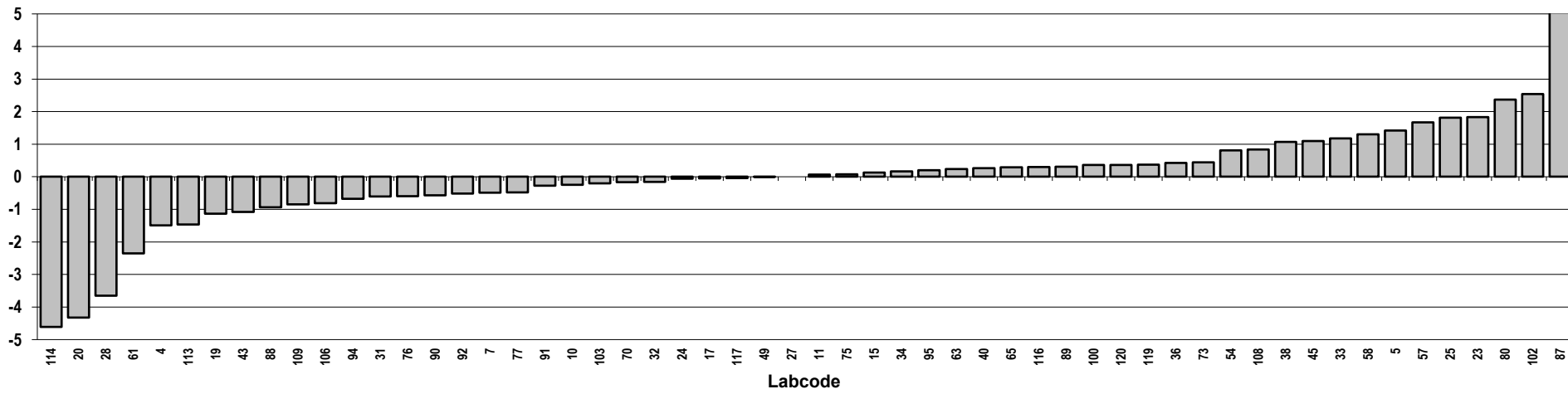
Brown meat
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,15	-1,4		102	0,24	0,74	
5	0,33	2,9		103	0,19	-0,52	
7	0,24	0,60		106	0,19	-0,57	
10	0,20	-0,33		108	0,17	-0,86	
11	0,25	0,84		109	0,18	-0,69	
15	0,21	0,095		113	0,28	1,6	
17	0,19	-0,55		114	0,015	-4,6	
19	0,23	0,42		116	0,20	-0,14	
20	0,19	-0,48		117	0,19	-0,43	
23	0,30	2,2		119	0,25	0,83	
24	0,21	0,098		120	0,21	-0,024	
25	0,19	-0,52					
27	0,22	0,18					
28	0,17	-0,95	ND				
31	0,22	0,16					
32	0,21	-0,071					
33	0,27	1,4					
34	0,22	0,32					
36	0,22	0,28					
38	0,23	0,57					
40	0,22	0,24					
43	0,20	-0,24					
45	0,20	-0,14					
49	0,23	0,48					
54	0,17	-0,95					
57	0,20	-0,16					
58	0,28	1,6					
61	0,19	-0,37					
63	0,21	0,071					
65	0,22	0,15					
70	0,22	0,24					
73	0,21	-0,054					
75	0,22	0,17					
76	0,19	-0,51					
77	0,22	0,30					
80	0,22	0,17					
87	0,50	6,8	Outlier				
88	0,20	-0,16					
89	0,23	0,54					
90	0,19	-0,54					
91	0,21	0,00					
92	0,24	0,76					
94	0,19	-0,48					
95	0,19	-0,38					
100	0,18	-0,83					

Consenus statistics

Consensus median, pg/g	0,21
Median all values pg/g	0,21
Consensus mean, pg/g	0,21
Standard deviation, pg/g	0,042
Relative standard deviation, %	20
No. of values reported	56
No. of values removed	1
No. of reported non-detects	1

1,2,3,4,7,8 HxCDD
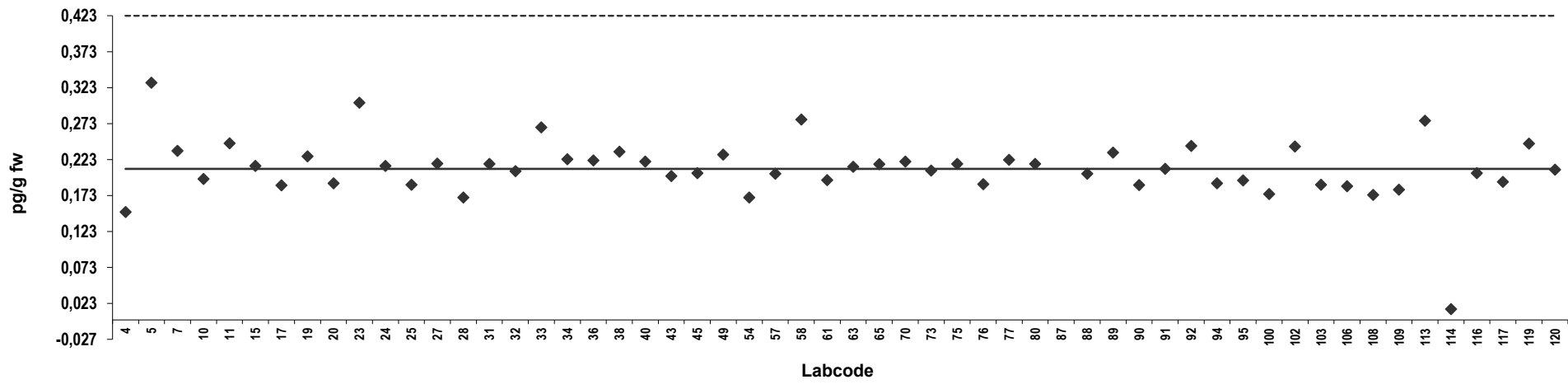
Z-score: 1,2,3,4,7,8 HxCDD
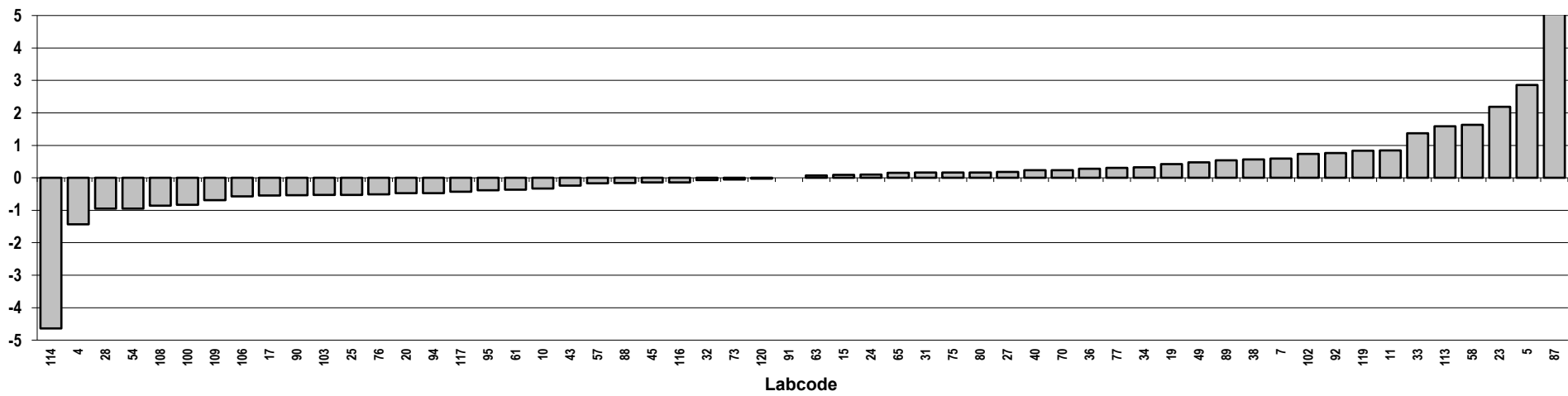
Brown meat
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,38	-0,90		102	0,49	0,26	
5	0,57	1,2		103	0,48	0,14	
7	0,45	-0,19		106	0,43	-0,37	
10	0,54	0,81		108	0,33	-1,4	
11	0,52	0,59		109	0,42	-0,52	
15	0,46	-0,096		113	0,52	0,60	
17	0,47	0,040		114	0,045	-4,5	
19	0,41	-0,59		116	0,47	0,024	
20	0,42	-0,47		117	0,39	-0,81	
23	0,49	0,29		119	0,52	0,63	
24	0,46	0,00		120	0,43	-0,37	
25	0,50	0,42					
27	0,43	-0,37					
28	0,63	1,8					
31	0,49	0,23					
32	0,48	0,15					
33	0,54	0,84					
34	0,67	2,2					
36	0,56	1,1					
38	0,49	0,28					
40	0,44	-0,26					
43	0,42	-0,47					
45	0,47	0,083					
49	0,53	0,71					
54	0,54	0,82					
57	0,43	-0,38					
58	0,60	1,5					
61	0,25	-2,3					
63	0,51	0,48					
65	0,53	0,73					
70	0,34	-1,3					
73	0,52	0,66					
75	0,46	-0,085					
76	0,42	-0,52					
77	0,61	1,6					
80	0,45	-0,16					
87	0,93	5,0	Outlier				
88	0,39	-0,80					
89	0,45	-0,15					
90	0,41	-0,63					
91	0,47	0,066					
92	0,38	-0,95					
94	0,43	-0,37					
95	0,41	-0,58					
100	0,45	-0,18					

Consensus statistics

Consensus median, pg/g	0,46
Median all values pg/g	0,47
Consensus mean, pg/g	0,46
Standard deviation, pg/g	0,095
Relative standard deviation, %	21
No. of values reported	56
No. of values removed	1
No. of reported non-detects	0
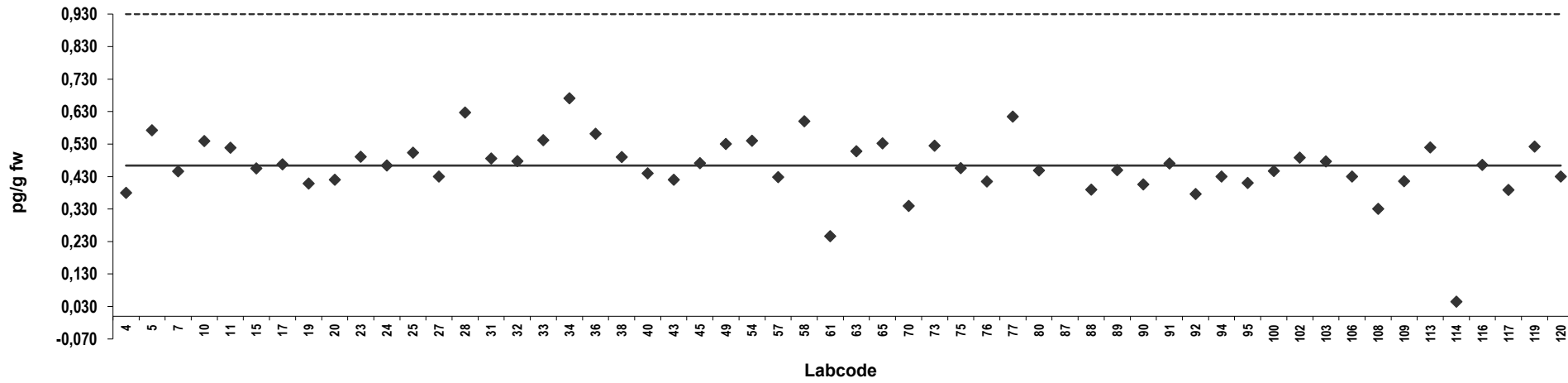
1,2,3,6,7,8 HxCDD

Z-score: 1,2,3,6,7,8 HxCDD
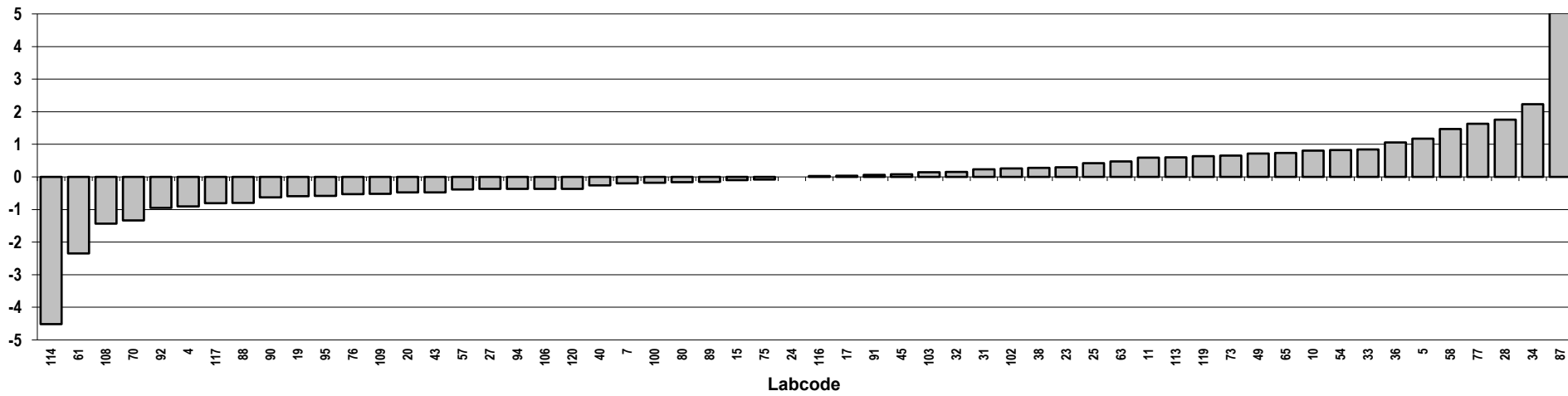
Brown meat
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,11	-1,8		102	0,049	-3,6	ND
5	0,21	1,2		103	0,17	0,058	
7	0,15	-0,64		106	0,16	-0,47	
10	0,21	0,99		108	0,12	-1,5	
11	0,18	0,20		109	0,15	-0,57	
15	0,17	0,00		113	0,24	1,9	
17	0,17	0,027		114	0,016	-4,5	
19	0,065	-3,1	ND	116	0,15	-0,47	
20	0,18	0,26		117	0,14	-0,99	
23	0,18	0,12		119	0,19	0,42	
24	0,18	0,23		120	0,16	-0,41	
25	0,20	0,76					
27	0,29	3,3					
28	0,16	-0,32	ND				
31	0,17	0,058					
32	0,19	0,47					
33	0,23	1,8					
34	0,18	0,36					
36	0,21	1,0					
38	0,10	-2,1	ND				
40	0,12	-1,5					
43	0,15	-0,61					
45	0,19	0,44					
49	0,18	0,26					
54	0,25	2,3					
57	0,18	0,23					
58	0,23	1,8					
61	0,11	-1,7					
63	0,17	-0,18					
65	0,19	0,41					
70	0,28	3,1					
73	0,17	-0,11					
75	0,17	-0,088					
76	0,17	0,0058					
77	0,22	1,3					
80	0,17	-0,18					
87	0,47	8,9	Outlier				
88	0,16	-0,42					
89	0,13	-1,1					
90	0,15	-0,48					
91	0,17	-0,029					
92	0,17	-0,16					
94	0,076	-2,8					
95	0,15	-0,76					
100	0,24	1,9					

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	0,050
Relative standard deviation, %	30
No. of values reported	56
No. of values removed	1
No. of reported non-detects	4

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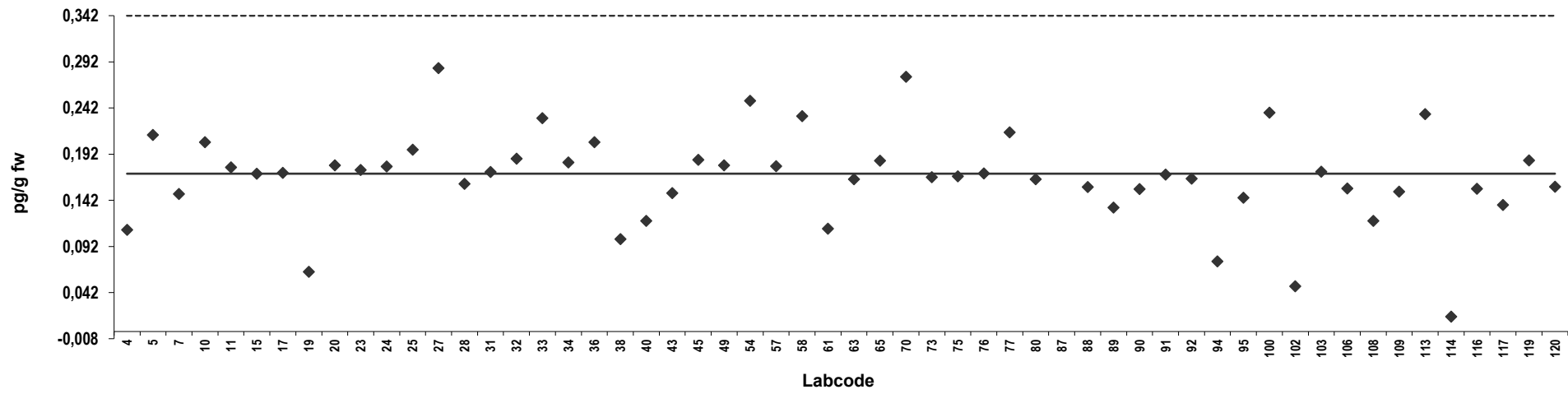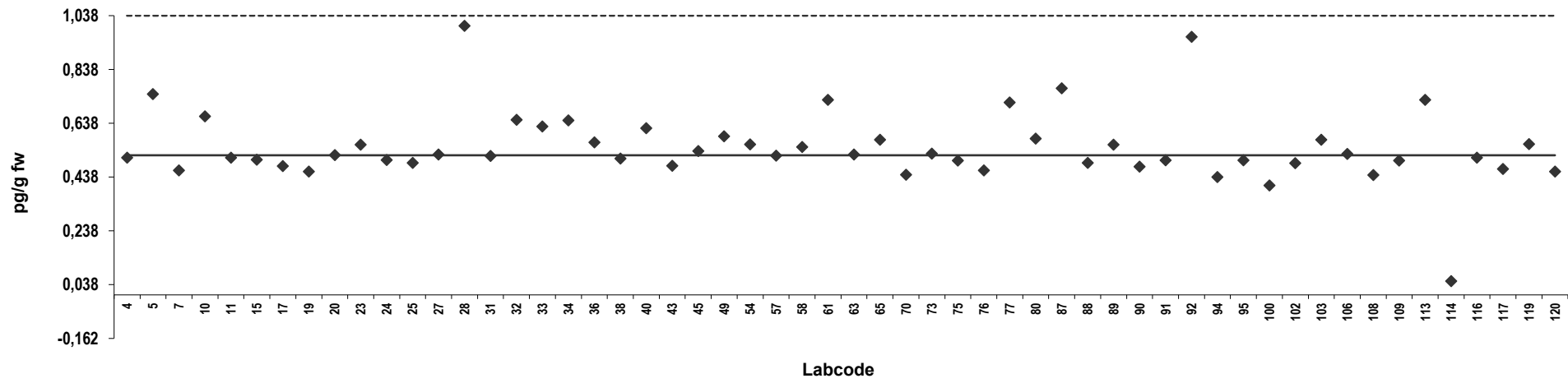

Z-score: 1,2,3,7,8,9 HxCDD
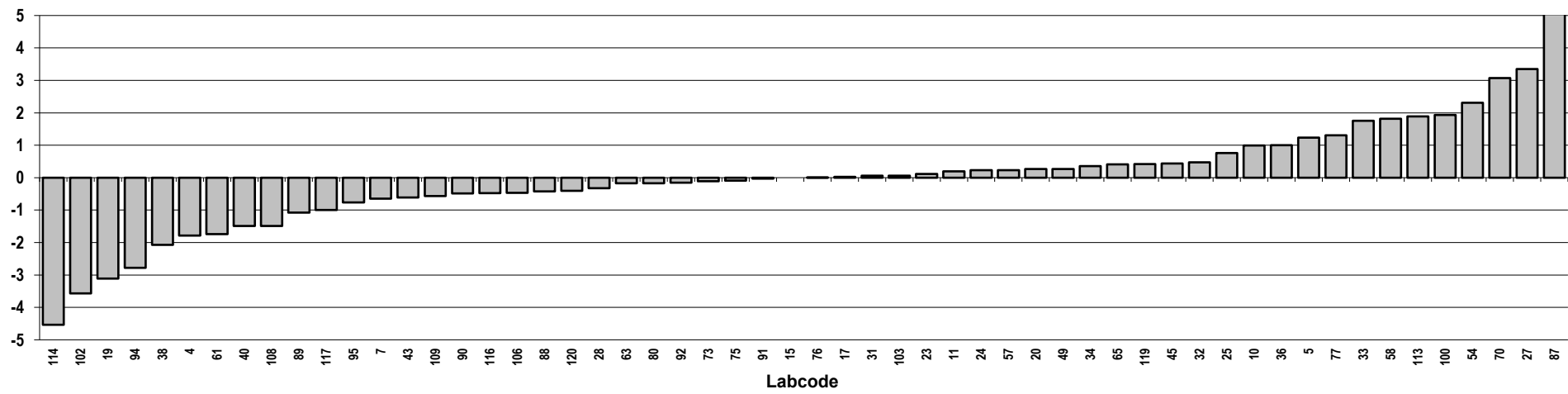
Brown meat
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,51	-0,087		102	0,49	-0,28	
5	0,75	2,2		103	0,58	0,56	
7	0,46	-0,54		106	0,52	0,048	
10	0,66	1,4		108	0,45	-0,70	
11	0,51	-0,082		109	0,50	-0,19	
15	0,50	-0,15		113	0,73	2,0	
17	0,48	-0,38		114	0,051	-4,5	
19	0,46	-0,58		116	0,51	-0,083	
20	0,52	0,0092		117	0,47	-0,49	
23	0,56	0,38		119	0,56	0,41	
24	0,50	-0,17		120	0,46	-0,59	
25	0,49	-0,28					
27	0,52	0,023					
28	1,0	4,6					
31	0,52	-0,024					
32	0,65	1,3					
33	0,63	1,0					
34	0,65	1,2					
36	0,57	0,46					
38	0,51	-0,12					
40	0,62	0,97					
43	0,48	-0,38					
45	0,53	0,15					
49	0,59	0,68					
54	0,56	0,39					
57	0,52	-0,0092					
58	0,55	0,30					
61	0,72	2,0					
63	0,52	0,028					
65	0,58	0,55					
70	0,45	-0,69					
73	0,52	0,054					
75	0,50	-0,19					
76	0,46	-0,55					
77	0,71	1,9					
80	0,58	0,60					
87	0,77	2,4					
88	0,49	-0,27					
89	0,56	0,38					
90	0,48	-0,41					
91	0,50	-0,18					
92	0,96	4,2					
94	0,44	-0,78					
95	0,50	-0,18					
100	0,41	-1,1					

Consenus statistics

|	
Consensus median, pg/g	0,52
Median all values pg/g	0,52
Consensus mean, pg/g	0,55
Standard deviation, pg/g	0,13
Relative standard deviation, %	24
No. of values reported	56
No. of values removed	0
No. of reported non-detects	0

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

Z-score: 1,2,3,4,6,7,8 HpCDD
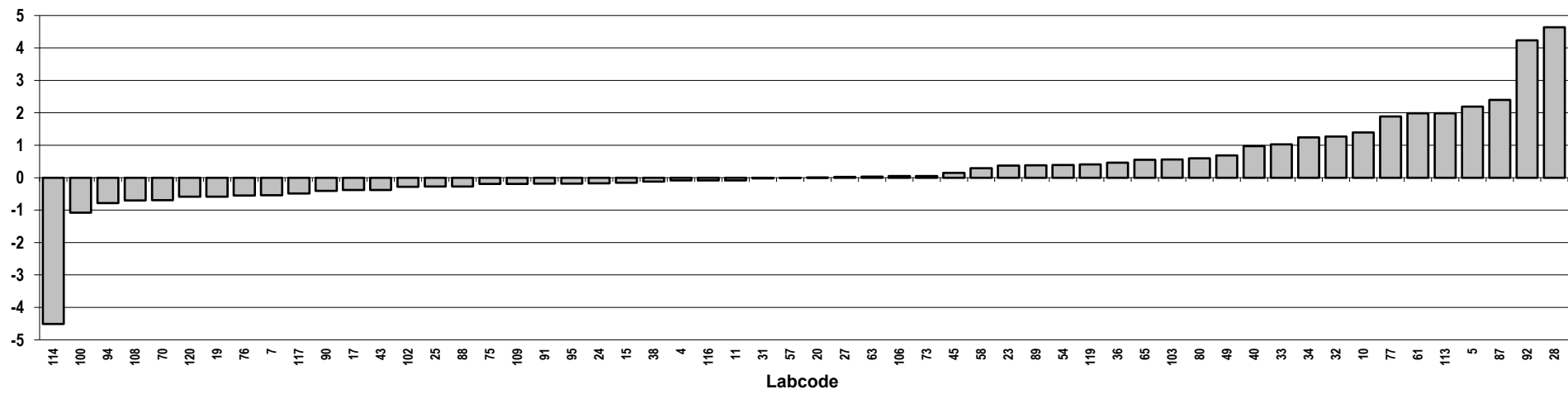
Brown meat
Congener: OCDD

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,52	0,014		102	0,39	-1,2	
5	0,64	1,2		103	0,79	2,6	
7	0,51	-0,053		106	0,64	1,2	
10	0,96	4,2		108	0,49	-0,31	
11	0,45	-0,63		109	0,58	0,57	
15	0,52	-0,014		113	0,67	1,4	
17	0,46	-0,56		114	0,075	-4,3	
19	0,45	-0,64		116	0,44	-0,77	
20	0,48	-0,37		117	0,55	0,31	
23	0,50	-0,23		119	0,70	1,7	
24	0,48	-0,41		120	0,48	-0,33	
25	0,50	-0,16					
27	0,49	-0,24					
28	2,4	18	Outlier				
31	0,90	3,7					
32	0,97	4,4					
33	0,76	2,4					
34	0,84	3,1					
36	0,53	0,15					
38	0,62	0,98					
40	0,34	-1,7					
43	0,47	-0,47					
45	0,53	0,14					
49	0,76	2,3					
54	0,67	1,5					
57	0,47	-0,46					
58	0,67	1,5					
61	0,72	2,0					
63	0,77	2,4					
65	0,64	1,2					
70	0,45	-0,64					
73	0,51	-0,034					
75	0,51	-0,053					
76	0,47	-0,46					
77	0,73	2,1					
80	0,78	2,6					
87	0,52	0,014					
88	0,47	-0,50					
89	0,38	-1,3					
90	0,48	-0,40					
91	0,44	-0,76					
92	2,2	16	Outlier				
94	0,52	0,024					
95	0,52	0,014					
100	0,41	-1,0					

Consenus statistics

Consensus median, pg/g	0,52
Median all values pg/g	0,52
Consensus mean, pg/g	0,57
Standard deviation, pg/g	0,16
Relative standard deviation, %	29
No. of values reported	56
No. of values removed	2
No. of reported non-detects	0

OCDD

Z-score: OCDD
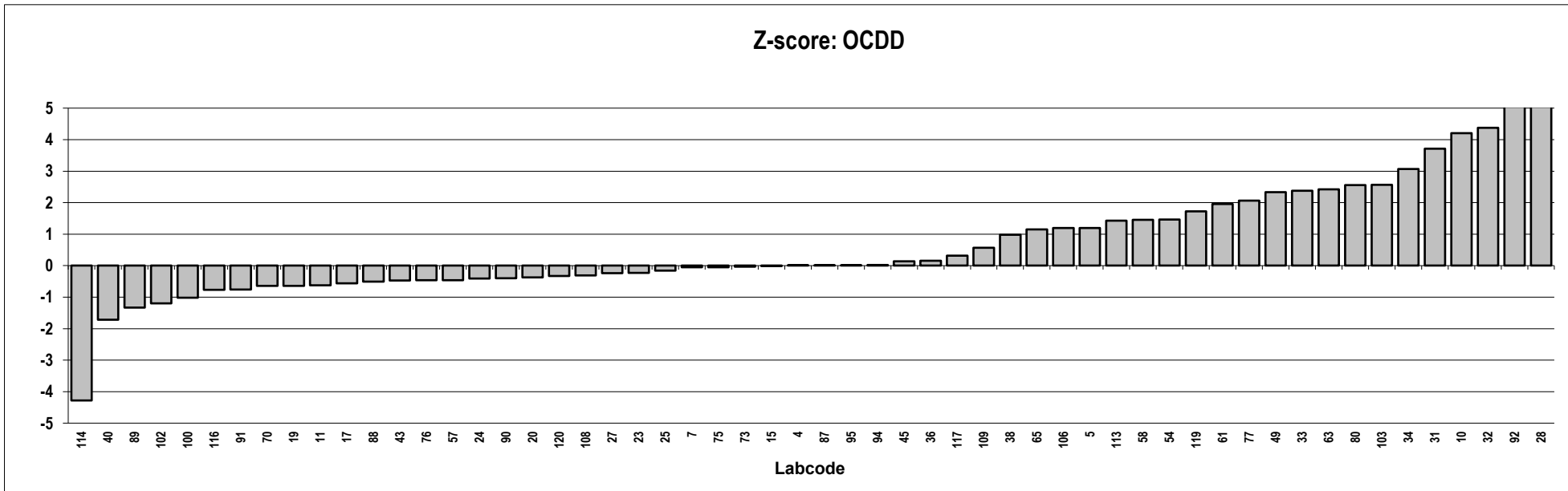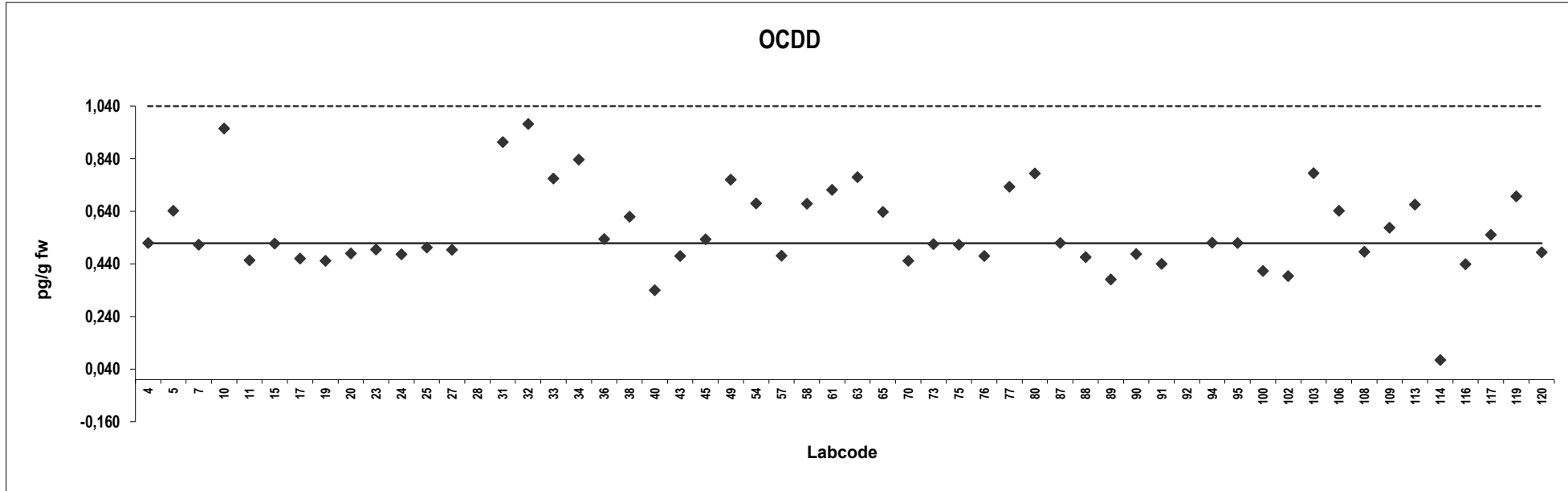
Brown meat
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	1,5	-1,8		102	2,1	-0,60	
5	3,1	1,5		103	2,1	-0,54	
7	1,9	-0,94		106	2,2	-0,24	
10	2,6	0,51		108	1,9	-1,1	
11	2,3	-0,020		109	2,0	-0,69	
15	2,4	0,064		113	2,7	0,8	
17	2,3	-0,050		114	0,30	-4,4	
19	2,5	0,34		116	2,5	0,25	
20	2,5	0,34		117	2,1	-0,47	
23	3,1	1,5		119	2,3	-0,15	
24	2,3	-0,019		120	2,2	-0,42	
25	1,7	-1,3					
27	2,4	0,11					
28	2,0	-0,66					
31	2,2	-0,23					
32	2,6	0,62					
33	2,8	0,86					
34	2,0	-0,74					
36	2,3	-0,17					
38	3,6	2,7					
40	2,6	0,44					
43	2,4	0,043					
45	2,4	0,20					
49	2,5	0,34					
54	2,5	0,28					
57	2,5	0,36					
58	2,7	0,79					
61	2,1	-0,63					
63	2,7	0,81					
65	2,6	0,45					
70	3,2	1,8					
73	2,3	-0,19					
75	2,4	0,043					
76	2,4	0,12					
77	2,3	-0,030					
80	2,4	0,032					
87	4,7	5,1	Outlier				
88	2,2	-0,31					
89	2,3	-0,20					
90	2,3	-0,20					
91	2,2	-0,32					
92	2,5	0,24					
94	2,4	0,00					
95	2,7	0,77					
100	1,8	-1,1					

Consenus statistics

|	
Consensus median, pg/g	2,4
Median all values pg/g	2,4
Consensus mean, pg/g	2,3
Standard deviation, pg/g	0,45
Relative standard deviation, %	19
No. of values reported	56
No. of values removed	1
No. of reported non-detects	0
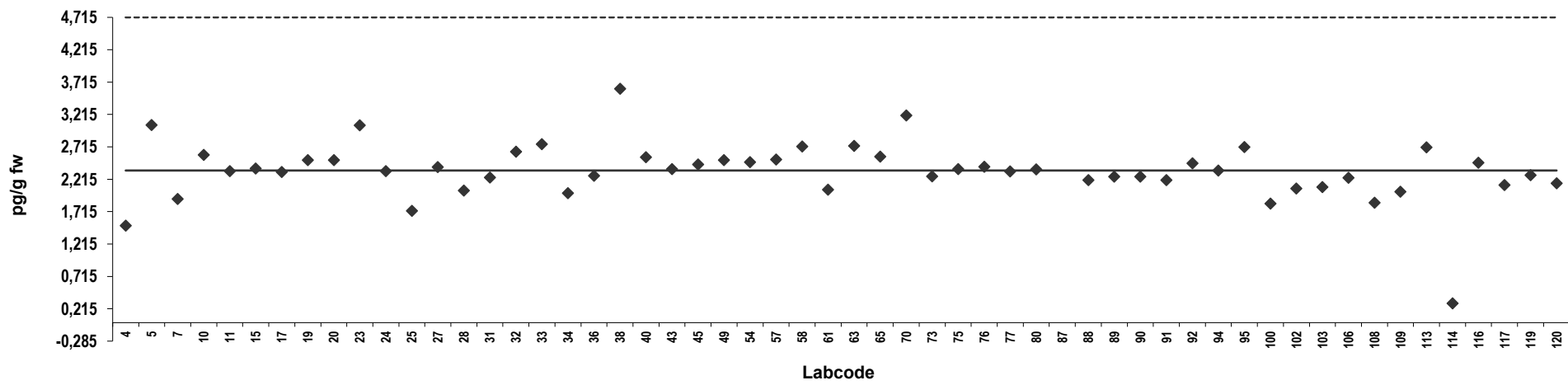
2,3,7,8 TCDF

Z-score: 2,3,7,8 TCDF
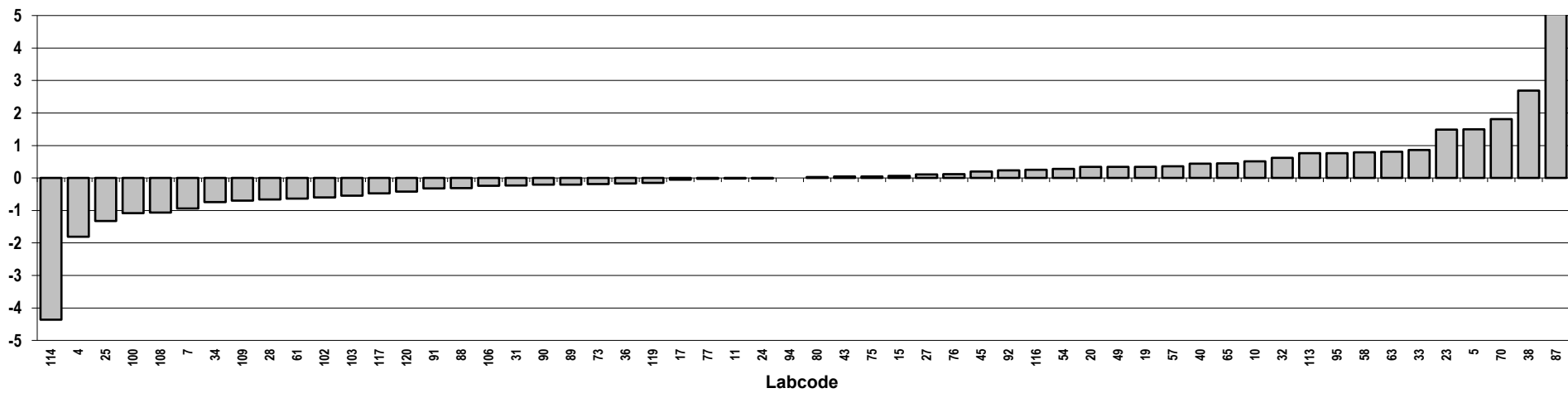
Brown meat
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,30	-0,83		102	0,36	-0,019	
5	0,47	1,6		103	0,35	-0,16	
7	0,33	-0,42		106	0,34	-0,34	
10	0,41	0,68		108	0,29	-0,91	
11	0,33	-0,41		109	0,28	-1,1	
15	0,36	0,023		113	0,39	0,5	
17	0,37	0,13		114	0,048	-4,3	
19	0,25	-1,5		116	0,36	0,016	
20	0,35	-0,13		117	0,37	0,18	
23	0,35	-0,13		119	0,39	0,48	
24	0,36	-0,016		120	0,32	-0,53	
25	0,35	-0,17					
27	0,44	1,2					
28	0,11	-3,5	ND				
31	0,35	-0,15					
32	0,37	0,15					
33	0,42	0,79					
34	0,35	-0,15					
36	0,40	0,51					
38	0,34	-0,31					
40	0,38	0,26					
43	0,32	-0,55					
45	0,36	-0,022					
49	0,33	-0,41					
54	0,40	0,57					
57	0,35	-0,20					
58	0,47	1,6					
61	0,28	-1,1					
63	0,39	0,36					
65	0,39	0,42					
70	0,41	0,75					
73	0,36	0,024					
75	0,36	0,037					
76	0,31	-0,63					
77	0,38	0,23					
80	0,37	0,16					
87	0,42	0,84					
88	0,35	-0,11					
89	0,37	0,11					
90	0,35	-0,19					
91	0,37	0,15					
92	0,46	1,4					
94	0,36	-0,060					
95	0,37	0,15					
100	0,38	0,26					

Consenus statistics	
Consensus median, pg/g	0,36
Median all values pg/g	0,36
Consensus mean, pg/g	0,35
Standard deviation, pg/g	0,069
Relative standard deviation, %	20
No. of values reported	56
No. of values removed	0
No. of reported non-detects	1

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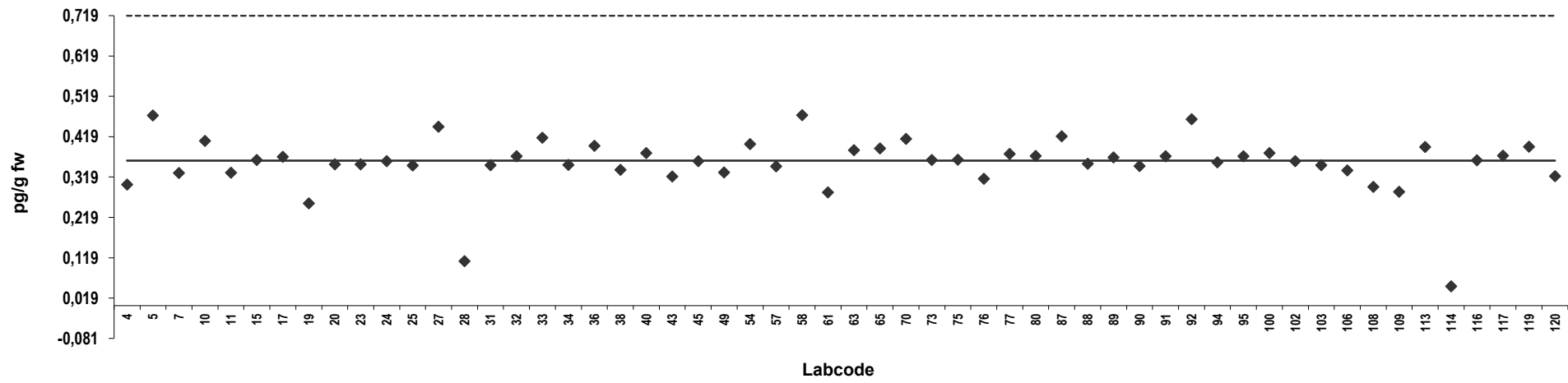
Z-score: 1,2,3,7,8 PeCDF
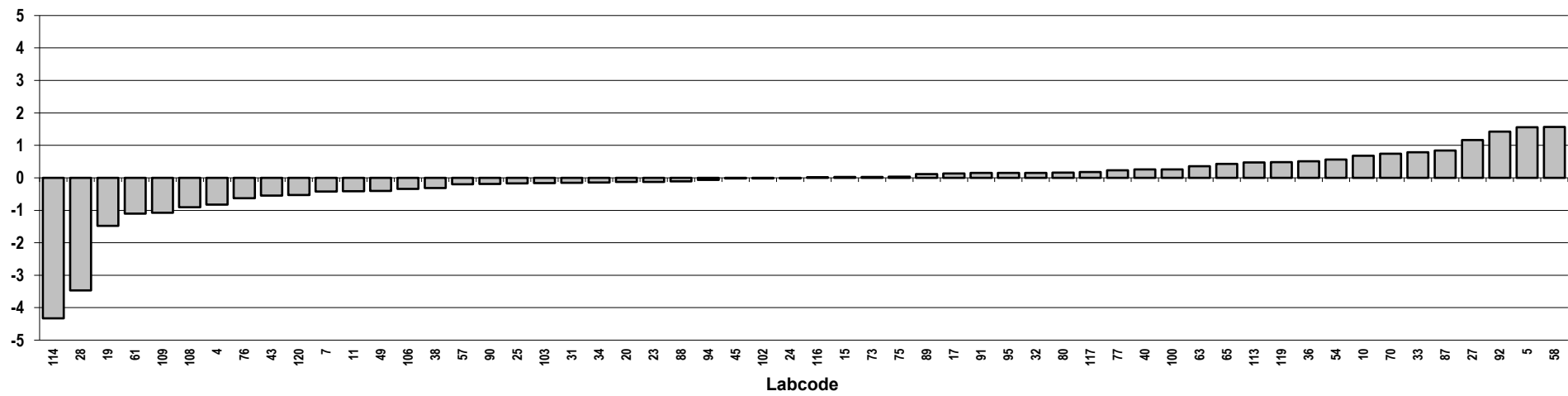
Brown meat

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	1,4	0,086		102	1,4	-0,093	
5	1,8	1,6		103	1,3	-0,31	
7	1,3	-0,22		106	1,5	0,23	
10	1,5	0,37		108	1,1	-1,1	
11	1,4	0,15		109	1,2	-0,71	
15	1,4	-0,16		113	1,4	0,2	
17	1,4	0,15		114	0,16	-4,4	
19	1,5	0,44		116	1,3	-0,44	
20	1,3	-0,24		117	1,3	-0,52	
23	1,9	1,7		119	1,5	0,53	
24	1,5	0,27		120	1,2	-0,87	
25	1,1	-0,90					
27	1,4	0,0054					
28	1,3	-0,52					
31	1,3	-0,35					
32	1,5	0,27					
33	1,6	0,80					
34	1,3	-0,42					
36	1,6	0,66					
38	1,4	-0,10					
40	1,4	0,014					
43	1,5	0,23					
45	1,3	-0,21					
49	1,5	0,52					
54	1,8	1,5					
57	1,6	0,73					
58	1,7	1,3					
61	1,3	-0,34					
63	1,5	0,26					
65	1,5	0,53					
70	1,2	-0,85					
73	1,3	-0,39					
75	1,3	-0,20					
76	1,4	-0,15					
77	1,3	-0,32					
80	1,3	-0,24					
87	1,5	0,30					
88	1,4	0,014					
89	1,4	-0,0054					
90	1,4	-0,13					
91	1,5	0,37					
92	1,3	-0,19					
94	1,4	0,14					
95	1,4	0,16					
100	1,1	-0,99					

Consensus statistics

Consensus median, pg/g	1,4
Median all values pg/g	1,4
Consensus mean, pg/g	1,4
Standard deviation, pg/g	0,24
Relative standard deviation, %	17
No. of values reported	56
No. of values removed	0
No. of reported non-detects	0

2,3,4,7,8 PeCDF

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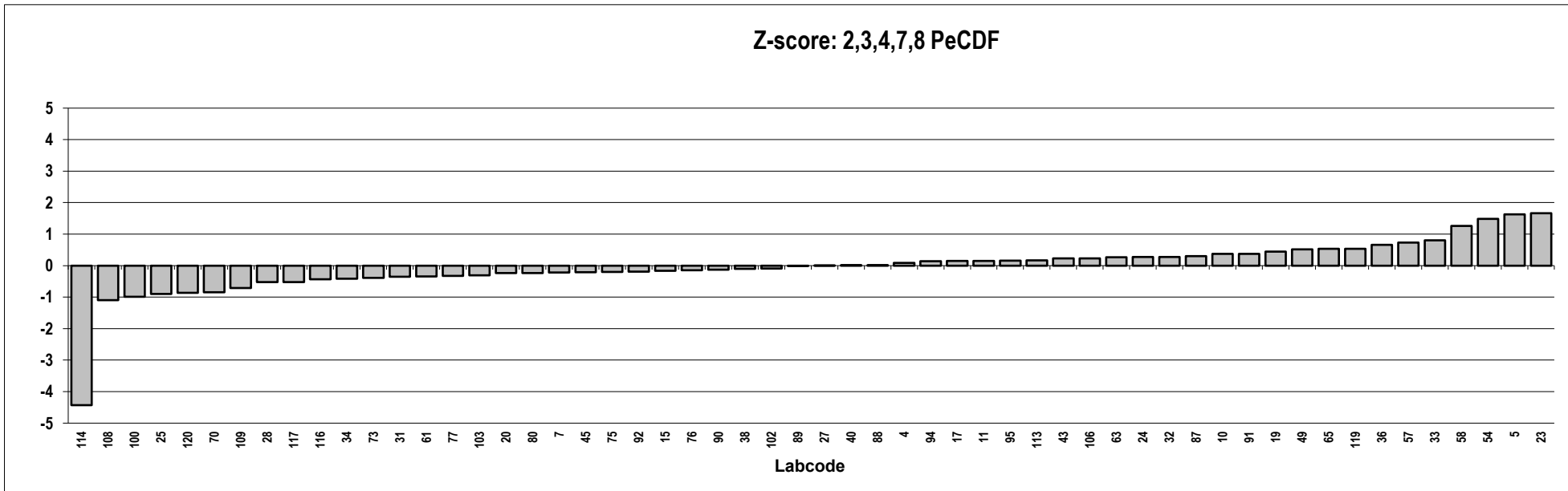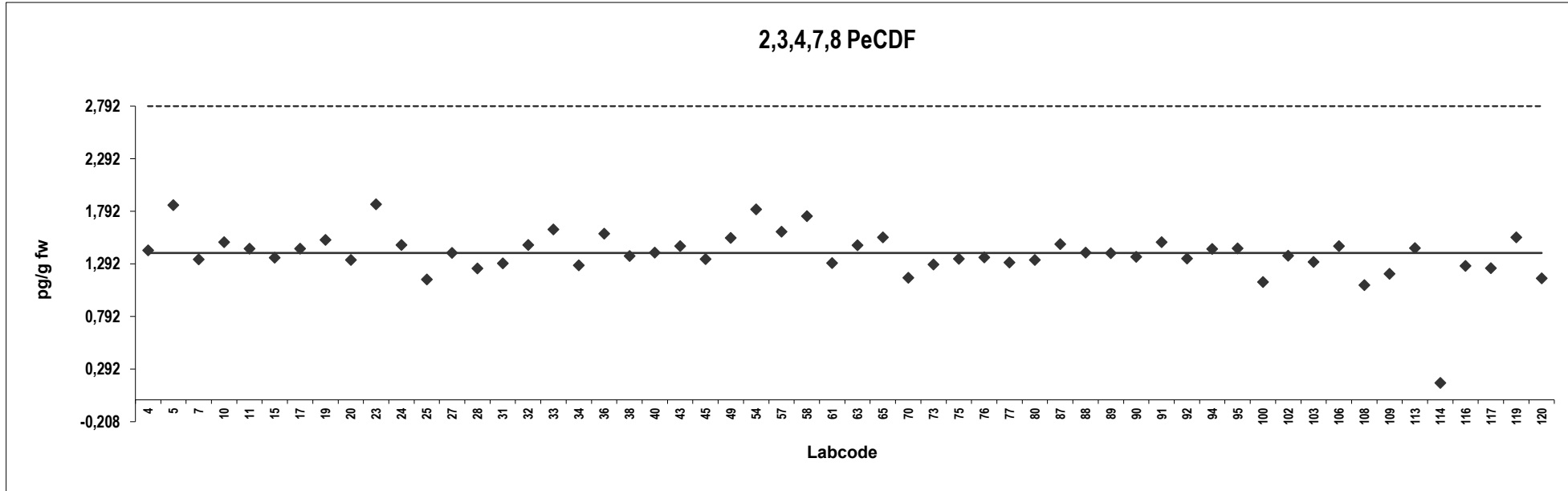
Brown meat

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,36	0,22		102	0,35	0,033	
5	0,44	1,3		103	0,32	-0,37	
7	0,29	-0,75		106	0,32	-0,29	
10	0,38	0,57		108	0,31	-0,58	
11	0,33	-0,22		109	0,29	-0,79	
15	0,34	-0,097		113	0,42	1,1	
17	0,36	0,21		114	0,039	-4,4	
19	0,35	0,032		116	0,33	-0,17	
20	0,34	-0,068		117	0,34	-0,010	
23	0,47	1,7		119	0,39	0,60	
24	0,34	-0,020		120	0,34	-0,083	
25	0,31	-0,52					
27	0,88	7,8	Outlier				
28	0,12	-3,3	ND				
31	0,32	-0,41					
32	0,40	0,76					
33	0,42	1,0					
34	0,36	0,25					
36	0,40	0,76					
38	0,68	4,9					
40	0,28	-0,97					
43	0,33	-0,21					
45	0,34	-0,021					
49	0,36	0,22					
54	0,36	0,22					
57	0,39	0,63					
58	0,42	1,1					
61	0,33	-0,19					
63	0,40	0,73					
65	0,38	0,46					
70	0,73	5,6	Outlier				
73	0,32	-0,37					
75	0,34	-0,068					
76	0,34	-0,077					
77	0,42	1,1					
80	0,38	0,48					
87	0,40	0,74					
88	0,30	-0,66					
89	0,33	-0,15					
90	0,35	0,010					
91	0,35	0,077					
92	0,44	1,4					
94	0,32	-0,39					
95	0,37	0,37					
100	0,21	-2,0					

Consenus statistics	
Consensus median, pg/g	0,34
Median all values pg/g	0,35
Consensus mean, pg/g	0,35
Standard deviation, pg/g	0,083
Relative standard deviation, %	24
No. of values reported	56
No. of values removed	2
No. of reported non-detects	1
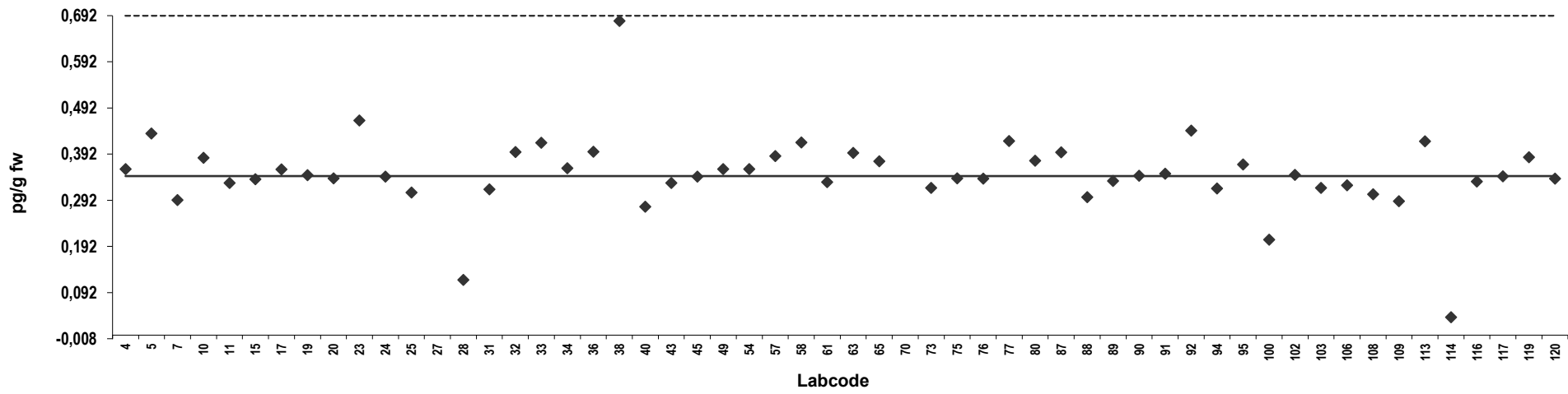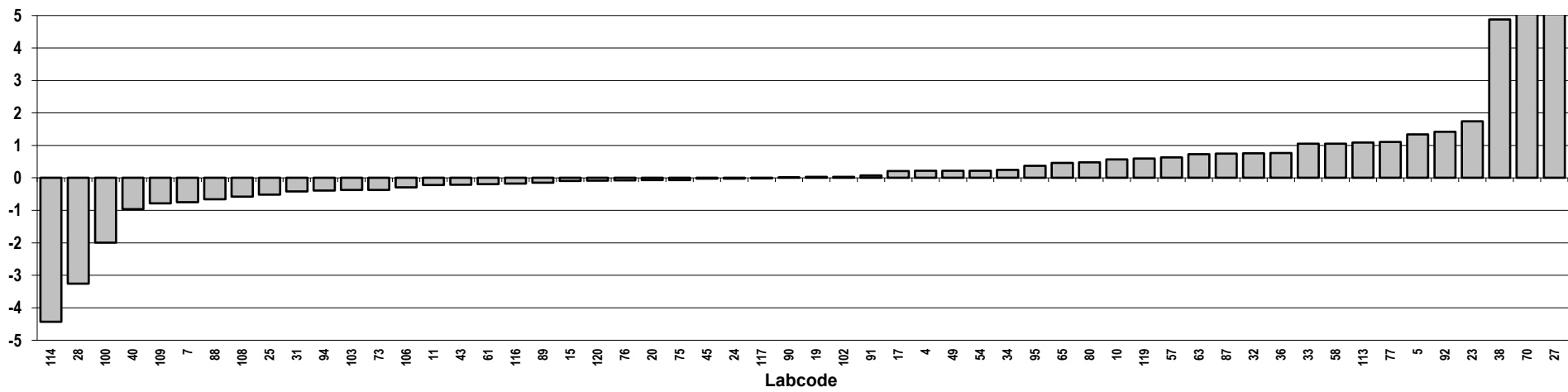
Brown meat
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,20	-0,12		102	0,22	0,44	
5	0,27	1,6		103	0,24	0,88	
7	0,20	-0,17		106	0,21	0,026	
10	0,24	0,78		108	0,16	-1,0	
11	0,20	-0,0018		109	0,18	-0,53	
15	0,20	-0,047		113	0,27	1,5	
17	0,22	0,27		114	0,025	-4,4	
19	0,17	-0,94		116	0,23	0,61	
20	0,20	-0,12		117	0,20	-0,12	
23	0,21	0,15		119	0,23	0,60	
24	0,20	-0,018		120	0,23	0,56	
25	0,20	-0,21					
27	0,24	0,75					
28	0,11	-2,3	ND				
31	0,19	-0,31					
32	0,20	-0,096					
33	0,25	1,0					
34	0,23	0,59					
36	0,24	0,91					
38	0,10	-2,6	ND				
40	0,17	-0,85					
43	0,17	-0,85					
45	0,21	0,17					
49	0,19	-0,36					
54	0,22	0,37					
57	0,21	0,065					
58	0,25	1,0					
61	0,12	-2,0					
63	0,22	0,27					
65	0,22	0,40					
70	0,21	0,0018					
73	0,22	0,27					
75	0,20	-0,071					
76	0,19	-0,32					
77	0,36	3,7					
80	0,23	0,49					
87	0,22	0,29					
88	0,18	-0,49					
89	0,21	0,059					
90	0,20	-0,030					
91	0,20	-0,12					
92	0,28	1,9					
94	0,18	-0,61					
95	0,18	-0,61					
100	0,15	-1,4					

Consenus statistics

Consensus median, pg/g	0,20
Median all values pg/g	0,20
Consensus mean, pg/g	0,20
Standard deviation, pg/g	0,047
Relative standard deviation, %	23
No. of values reported	56
No. of values removed	0
No. of reported non-detects	2

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

Z-score: 1,2,3,6,7,8 HxCDF
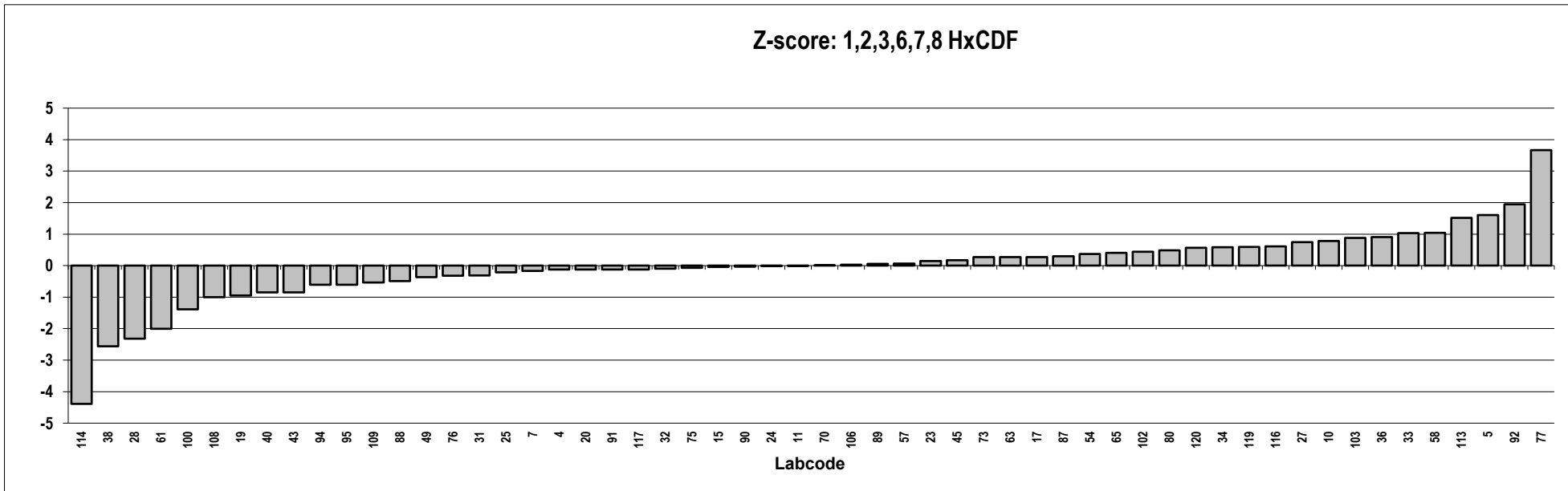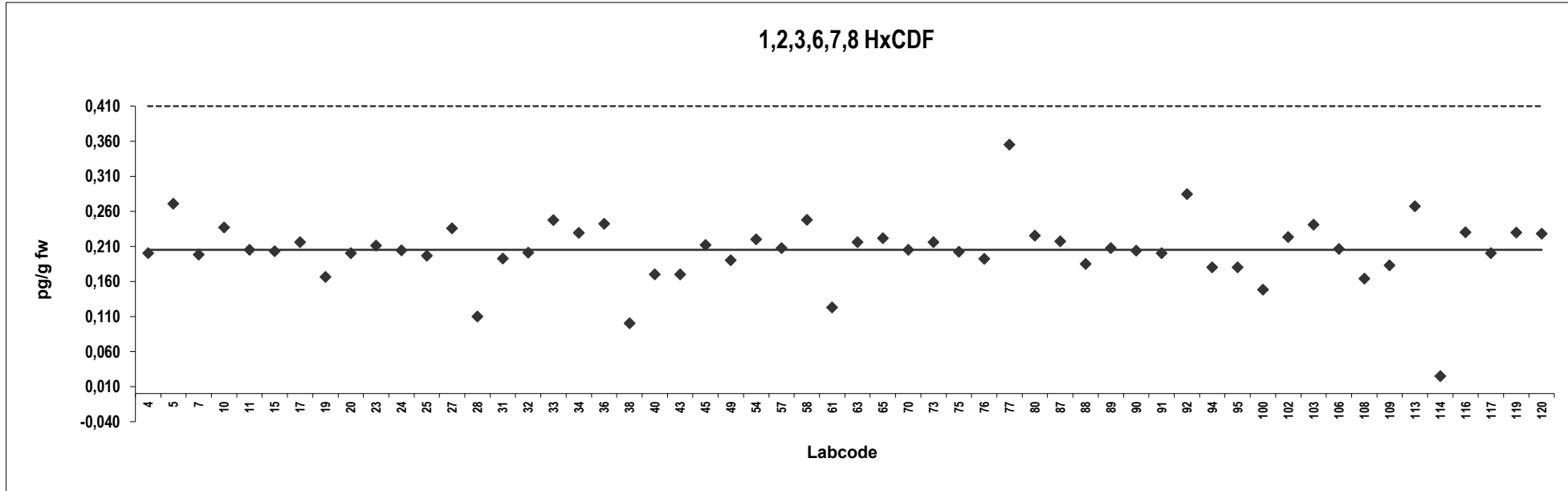
Brown meat
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,49	-0,37		102	0,58	0,44	
5	0,73	1,9		103	0,59	0,54	
7	0,55	0,20		106	0,51	-0,16	
10	0,56	0,30		108	0,41	-1,1	
11	0,49	-0,36		109	0,47	-0,58	
15	0,52	-0,082		113	0,67	1,3	
17	0,52	-0,10		114	0,057	-4,5	
19	0,53	-0,013		116	0,52	-0,12	
20	0,51	-0,18		117	0,52	-0,13	
23	0,54	0,088		119	0,59	0,59	
24	0,53	-0,019		120	0,51	-0,22	
25	0,050	-4,5					
27	0,56	0,33					
28	0,62	0,89					
31	0,49	-0,34					
32	0,57	0,43					
33	0,68	1,4					
34	0,49	-0,33					
36	0,61	0,77					
38	0,59	0,61					
40	0,49	-0,37					
43	0,49	-0,37					
45	0,53	-0,018					
49	0,52	-0,082					
54	0,67	1,3					
57	0,56	0,30					
58	0,67	1,4					
61	0,41	-1,1					
63	0,59	0,61					
65	0,60	0,66					
70	0,50	-0,32					
73	0,55	0,18					
75	0,51	-0,17					
76	0,47	-0,55					
77	0,60	0,65					
80	0,56	0,27					
87	0,54	0,14					
88	0,58	0,52					
89	0,55	0,19					
90	0,50	-0,29					
91	0,55	0,20					
92	0,53	0,050					
94	0,48	-0,47					
95	0,53	0,013					
100	0,42	-1,1					

Consensus statistics

Consensus median, pg/g	0,53
Median all values pg/g	0,53
Consensus mean, pg/g	0,53
Standard deviation, pg/g	0,11
Relative standard deviation, %	21
No. of values reported	56
No. of values removed	0
No. of reported non-detects	0

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

Labcode
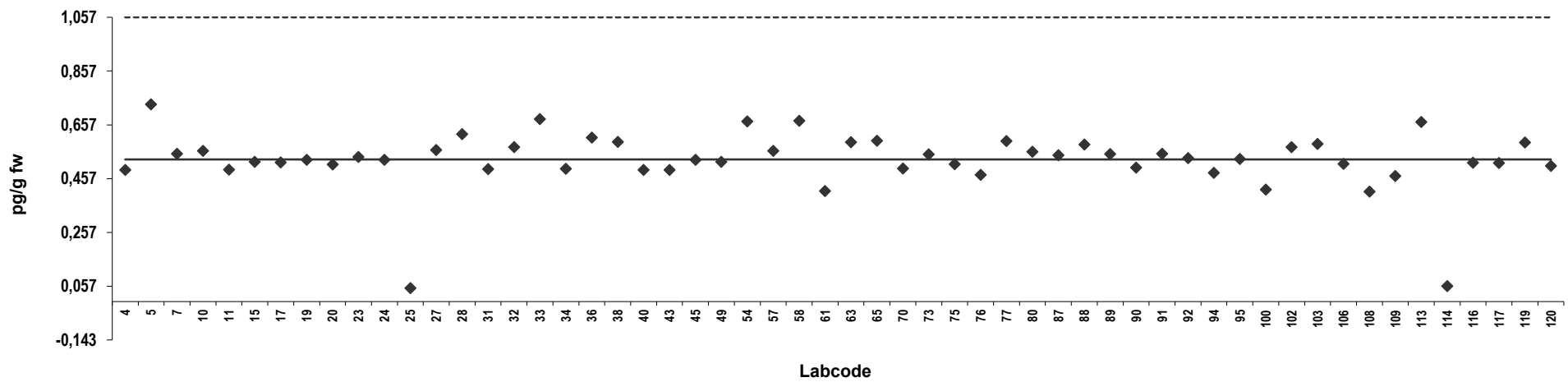
pg/g fw

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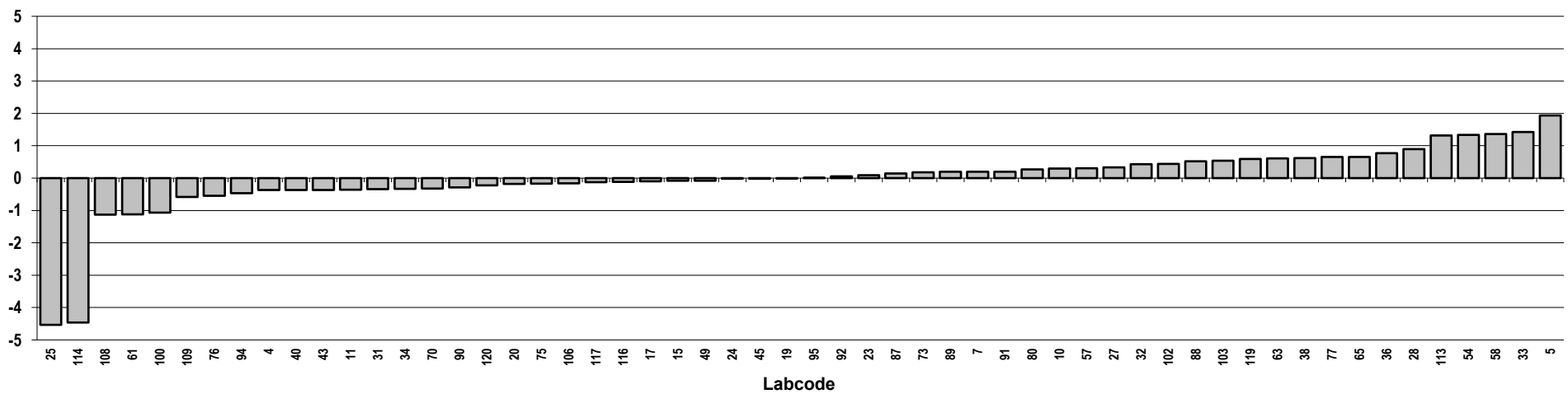
Labcode

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	6,9	Outlier,ND	102	0,035	3,3	ND
5	0,045	5,6		103	0,031	2,4	
7	0,0020	-4,5		106	0,022	0,24	ND
10	0,0053	-3,7		108	0,033	2,9	
11	0,0045	-3,9	ND	109	0,010	-2,6	ND
15	0,017	-0,95		113	0,020	-0,14	
17	0,0037	-4,1		114	0,011	-2,4	
19	0,075	13	Outlier,ND	116	0,034	3,2	
20	0,050	6,9	Outlier,ND	117	0,022	0,24	
23	0,038	4,0	ND	119	0,0052	-3,8	
24	0,0096	-2,7		120	0,020	-0,24	
25	0,41	93	Outlier				
27	0,029	1,8	ND				
28	0,32	71	Outlier				
31	0,0045	-3,9	ND				
32	0,027	1,4					
33	0,022	0,21					
34	0,0056	-3,7	ND				
36	0,020	-0,24	ND				
38	0,10	19	Outlier,ND				
40	0,012	-2,1	ND				
43	0,030	2,1	ND				
45	0,033	2,8					
49	0,012	-2,1					
54	0,0072	-3,3					
57	0,028	1,7					
58	0,050	6,9	Outlier,ND				
61	0,025	1,1					
63	0,022	0,24					
65	0,021	0,00					
70	0,11	21	Outlier,ND				
73	0,042	5,1					
75	0,018	-0,71					
76	0,025	1,0					
77	0,10	19	Outlier,ND				
80	0,025	0,95	ND				
87	0,023	0,48					
88	0,031	2,5					
89	0,026	1,3					
90	0,016	-1,3					
91	0,0040	-4,0	ND				
92	0,14	28	Outlier				
94	0,0070	-3,3	ND				
95	0,050	6,9	Outlier,ND				
100	0,017	-0,86	ND				

Consenus statistics	
Consensus median, pg/g	0,021
Median all values pg/g	0,024
Consensus mean, pg/g	0,020
Standard deviation, pg/g	0,011
Relative standard deviation, %	56
No. of values reported	56
No. of values removed	11
No. of reported non-detects	23

1,2,3,7,8,9 HxCDF
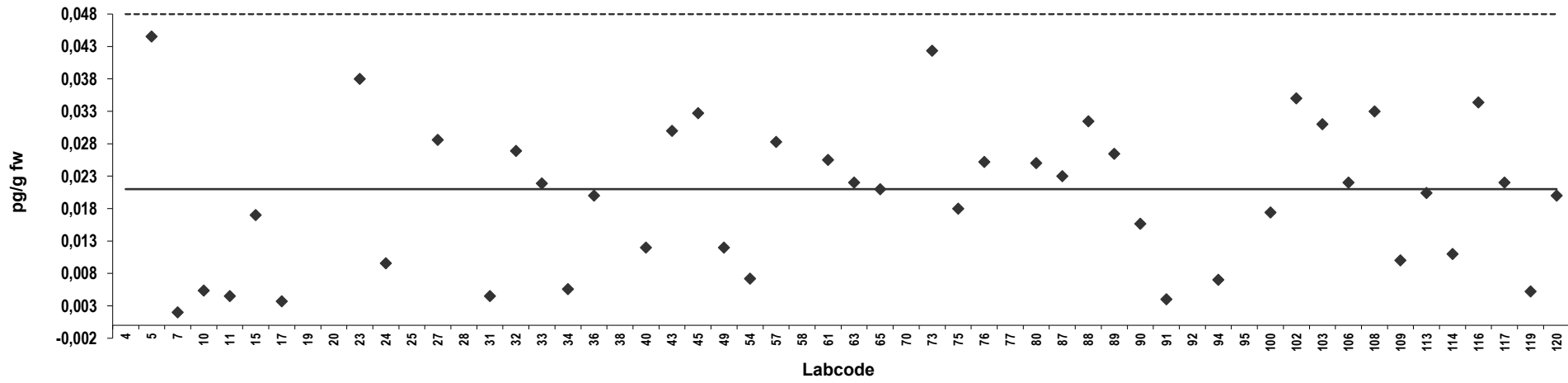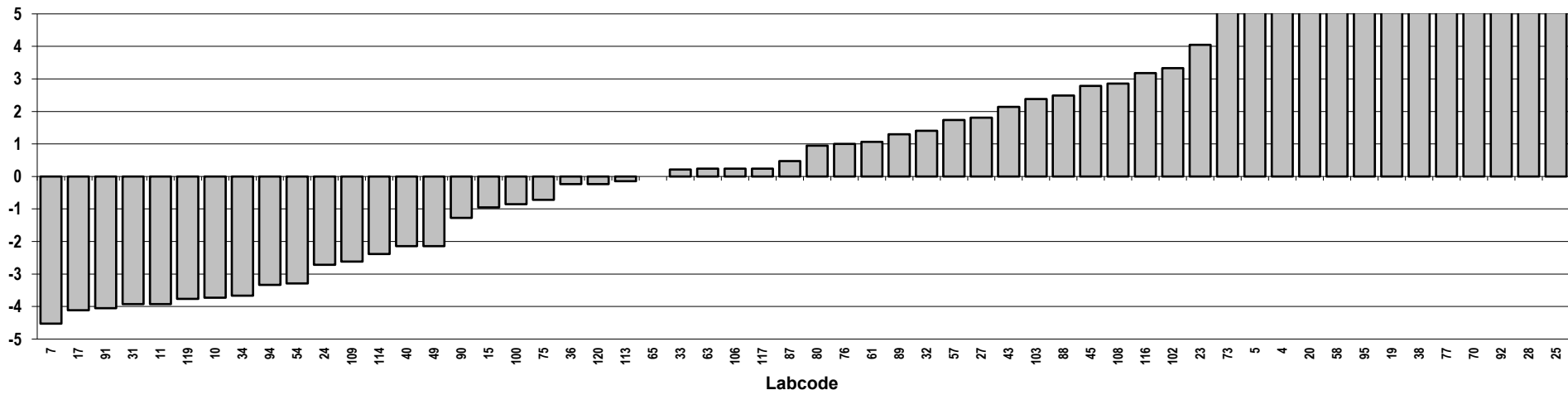
pg/g fw

Labcode

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

Labcode

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

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,54	-0,030		102	0,52	-0,23	
5	0,75	1,9		103	0,59	0,39	
7	0,49	-0,50		106	0,54	-0,048	
10	0,57	0,28		108	0,41	-1,3	
11	0,53	-0,094		109	0,43	-1,1	
15	0,54	-0,021		113	0,68	1,3	
17	0,50	-0,43		114	0,053	-4,5	
19	0,55	0,093		116	0,51	-0,30	
20	0,51	-0,31		117	0,56	0,14	
23	0,54	-0,012		119	0,62	0,69	
24	0,54	0,012		120	0,54	-0,012	
25	0,43	-1,0					
27	0,57	0,22					
28	0,92	3,5					
31	0,57	0,29					
32	0,57	0,24					
33	0,64	0,92					
34	0,50	-0,39					
36	0,61	0,57					
38	0,55	0,055					
40	0,51	-0,31					
43	0,49	-0,49					
45	0,55	0,053					
49	0,51	-0,31					
54	0,66	1,1					
57	0,51	-0,31					
58	0,59	0,41					
61	0,46	-0,77					
63	0,55	0,053					
65	0,63	0,76					
70	0,48	-0,61					
73	0,54	-0,051					
75	0,54	-0,012					
76	0,48	-0,59					
77	0,72	1,7					
80	0,57	0,23					
87	0,58	0,31					
88	0,57	0,26					
89	0,57	0,22					
90	0,50	-0,43					
91	0,54	-0,030					
92	0,57	0,24					
94	0,56	0,12					
95	0,56	0,15					
100	0,45	-0,87					

Consenus statistics

Consensus median, pg/g	0,54
Median all values pg/g	0,54
Consensus mean, pg/g	0,55
Standard deviation, pg/g	0,11
Relative standard deviation, %	19
No. of values reported	56
No. of values removed	0
No. of reported non-detects	0

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

Z-score: 1,2,3,4,6,7,8 HpCDF
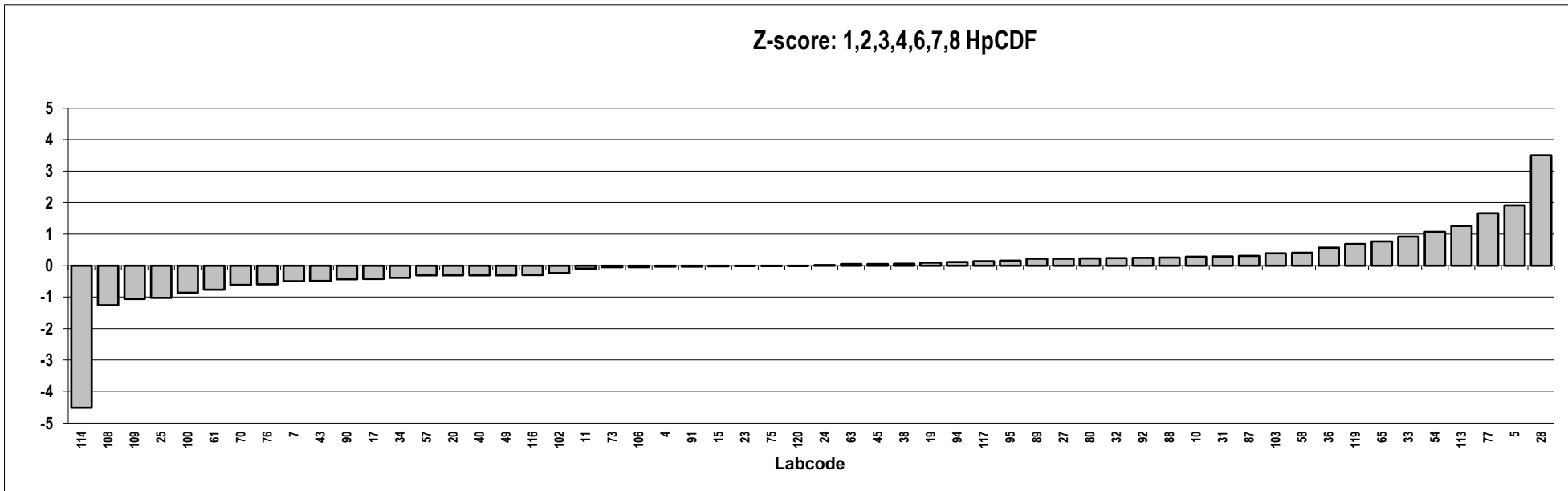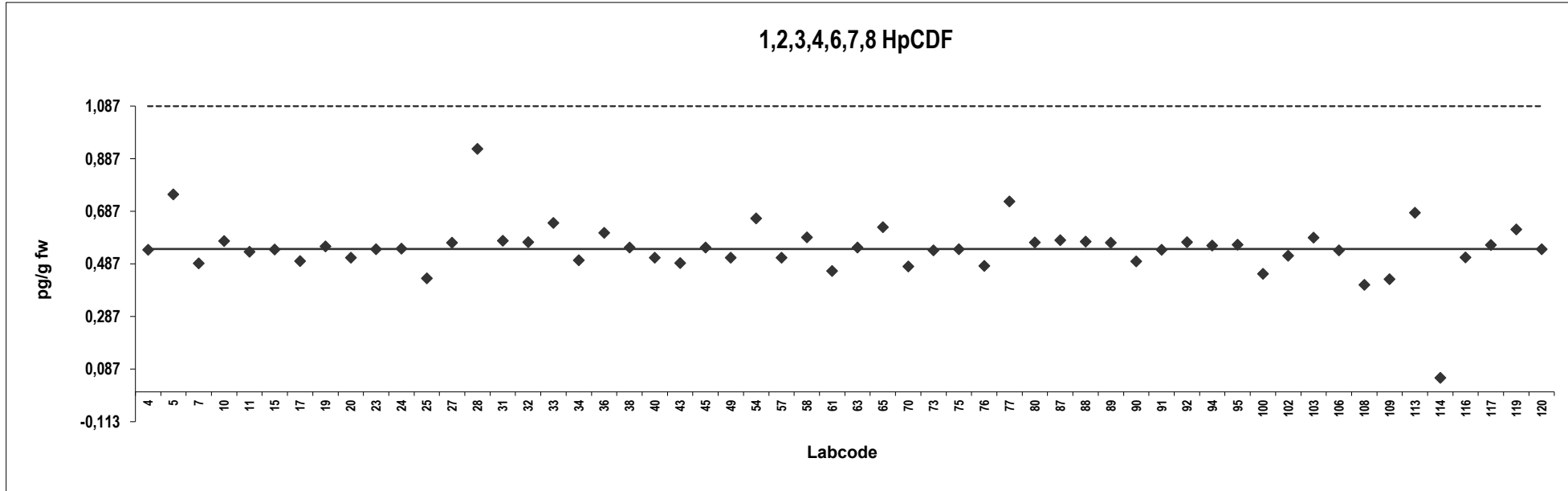
Brown meat
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,050	24	Outlier,ND	102	0,021	7,1	Outlier,ND
5	0,011	1,4		103	0,013	2,5	
7	0,0040	-2,7		106	0,011	1,3	
10	0,0071	-0,93		108	0,020	6,5	ND
11	0,0056	-1,8	ND	109	0,020	6,5	ND
15	0,0080	-0,39		113	0,0090	0,19	
17	0,0086	-0,017		114	0,0087	0,017	ND
19	0,040	18	Outlier,ND	116	0,018	5,4	ND
20	0,010	0,77		117	0,015	3,6	ND
23	0,029	11	Outlier,ND	119	0,0062	-1,4	
24	0,0050	-2,1		120	0,011	1,3	
25	0,0053	-1,9					
27	0,026	9,8	Outlier,ND				
28	0,072	37	Outlier,ND				
31	0,0090	0,18	ND				
32	0,0044	-2,5	ND				
33	0,0066	-1,2					
34	0,0087	0,017					
36	0,0060	-1,5	ND				
38	0,10	53	Outlier,ND				
40	0,013	2,5	ND				
43	0,030	12	Outlier,ND				
45	0,014	3,0	ND				
49	0,0060	-1,5					
54	0,19	105	Outlier				
57	0,0073	-0,79					
58	0,050	24	Outlier,ND				
61	0,045	21	Outlier				
63	0,0070	-0,96	ND				
65	0,020	6,5					
70	0,10	55	Outlier,ND				
73	0,010	0,75					
75	0,010	0,77					
76	0,010	0,77	ND				
77	0,15	81	Outlier,ND				
80	0,050	24	Outlier,ND				
87	0,0030	-3,3					
88	0,0079	-0,47					
89	0,0069	-1,0					
90	0,0063	-1,4					
91	0,0030	-3,3	ND				
92	0,0087	0,042					
94	0,0035	-3,0					
95	0,060	30	Outlier,ND				
100	0,023	8,2	Outlier				

Consensus statistics

|	
Consensus median, pg/g	0,0087
Median all values pg/g	0,010
Consensus mean, pg/g	0,0092
Standard deviation, pg/g	0,0045
Relative standard deviation, %	49
No. of values reported	56
No. of values removed	16
No. of reported non-detects	27

1,2,3,4,7,8,9 HpCDF
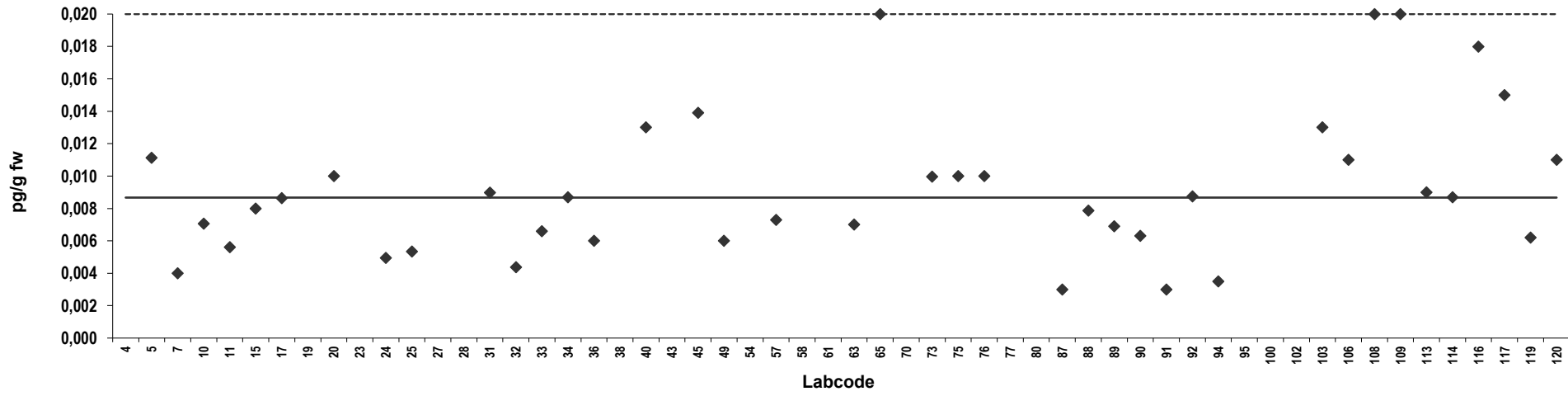
Z-score: 1,2,3,4,7,8,9 HpCDF
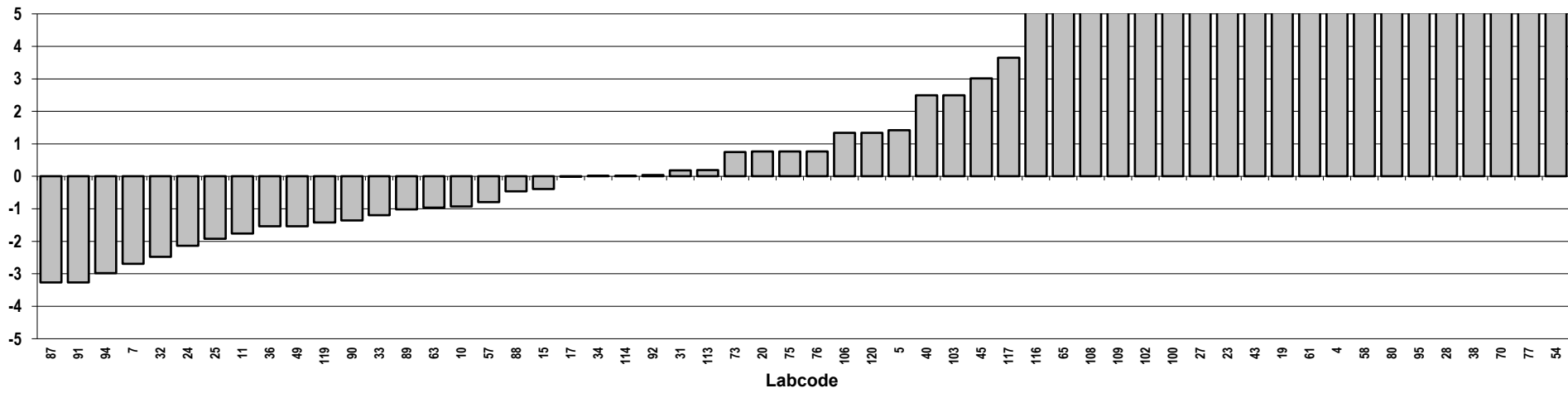
Brown meat
Congener: OCDF

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	0,20	25	Outlier,ND	102	0,048	2,1	ND
5	0,053	2,8		103	0,045	1,7	
7	0,039	0,79		106	0,031	-0,43	
10	0,028	-0,80		108	0,050	2,4	ND
11	0,028	-0,87	ND	109	0,041	1,0	
15	0,040	0,94		113	0,015	-2,8	
17	0,026	-1,2		114	0,0087	-3,7	ND
19	0,042	1,2		116	0,014	-2,9	
20	0,030	-0,55		117	0,037	0,49	
23	0,043	1,3	ND	119	0,027	-1,1	
24	0,031	-0,44		120	0,081	7,0	Outlier
25	0,060	3,9					
27	0,027	-0,95					
28	1,1	154	Outlier				
31	0,024	-1,5					
32	0,030	-0,55					
33	0,032	-0,20					
34	0,020	-2,0					
36	0,036	0,27					
38	0,20	25	Outlier,ND				
40	0,027	-0,99	ND				
43	0,050	2,4	ND				
45	0,029	-0,74					
49	0,038	0,64					
54	0,084	7,5	Outlier				
57	0,033	-0,12					
58	0,050	2,4	ND				
61	0,096	9,3	Outlier				
63	0,024	-1,4					
65	0,045	1,7					
70	0,092	8,6	Outlier,ND				
73	0,042	1,2					
75	0,038	0,64					
76	0,020	-2,0	ND				
77	0,30	40	Outlier,ND				
80	0,10	9,8	Outlier,ND				
87	0,036	0,35					
88	0,037	0,49					
89	0,034	0,12					
90	0,037	0,49					
91	0,018	-2,3					
92	0,26	33	Outlier				
94	0,018	-2,3					
95	0,026	-1,1	ND				
100	0,052	2,7					

Consenus statistics

Consensus median, pg/g	0,034
Median all values pg/g	0,037
Consensus mean, pg/g	0,034
Standard deviation, pg/g	0,011
Relative standard deviation, %	34
No. of values reported	56
No. of values removed	10
No. of reported non-detects	15

OCDF

pg/g fw

Labcode

Z-score: OCDF
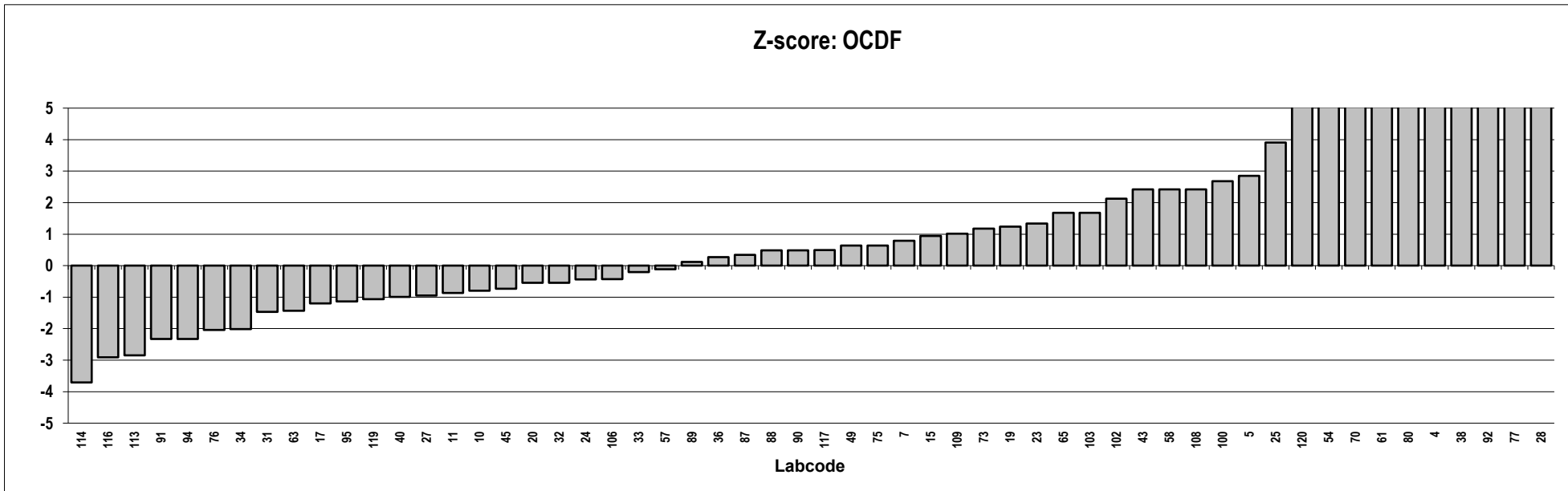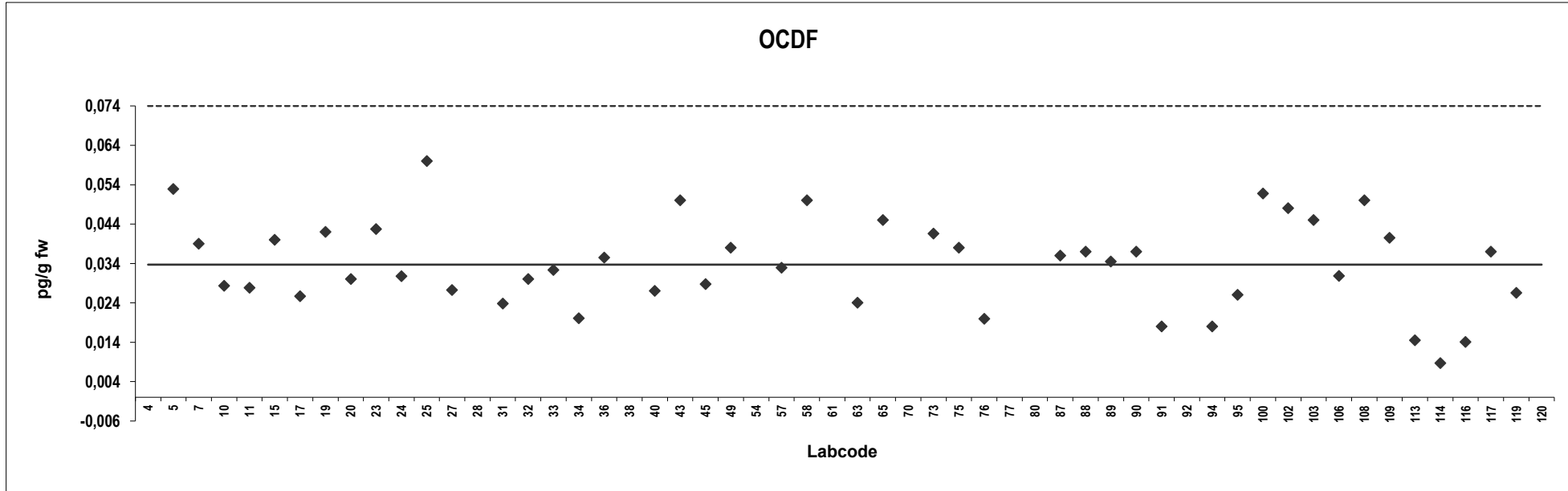
Labcode

Brown meat

Congener: PCB 77

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	25	-0,13		106	22	-0,69	
5	35	1,8		108	26	0,093	
7	24	-0,45		109	24	-0,46	
10	27	0,17		113	38	2,4	
11	28	0,33		114	3,4	-4,3	
15	28	0,46		116	28	0,35	
17	28	0,46		117	28	0,31	
19	21	-0,93		119	25	-0,16	
20	24	-0,33		120	25	-0,14	
23	28	0,40					
24	25	-0,10					
25	21	-1,0					
27	23	-0,56					
28	26	0,016					
31	26	0,013					
32	23	-0,59					
33	38	2,3					
34	24	-0,31					
36	24	-0,38					
38	29	0,63					
40	34	1,6					
43	24	-0,39					
45	26	0,11					
49	24	-0,31					
54	24	-0,39					
57	26	0,053					
58	35	1,7					
61	22	-0,84					
63	26	-0,061					
65	28	0,43					
70	22	-0,68					
75	28	0,36					
77	34	1,6					
80	26	-0,013					
87	25	-0,17					
88	25	-0,26					
89	22	-0,71					
90	28	0,37					
91	28	0,40					
92	27	0,12					
94	24	-0,45					
95	30	0,71					
100	28	0,32					
102	28	0,40					
103	22	-0,79					

Consensus statistics

Consensus median, pg/g	26
Median all values pg/g	26
Consensus mean, pg/g	26
Standard deviation, pg/g	5,1
Relative standard deviation, %	19
No. of values reported	54
No. of values removed	0
No. of reported non-detects	0

PCB 77

Z-score: PCB 77
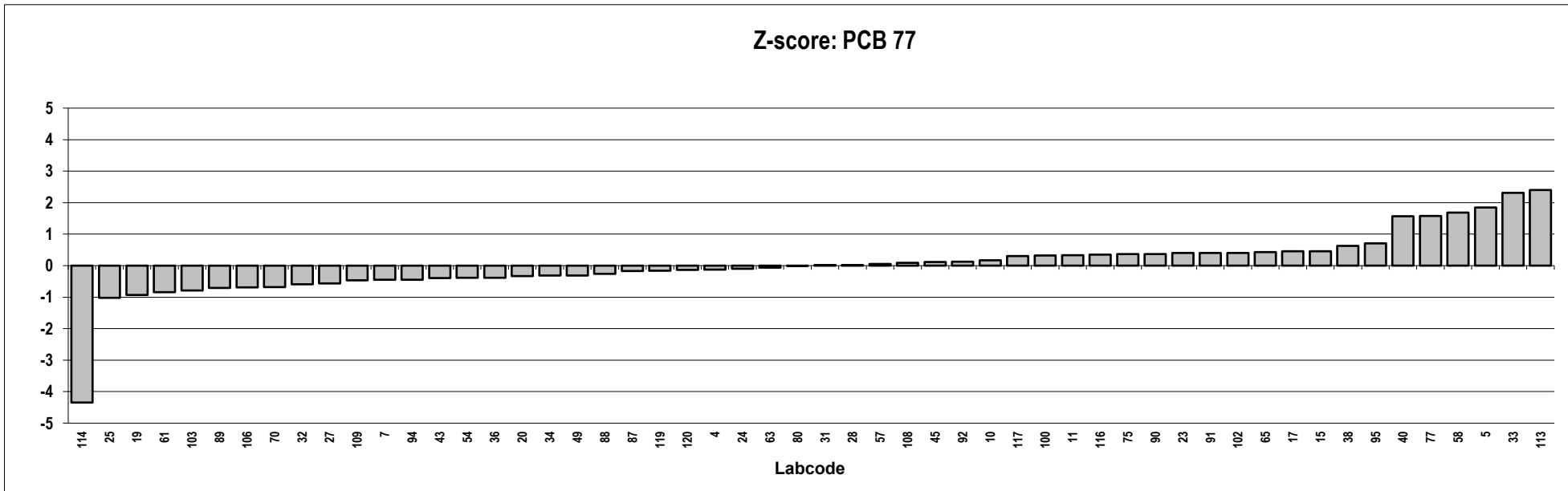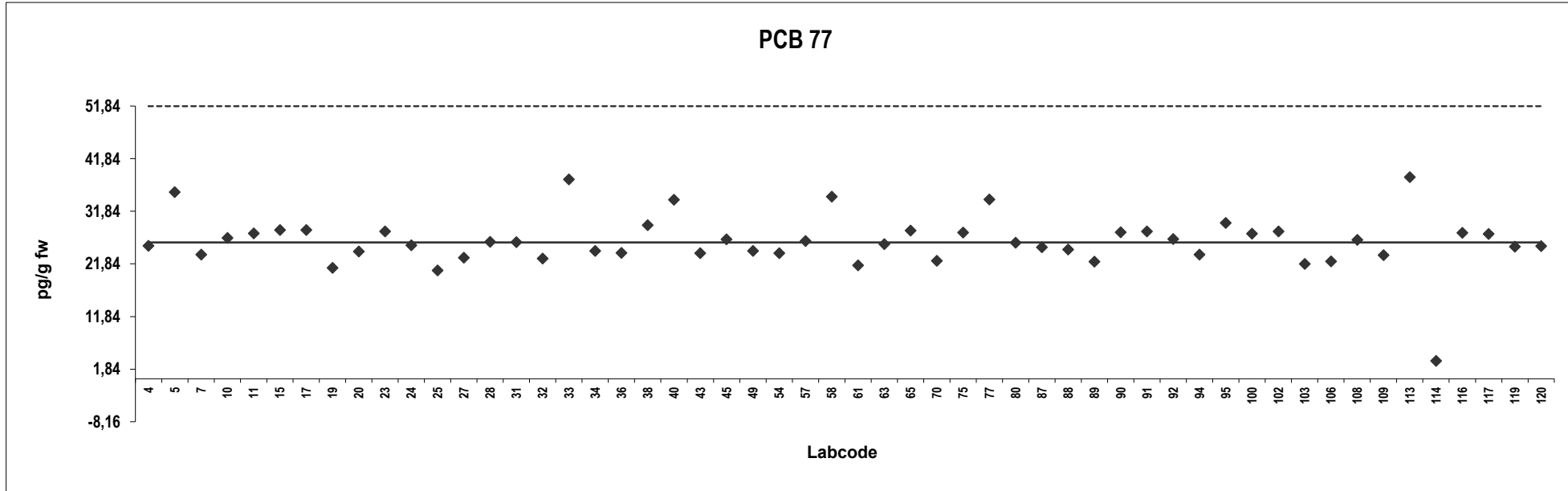
Brown meat
Congener: PCB 126

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	8,7	0,20		106	7,4	-0,59	
5	12	2,4		108	8,4	0,023	
7	8,9	0,30		109	7,6	-0,46	
10	9,2	0,50		113	12,6	2,5	
11	8,4	0,011		114	0,90	-4,5	
15	8,8	0,23		116	9,8	0,86	
17	9,1	0,41		117	7,8	-0,33	
19	7,5	-0,50		119	8,1	-0,17	
20	7,6	-0,44		120	8,2	-0,12	
23	9,7	0,81					
24	8,6	0,13					
25	8,9	0,34					
27	7,8	-0,34					
28	8,8	0,24					
31	8,0	-0,24					
32	5,6	-1,7					
33	12	2,1					
34	7,4	-0,58					
36	7,7	-0,38					
38	9,5	0,68					
40	7,8	-0,37					
43	7,3	-0,65					
45	8,6	0,14					
49	7,3	-0,62					
54	8,4	0,0053					
57	8,4	-0,0053					
58	12	2,0					
61	5,1	-1,9					
63	8,8	0,26					
65	8,7	0,17					
70	3,2	-3,1	ND				
75	8,8	0,28					
77	10	1,2					
80	7,6	-0,47					
87	8,2	-0,13					
88	8,4	-0,0094					
89	8,0	-0,25					
90	8,3	-0,022					
91	8,7	0,20					
92	8,6	0,15					
94	7,6	-0,45					
95	9,3	0,55					
100	7,7	-0,39					
102	8,7	0,18					
103	8,0	-0,24					

Consenus statistics

Consensus median, pg/g	8,4
Median all values pg/g	8,4
Consensus mean, pg/g	8,3
Standard deviation, pg/g	1,8
Relative standard deviation, %	22
No. of values reported	54
No. of values removed	0
No. of reported non-detects	1

PCB 126

Z-score: PCB 126
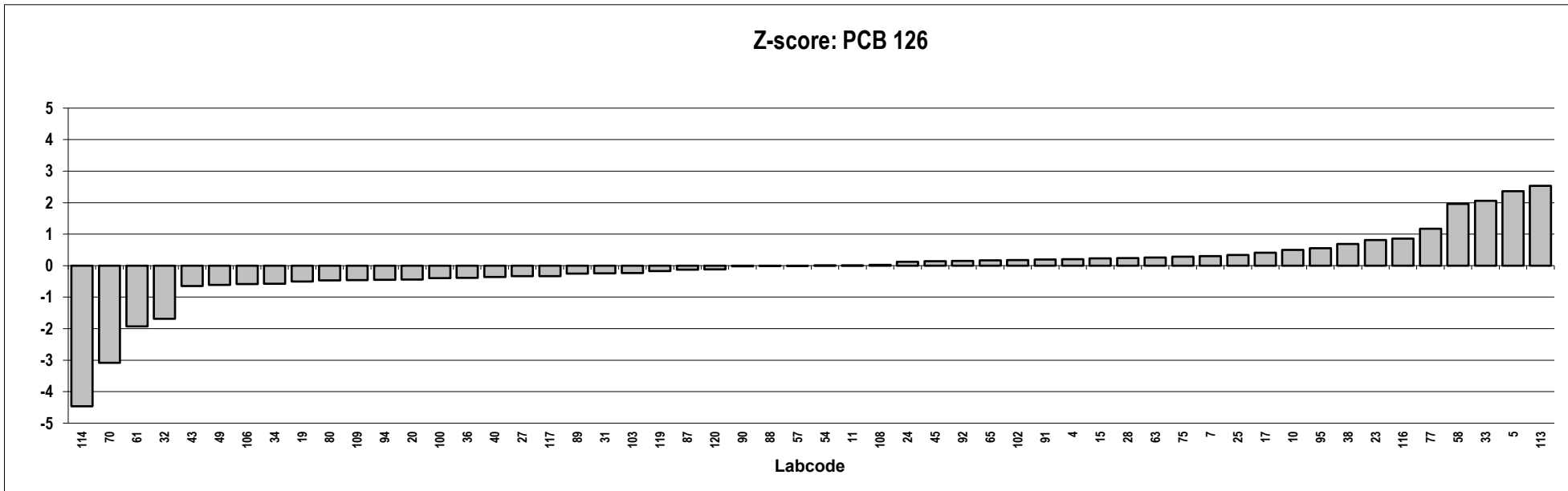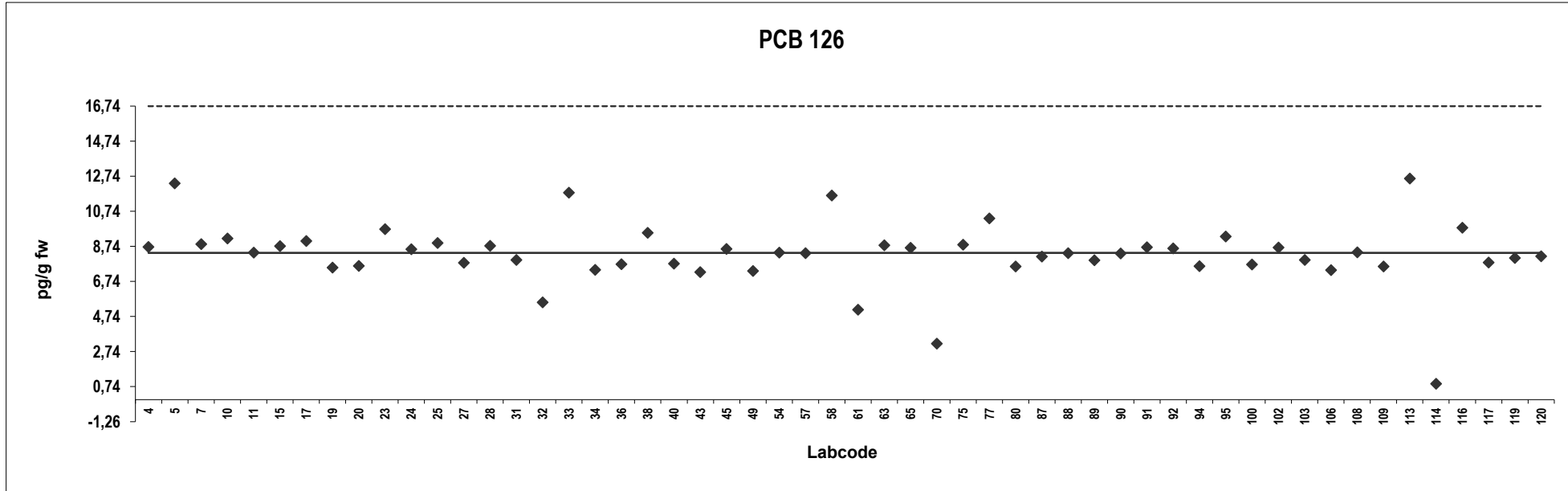
Brown meat
Congener: PCB 169

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	3,0	0,19		106	2,8	-0,16	
5	4,0	1,9		108	2,9	-0,016	
7	3,2	0,49		109	2,8	-0,15	
10	3,3	0,68		113	2,2	-1,1	
11	3,0	0,19		114	0,30	-4,5	
15	3,1	0,32		116	2,1	-1,3	
17	3,2	0,59		117	2,6	-0,51	
19	2,5	-0,62		119	2,9	0,075	
20	2,3	-1,0		120	2,9	0,038	
23	2,9	0,0017					
24	2,9	-0,018					
25	2,4	-0,80					
27	2,6	-0,45					
28	2,6	-0,54					
31	2,9	0,0047					
32	2,8	-0,077					
33	4,3	2,5					
34	2,7	-0,36					
36	2,8	-0,063					
38	3,0	0,26					
40	3,4	1,0					
43	2,7	-0,22					
45	3,1	0,33					
49	2,6	-0,42					
54	1,8	-1,8					
57	3,0	0,31					
58	4,3	2,5					
61	2,4	-0,90					
63	3,6	1,2					
65	2,9	0,12					
70	3,5	1,1	ND				
75	3,0	0,26					
77	3,8	1,6					
80	2,2	-1,2					
87	2,9	-0,0017					
88	3,0	0,29					
89	2,4	-0,76					
90	2,8	-0,089					
91	3,1	0,40					
92	2,9	0,066					
94	2,8	-0,051					
95	2,8	-0,12					
100	2,4	-0,83					
102	3,4	0,84					
103	3,1	0,46					

Consenus statistics

Consensus median, pg/g	2,9
Median all values pg/g	2,9
Consensus mean, pg/g	2,9
Standard deviation, pg/g	0,60
Relative standard deviation, %	21
No. of values reported	54
No. of values removed	0
No. of reported non-detects	1

PCB 169

Z-score: PCB 169
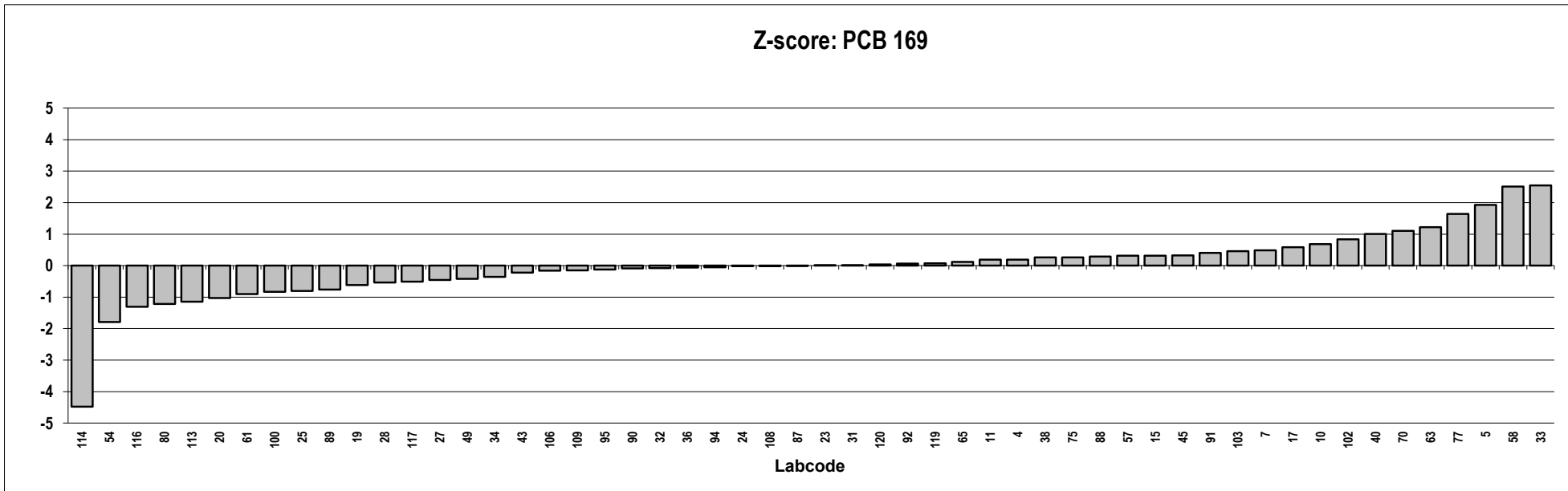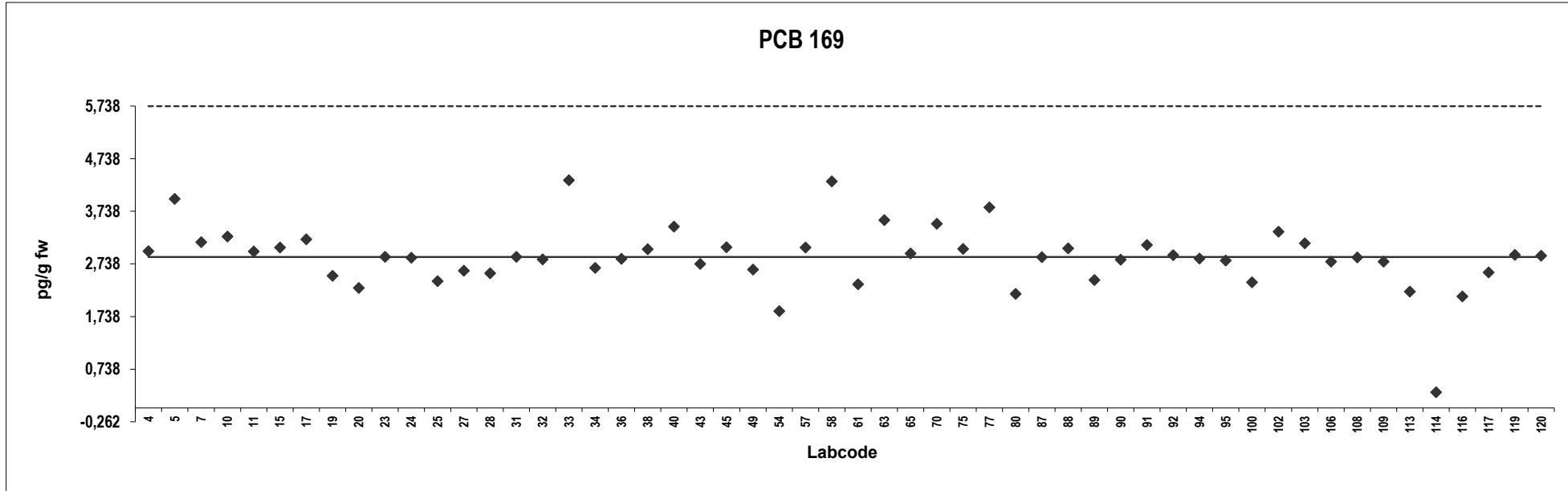
Brown meat
Congener: PCB 81

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	2,0	0,80	ND	106	1,6	-0,39	
5	2,6	2,6		108	1,8	0,28	
7	1,8	0,22		109	1,6	-0,38	
10	1,8	0,25		113	1,6	-0,26	
11	1,5	-0,56		114	0,30	-4,1	
15	1,9	0,54		116	0,99	-2,1	
17	0,79	-2,7		117	1,9	0,37	
19	1,5	-0,74		119	1,8	0,32	
20	1,6	-0,27		120	1,6	-0,47	
23	2,1	1,0					
24	1,6	-0,44					
25	1,2	-1,6					
27	1,3	-1,2					
28	0,26	-4,2	ND				
31	1,7	-0,12					
32	1,0	-2,1					
33	2,5	2,2					
34	1,6	-0,37					
36	1,7	-0,088					
38	1,8	0,24					
40	0,58	-3,3					
43	2,7	2,9					
45	1,7	0,06					
49	1,8	0,13					
54	1,8	0,074					
57	3,6	5,5	Outlier				
58	2,6	2,5					
61	1,4	-1,0					
63	2,0	0,71					
65	1,8	0,27					
70	3,3	4,6	ND				
75	1,9	0,60					
77	2,0	0,80					
80	1,6	-0,24					
87	1,8	0,34					
88	1,7	0,00					
89	1,5	-0,60					
90	1,7	-0,11					
91	2,0	0,80					
92	1,8	0,28					
94	1,8	0,16					
95	1,7	-0,16					
100	1,3	-1,2					
102	1,9	0,36					
103	1,0	-2,1					

Consenus statistics

Consensus median, pg/g	1,7
Median all values pg/g	1,7
Consensus mean, pg/g	1,7
Standard deviation, pg/g	0,54
Relative standard deviation, %	32
No. of values reported	54
No. of values removed	1
No. of reported non-detects	3

PCB 81

Z-score: PCB 81
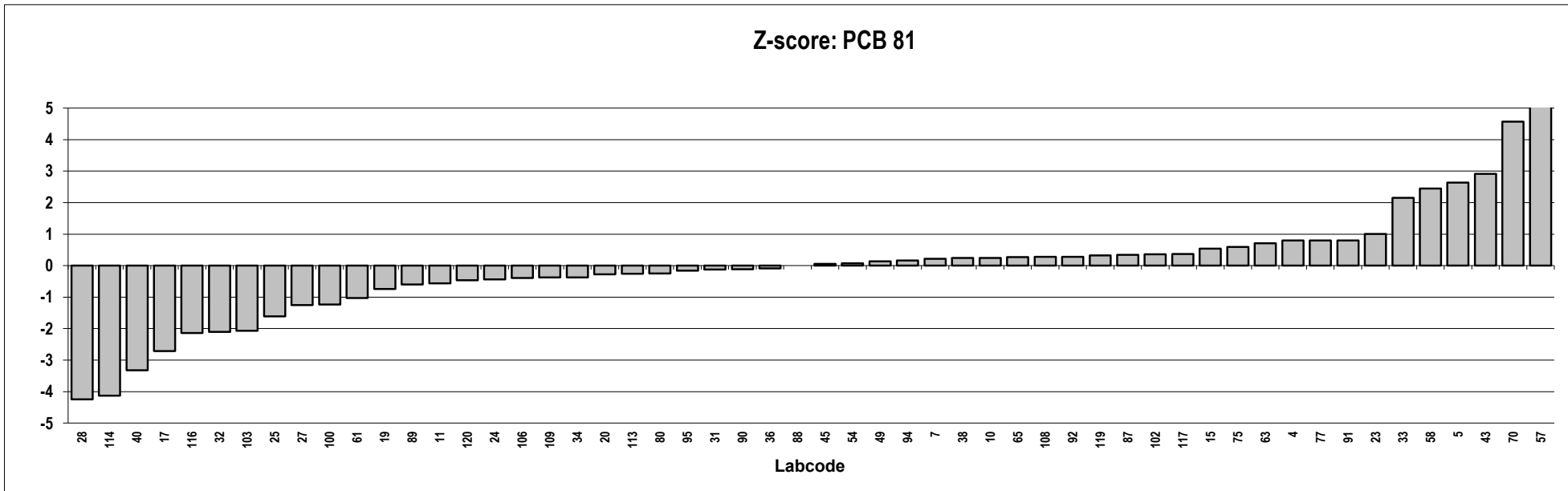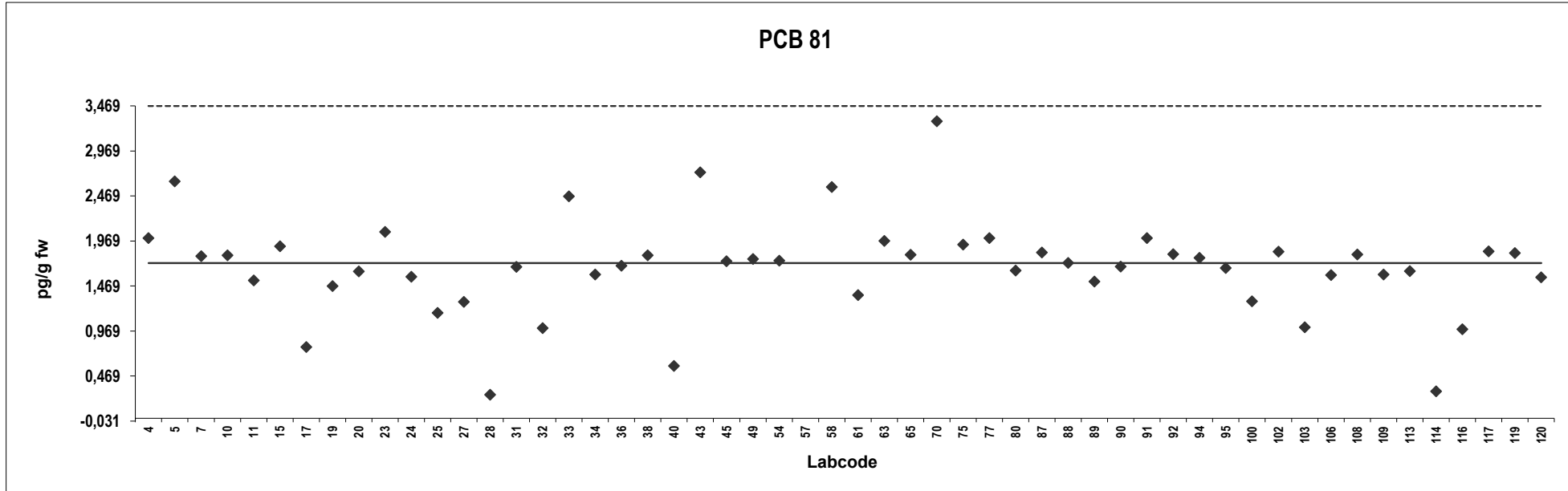
Brown meat
Congener: PCB 105

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	311	0,59		106	244	-0,62	
5	379	1,8		108	278	-0,0057	
7	273	-0,095		109	248	-0,54	
10	295	0,30		113	403	2,2	
11	288	0,18		114	240	-0,69	
15	302	0,43		116	290	0,21	
17	302	0,43		117	271	-0,14	
19	240	-0,68		119	269	-0,16	
20	264	-0,25		120	305	0,49	
23	285	0,12					
24	298	0,35					
25	276	-0,042					
27	266	-0,22					
28	272	-0,11					
31	271	-0,12					
32	277	-0,015					
33	419	2,5					
34	268	-0,18					
36	264	-0,26					
38	310	0,57					
40	362	1,5					
43	249	-0,53					
45	235	-0,78					
49	267	-0,20					
54	520	4,3					
57	300	0,38					
58	316	0,68					
61	283	0,093					
63	272	-0,11					
65	285	0,13					
70	262	-0,29					
75	300	0,39					
77	319	0,73					
80	293	0,27					
87	264	-0,27					
88	270	-0,14					
89	279	0,0057					
90	293	0,26					
91	297	0,34					
92	329	0,90					
94	254	-0,44					
95	253	-0,45					
100	270	-0,15					
102	286	0,14					
103	272	-0,11					

Consenus statistics

Consensus median, pg/g	278
Median all values pg/g	278
Consensus mean, pg/g	291
Standard deviation, pg/g	48
Relative standard deviation, %	17
No. of values reported	54
No. of values removed	0
No. of reported non-detects	0

PCB 105

y-axis: pg/g fw
556,6
456,6
356,6
256,6
156,6
56,6
-43,4

x-axis (Labcode): 4, 5, 7, 10, 11, 15, 17, 19, 20, 23, 24, 25, 27, 28, 31, 32, 33, 34, 36, 38, 40, 43, 45, 49, 54, 57, 58, 61, 63, 65, 70, 75, 77, 80, 87, 88, 89, 90, 91, 92, 94, 95, 100, 102, 103, 106, 108, 109, 113, 114, 116, 117, 119, 120

Z-score: PCB 105

y-axis: 5, 4, 3, 2, 1, 0, -1, -2, -3, -4, -5

x-axis (Labcode): 45, 114, 19, 106, 109, 43, 95, 94, 70, 87, 36, 20, 27, 49, 34, 119, 100, 88, 117, 31, 28, 63, 103, 7, 25, 32, 108, 89, 61, 23, 65, 102, 11, 116, 90, 80, 10, 91, 24, 57, 75, 15, 17, 120, 38, 4, 58, 77, 92, 40, 5, 113, 33, 54
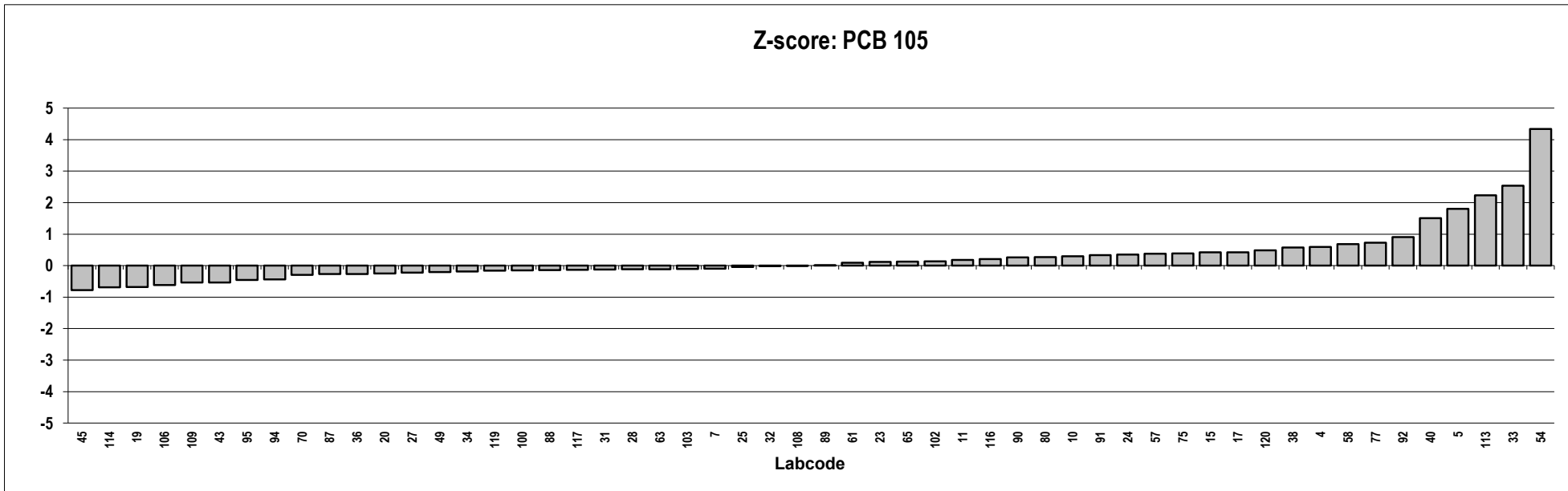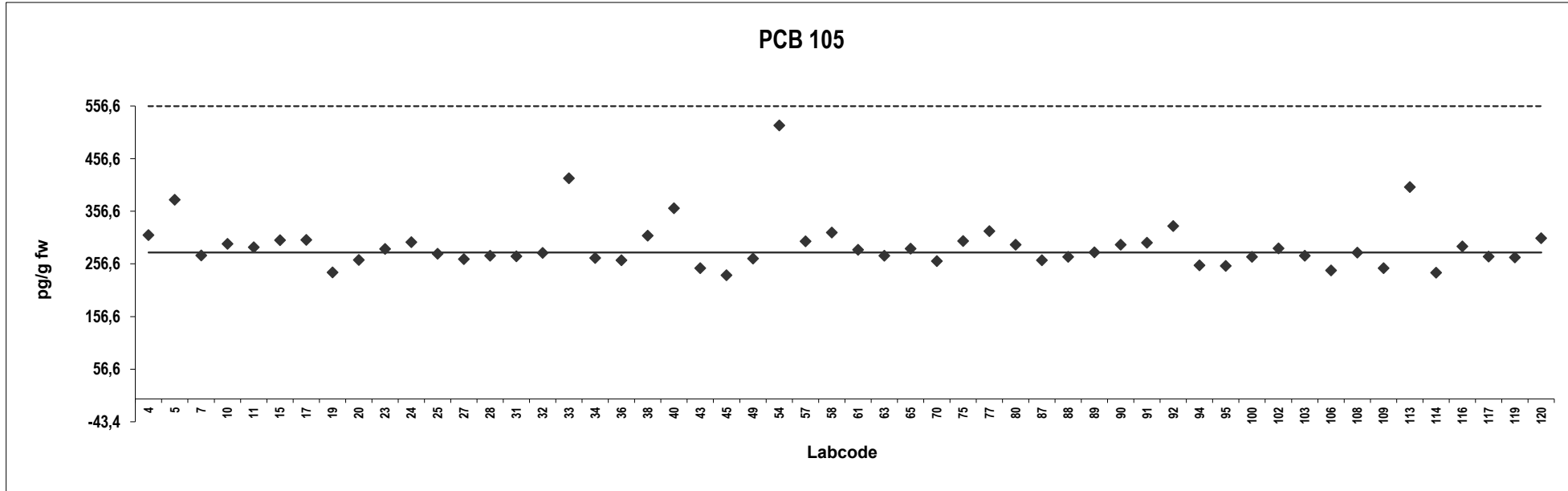
Brown meat
Congener: PCB 114

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	13	0,90		106	20	4,0	
5	16	2,4		108	13	0,75	
7	8,6	-1,1		109	11	-0,010	
10	11	0,16		113	28	7,8	Outlier
11	11	0,16		114	21	4,5	ND
15	12	0,44		116	11	-0,068	
17	11	-0,085		117	11	0,045	
19	12	0,50		119	11	0,029	
20	9,6	-0,63		120	12	0,32	
23	9,7	-0,59					
24	12	0,34					
25	8,3	-1,3					
27	6,0	-2,3					
28	12	0,35					
31	9,2	-0,83					
32	13	0,69					
33	32	9,6	Outlier				
34	9,1	-0,86					
36	10	-0,32					
38	10	-0,25					
40	15	1,7					
43	11	0,16					
45	11	-0,15					
49	11	0,074					
54	11	-0,11					
57	11	-0,22					
58	14	1,3					
61	9,0	-0,94					
63	21	4,4					
65	12	0,29					
70	11	-0,017					
75	12	0,48					
77	20	4,1	ND				
80	12	0,42					
87	25	6,3	Outlier				
88	10	-0,25					
89	8,4	-1,2					
90	11	0,00					
91	11	-0,017					
92	12	0,35					
94	8,1	-1,3					
95	9,2	-0,83					
100	9,0	-0,94					
102	11	-0,017					
103	8,6	-1,1					

Consensus statistics

Consensus median, pg/g	11
Median all values pg/g	11
Consensus mean, pg/g	12
Standard deviation, pg/g	3,1
Relative standard deviation, %	27
No. of values reported	54
No. of values removed	3
No. of reported non-detects	2

PCB 114

Z-score: PCB 114
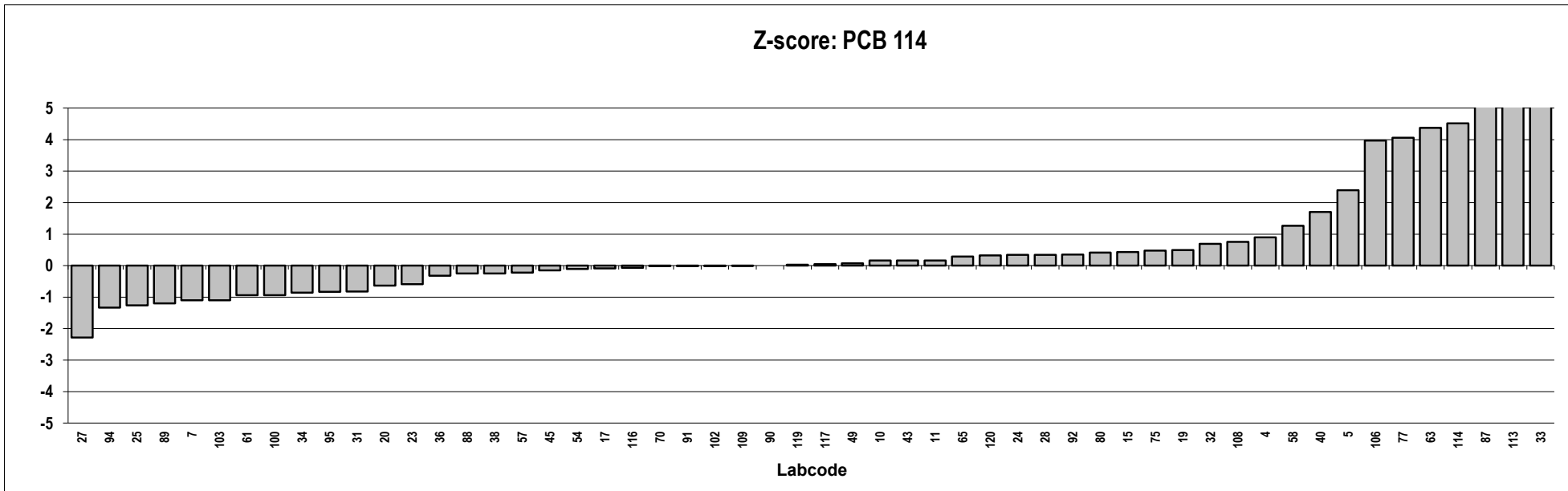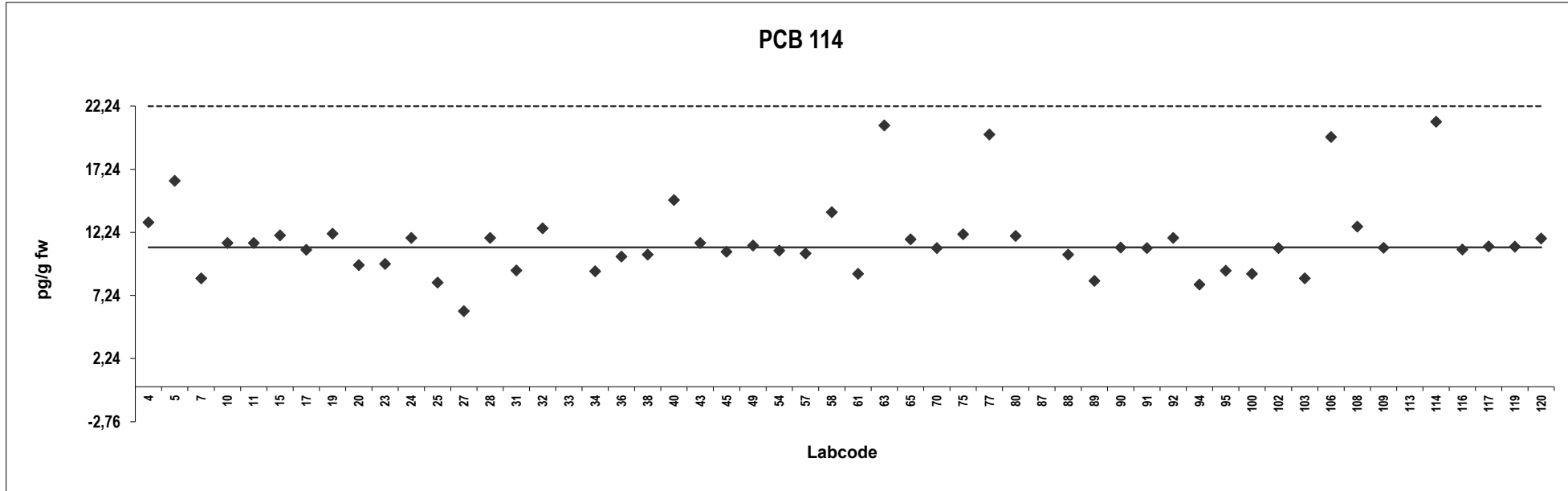
Brown meat
Congener: PCB 118

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	1135	1,1		106	780	-0,78	
5	1234	1,7		108	906	-0,099	
7	1060	0,73		109	1029	0,56	
10	926	0,0095		113	1337	2,2	
11	934	0,050		114	930	0,031	
15	918	-0,034		116	1080	0,84	
17	973	0,26		117	897	-0,15	
19	833	-0,49		119	909	-0,084	
20	813	-0,60		120	992	0,36	
23	960	0,19					
24	984	0,32					
25	888	-0,20					
27	899	-0,14					
28	869	-0,30					
31	911	-0,072					
32	938	0,073					
33	1298	2,0					
34	830	-0,51					
36	834	-0,49					
38	995	0,38					
40	1177	1,37					
43	869	-0,30					
45	760	-0,89					
49	874	-0,27					
54	844	-0,43					
57	815	-0,59					
58	998	0,40					
61	889	-0,19					
63	918	-0,034					
65	1027	0,55					
70	857	-0,36					
75	907	-0,093					
77	1123	1,1					
80	991	0,36					
87	832	-0,50					
88	946	0,12					
89	807	-0,63					
90	925	0,0029					
91	956	0,17					
92	1048	0,67					
94	885	-0,21					
95	742	-0,99					
100	935	0,058					
102	956	0,17					
103	924	-0,0029					

Consenus statistics

Consensus median, pg/g	924
Median all values pg/g	924
Consensus mean, pg/g	946
Standard deviation, pg/g	124
Relative standard deviation, %	13
No. of values reported	54
No. of values removed	0
No. of reported non-detects	0

PCB 118

Z-score: PCB 118
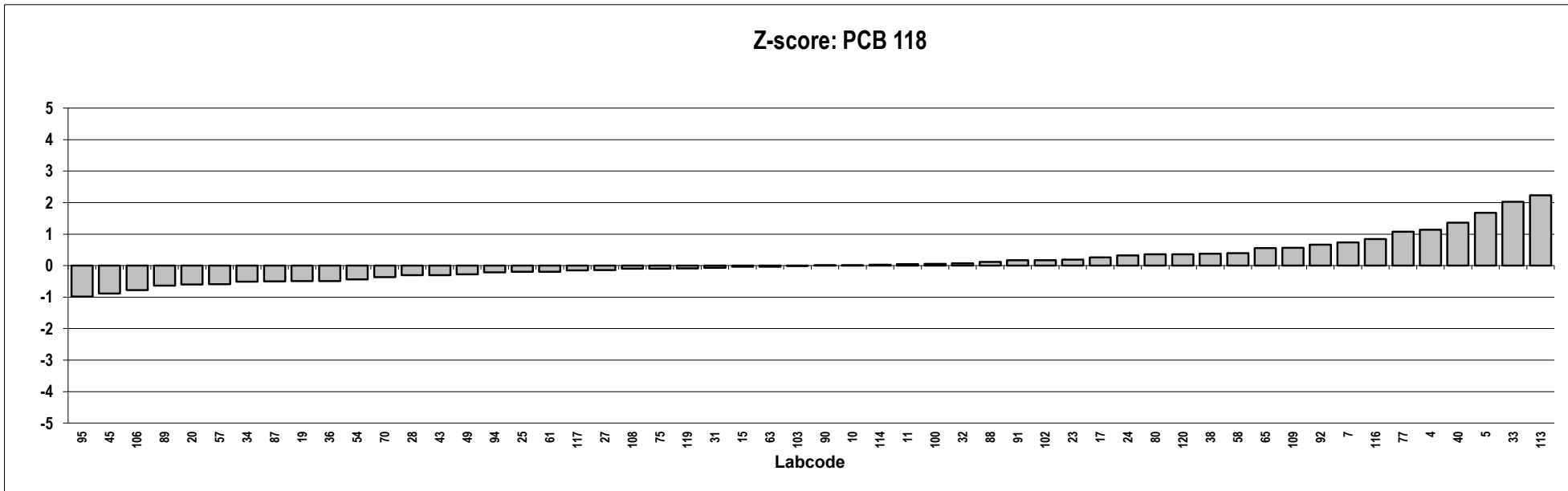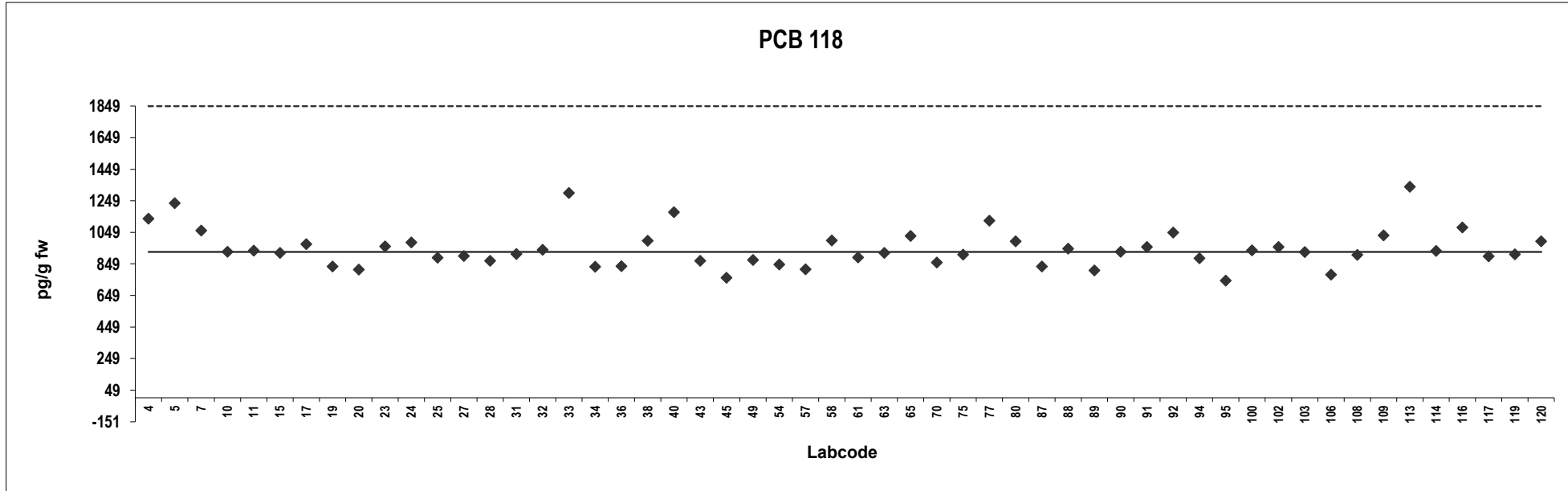
Brown meat

Congener: PCB 123

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	14	-0,058		106	14	-0,073	
5	14	0,23		108	14	0,22	
7	16	0,69		109	4,7	-3,3	
10	14	0,00		113	15	0,48	
11	15	0,64		114	68	20	Outlier,ND
15	18	1,4		116	12	-0,61	
17	32	6,7	Outlier	117	11	-1,1	
19	7,3	-2,3		119	11	-1,0	
20	23	3,3		120	22	2,9	
23	13	-0,36					
24	14	0,063					
25	14	-0,036					
27	15	0,59					
28	27	4,9					
31	13	-0,17					
32	15	0,53					
33	23	3,4					
34	13	-0,22					
36	8,0	-2,1					
38	18	1,7					
40	18	1,4					
43	21	2,6					
45	10	-1,3					
49	11	-1,1					
54	18	1,7					
57	0,030	-5,0	ND				
58	39	9,2	Outlier				
61	104	33	Outlier				
63	13	-0,15					
65	9,6	-1,5					
70	8,9	-1,8					
75	18	1,4					
77	20	2,3	ND				
80	14	0,0036					
87	11	-0,93					
88	16	0,96					
89	11	-1,0					
90	15	0,59					
91	14	0,11					
92	31	6,4	Outlier				
94	13	-0,11					
95	14	0,00					
100	12	-0,77					
102	16	0,91					
103	12	-0,49					

Consenus statistics	
Consensus median, pg/g	14
Median all values pg/g	14
Consensus mean, pg/g	14
Standard deviation, pg/g	4,7
Relative standard deviation, %	33
No. of values reported	54
No. of values removed	5
No. of reported non-detects	3

PCB 123

Z-score: PCB 123
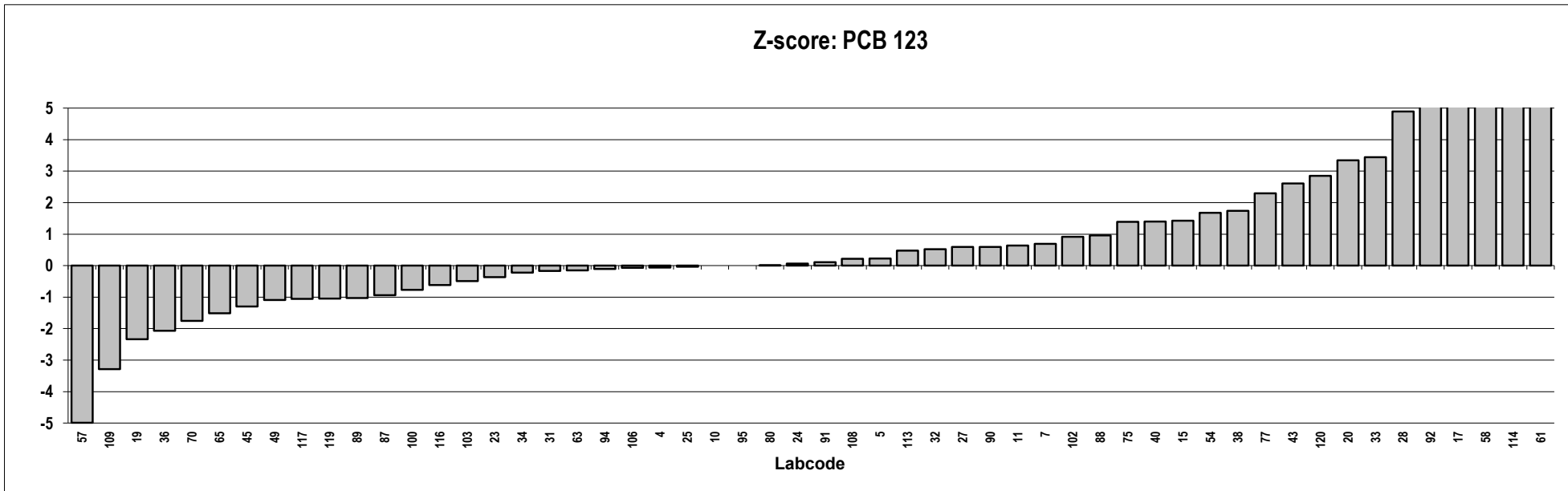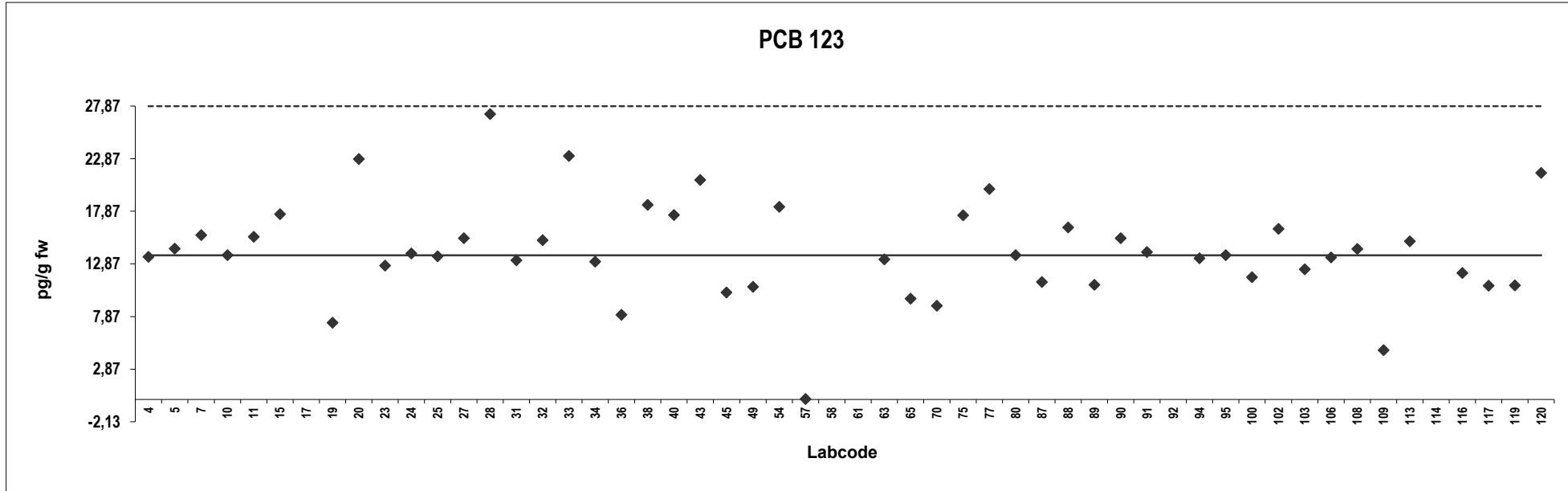
Brown meat
Congener: PCB 156

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	122	0,66		106	97	-0,49	
5	144	1,7		108	98	-0,43	
7	108	0,019		109	96	-0,53	
10	114	0,30		113	147	1,8	
11	114	0,31		114	100	-0,35	
15	106	-0,073		116	127	0,91	
17	122	0,69		117	100	-0,34	
19	93	-0,65		119	103	-0,21	
20	91	-0,75		120	114	0,30	
23	99	-0,40					
24	111	0,14					
25	84	-1,1					
27	109	0,049					
28	103	-0,21					
31	103	-0,20					
32	107	-0,019					
33	140	1,5					
34	99	-0,41					
36	113	0,24					
38	116	0,41					
40	137	1,4					
43	104	-0,16					
45	88	-0,92					
49	104	-0,17					
54	98	-0,46					
57	113	0,23					
58	125	0,82					
61	114	0,28					
63	112	0,21					
65	105	-0,14					
70	122	0,67					
75	104	-0,17					
77	124	0,76					
80	121	0,61					
87	108	0,038					
88	102	-0,26					
89	88	-0,91					
90	111	0,14					
91	109	0,066					
92	122	0,67					
94	96	-0,53					
95	98	-0,46					
100	101	-0,31					
102	114	0,30					
103	100	-0,36					

Consensus statistics

Consensus median, pg/g	108
Median all values pg/g	108
Consensus mean, pg/g	109
Standard deviation, pg/g	14
Relative standard deviation, %	13
No. of values reported	54
No. of values removed	0
No. of reported non-detects	0
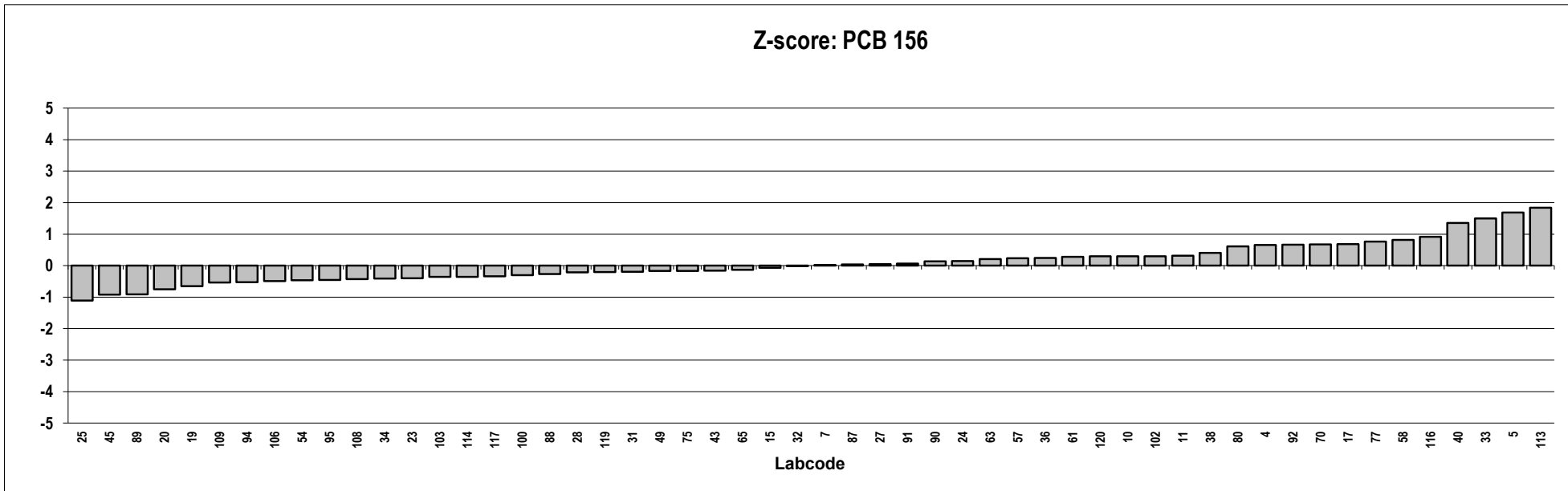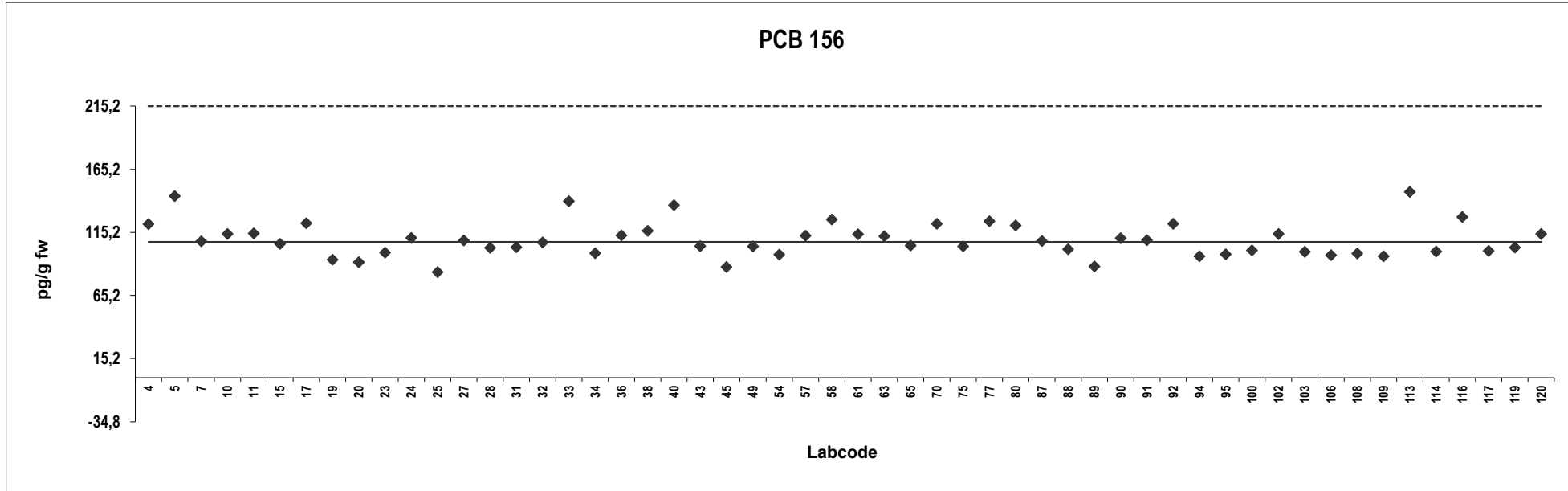
PCB 156

Brown meat

Congener: PCB 157

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	46	2,3		106	32	0,056	
5	40	1,4		108	31	-0,0079	
7	34	0,42		109	29	-0,44	
10	36	0,69		113	40	1,3	
11	35	0,59		114	30	-0,23	
15	33	0,21		116	34	0,41	
17	36	0,76		117	31	-0,14	
19	28	-0,47		119	31	-0,14	
20	93	9,7	Outlier	120	34	0,33	
23	22	-1,4					
24	33	0,17					
25	26	-0,88					
27	30	-0,16					
28	30	-0,31					
31	32	0,14					
32	31	-0,041					
33	45	2,1					
34	29	-0,32					
36	33	0,31					
38	33	0,30					
40	41	1,6					
43	30	-0,18					
45	29	-0,39					
49	30	-0,29					
54	32	0,0079					
57	31	-0,082					
58	36	0,71					
61	29	-0,32					
63	33	0,17					
65	34	0,46					
70	122	14	Outlier				
75	32	0,087					
77	24	-1,1					
80	33	0,31					
87	31	-0,12					
88	30	-0,21					
89	29	-0,34					
90	33	0,24					
91	33	0,25					
92	35	0,61					
94	28	-0,55					
95	29	-0,37					
100	31	-0,087					
102	29	-0,36					
103	31	-0,13					

Consensus statistics

Consensus median, pg/g	31
Median all values pg/g	32
Consensus mean, pg/g	32
Standard deviation, pg/g	4,3
Relative standard deviation, %	13
No. of values reported	54
No. of values removed	2
No. of reported non-detects	0

PCB 157

Z-score: PCB 157
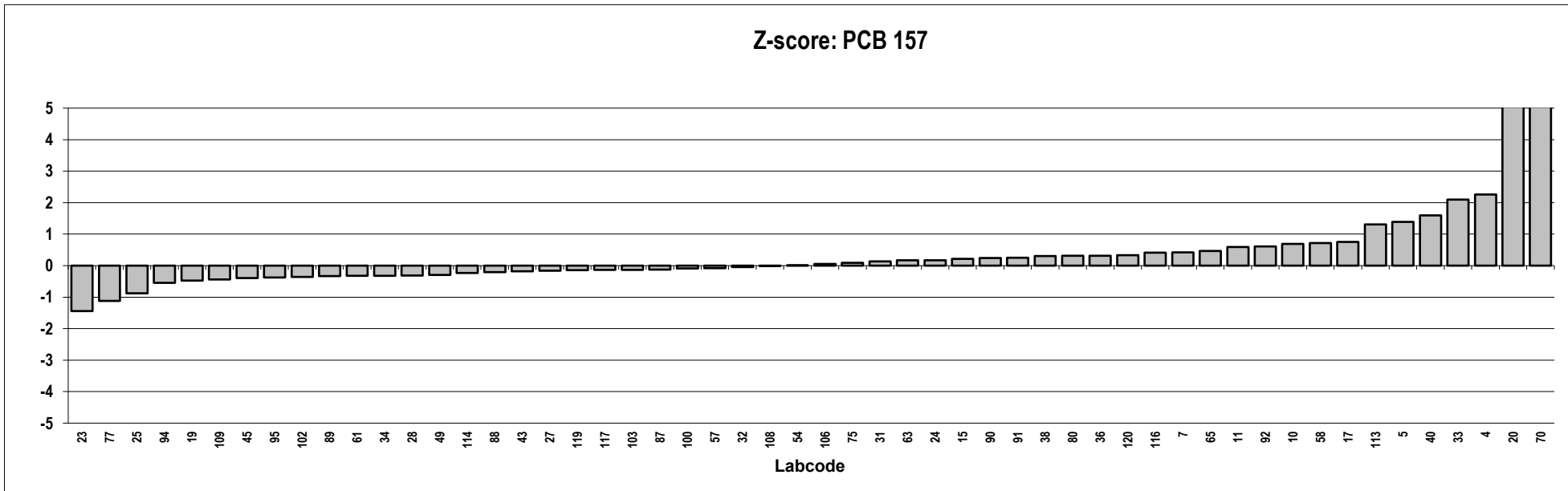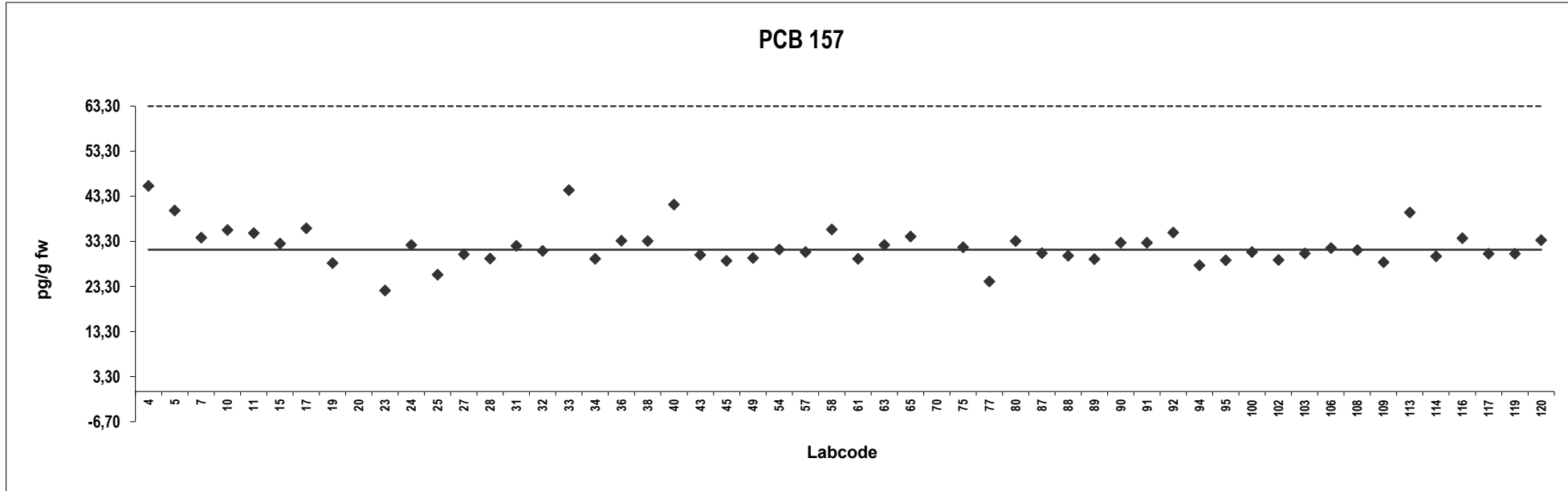
Brown meat
Congener: PCB 167

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	84	-0,056		106	83	-0,10	
5	107	1,3		108	104	1,1	
7	83	-0,14		109	74	-0,61	
10	89	0,27		113	108	1,3	
11	89	0,27		114	190	6,2	Outlier,ND
15	87	0,13		116	99	0,82	
17	86	0,080		117	72	-0,76	
19	73	-0,67		119	81	-0,20	
20	70	-0,90		120	93	0,51	
23	104	1,1					
24	81	-0,21					
25	65	-1,2					
27	80	-0,26					
28	50	-2,0					
31	82	-0,14					
32	86	0,061					
33	108	1,4					
34	75	-0,60					
36	84	-0,052					
38	212	7,5	Outlier				
40	106	1,2					
43	87	0,12					
45	79	-0,34					
49	83	-0,13					
54	90	0,32					
57	0,17	-5,0	ND				
58	90	0,33					
61	84	-0,047					
63	86	0,070					
65	85	0,0069					
70	73	-0,72					
75	88	0,19					
77	108	1,4					
80	88	0,17					
87	85	-0,0069					
88	78	-0,42					
89	72	-0,75					
90	86	0,087					
91	89	0,25					
92	91	0,38					
94	79	-0,37					
95	91	0,35					
100	84	-0,030					
102	88	0,19					
103	79	-0,35					

Consenus statistics	
Consensus median, pg/g	85
Median all values pg/g	85
Consensus mean, pg/g	84
Standard deviation, pg/g	16
Relative standard deviation, %	20
No. of values reported	54
No. of values removed	2
No. of reported non-detects	2

PCB 167

pg/g fw

Labcode

Z-score: PCB 167
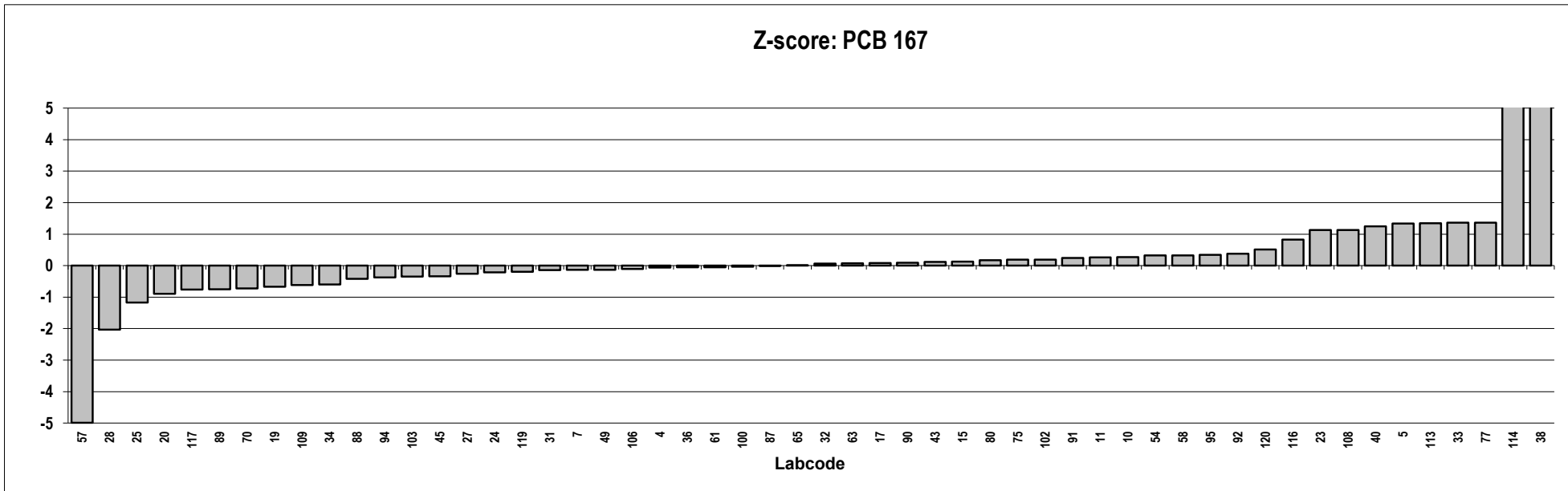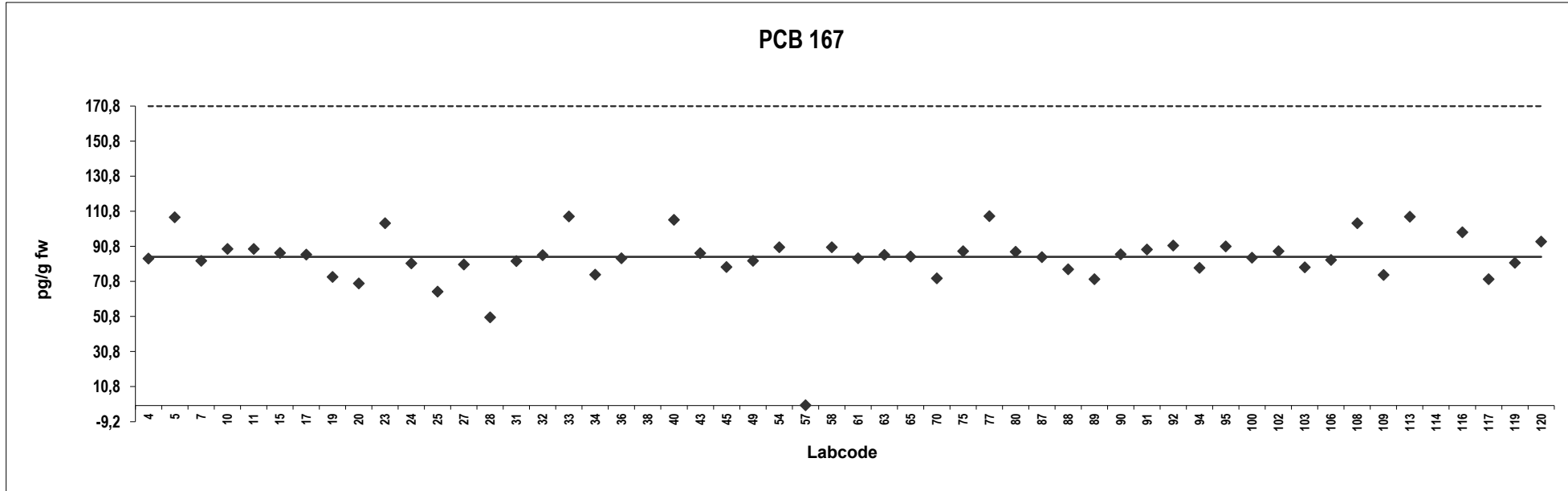
Labcode

Brown meat

Congener: PCB 189

Lab code	Conc. pg/g fw.	Z-scores	Notes	Lab code	Conc. pg/g fw.	Z-scores	Notes
4	15	0,68		106	13	-0,0086	
5	16	1,1		108	12	-0,36	
7	13	-0,12		109	12	-0,17	
10	12	-0,28		113	14	0,29	
11	13	0,0086		114	14	0,42	ND
15	14	0,26		116	8,8	-1,6	
17	14	0,40		117	11	-0,66	
19	11	-0,60		119	12	-0,26	
20	11	-0,90		120	13	-0,12	
23	13	-0,12					
24	13	-0,11					
25	11	-0,63					
27	11	-0,84					
28	13	-0,16					
31	13	0,062					
32	13	-0,027					
33	17	1,5					
34	13	-0,059					
36	13	0,20					
38	13	0,087					
40	15	0,98					
43	14	0,29					
45	11	-0,79					
49	13	-0,047					
54	15	0,61					
57	13	0,21					
58	15	0,80					
61	13	0,14					
63	13	0,11					
65	13	-0,14					
70	11	-0,59					
75	14	0,34					
77	20	2,7	ND				
80	16	1,0					
87	14	0,29					
88	11	-0,64					
89	11	-0,87					
90	14	0,26					
91	13	0,030					
92	14	0,44					
94	11	-0,82					
95	13	-0,047					
100	13	-0,0086					
102	15	0,65					
103	17	1,4					

Consensus statistics

Consensus median, pg/g	13
Median all values pg/g	13
Consensus mean, pg/g	13
Standard deviation, pg/g	1,8
Relative standard deviation, %	14
No. of values reported	54
No. of values removed	0
No. of reported non-detects	2

PCB 189

Z-score: PCB 189
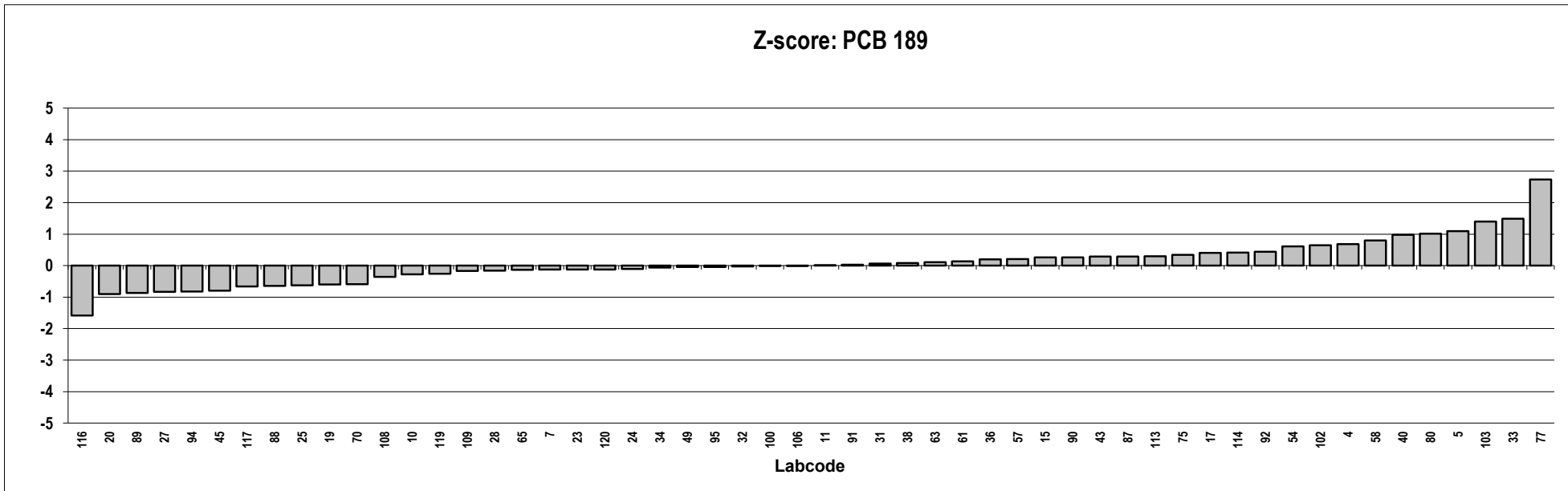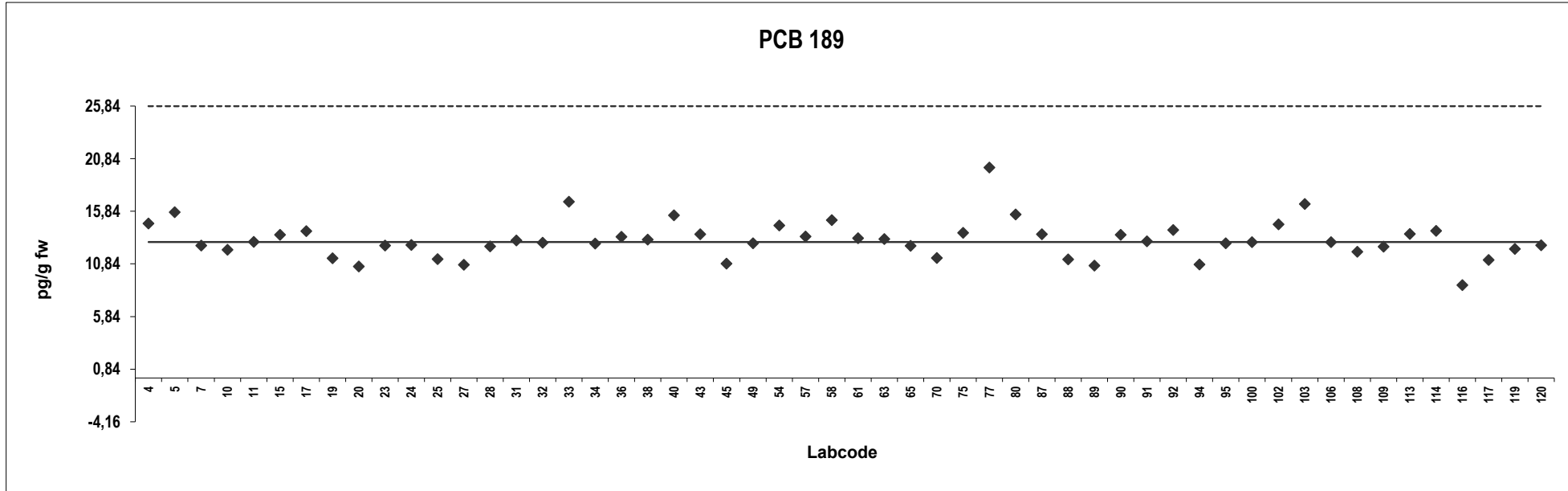
Brown meat
Congener: PCB 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	170	0,99		117	527	14	Outlier
5	170	0,99		120	93	-1,7	
7	132	-0,35					
10	123	-0,67					
11	166	0,84					
15	178	1,3					
17	153	0,39					
19	139	-0,12					
23	160	0,63					
24	169	0,93					
25	149	0,25					
27	101	-1,4					
28	140	-0,070					
31	128	-0,51					
32	140	-0,059					
34	169	0,93					
38	154	0,41					
40	731	21	Outlier				
43	139	-0,11					
45	168	0,91					
49	139	-0,11					
54	119	-0,81					
57	139	-0,10					
58	159	0,59					
61	310	5,9	Outlier				
63	166	0,83					
65	463	11	Outlier				
70	101	-1,4					
75	180	1,3					
77	310	5,9	Outlier,ND				
80	154	0,42					
81	100	-1,5					
87	127	-0,53					
90	0,14	-5,0					
94	167	0,88					
95	142	0,00					
100	362	7,7	Outlier				
102	147	0,18					
103	90	-1,8					
105	85	-2,0					
106	121	-0,74					
108	297	5,5					
109	156	0,50					
113	201	2,1					
114	130	-0,42					

Consenus statistics

Consensus median, pg/g	142
Median all values pg/g	153
Consensus mean, pg/g	143
Standard deviation, pg/g	43
Relative standard deviation, %	30
No. of values reported	47
No. of values removed	6
No. of reported non-detects	1

PCB 28

Z-score: PCB 28
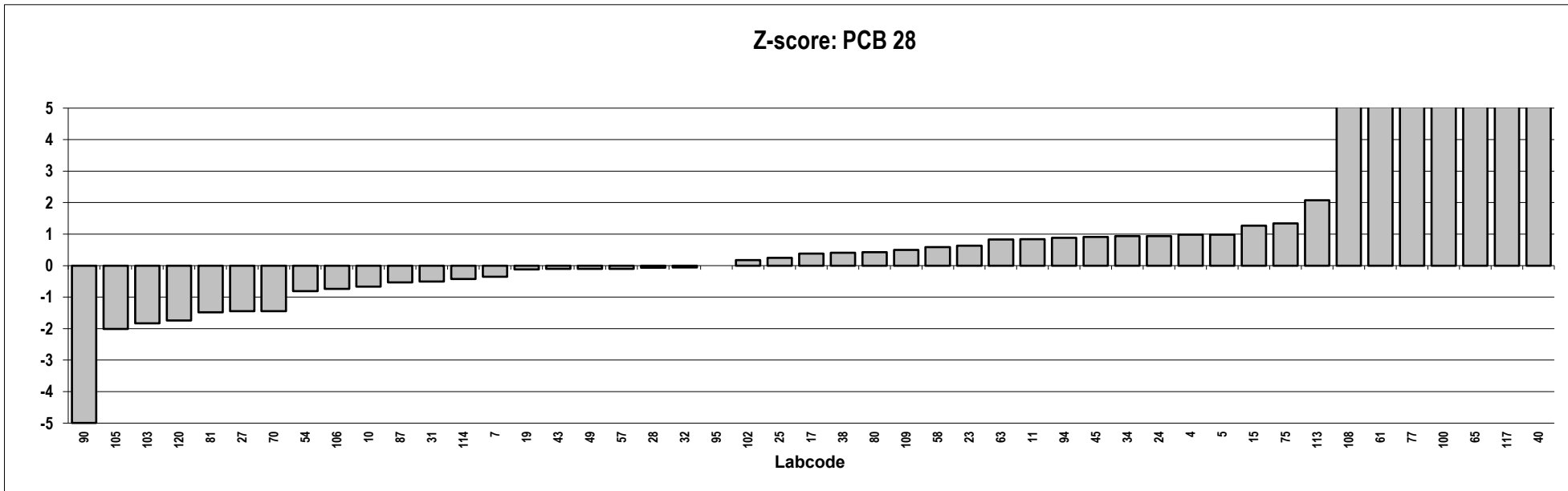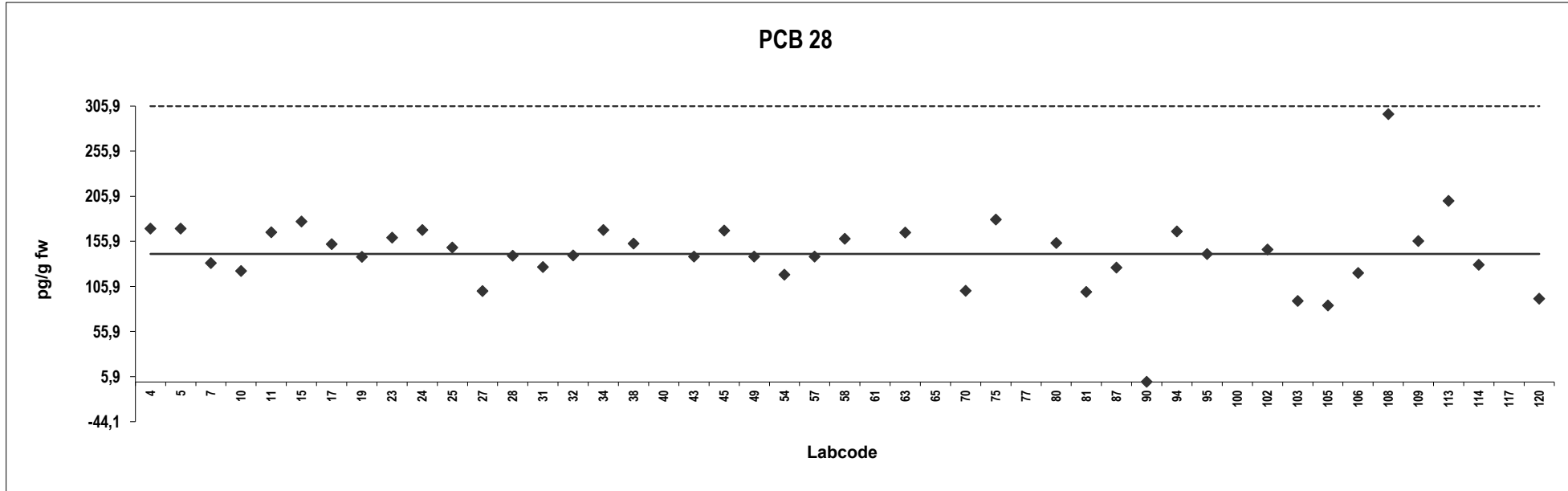
Brown meat
Congener: PCB 52

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	60	2,6		117	287	31	Outlier
5	60	2,6		120	68	3,6	
7	44	0,62					
10	39	-0,11					
11	39	-0,038					
15	61	2,7					
17	36	-0,42					
19	56	2,1					
23	61	2,8					
24	42	0,27					
25	28	-1,4					
27	35	-0,59					
28	26	-1,7					
31	37	-0,31					
32	47	0,92					
34	32	-0,90					
38	44	0,52					
40	406	46	Outlier				
43	34	-0,70					
45	31	-1,1					
49	40	0,038					
54	30	-1,2					
57	35	-0,57					
58	50	1,3	ND				
61	43	0,41					
63	43	0,42					
65	257	28	Outlier				
70	25	-1,9					
75	56	2,1					
77	270	29	Outlier,ND				
80	37	-0,37					
81	30	-1,2					
87	39	-0,076					
90	0,041	-5,0					
94	59	2,5					
95	41	0,13					
100	182	18	Outlier				
102	38	-0,16					
103	38	-0,19					
105	47	0,95					
106	34	-0,73					
108	149	14	Outlier				
109	44	0,63					
113	61	2,7					
114	83	5,5					

Consensus statistics

Consensus median, pg/g	40
Median all values pg/g	43
Consensus mean, pg/g	43
Standard deviation, pg/g	14
Relative standard deviation, %	34
No. of values reported	47
No. of values removed	6
No. of reported non-detects	2

PCB 52
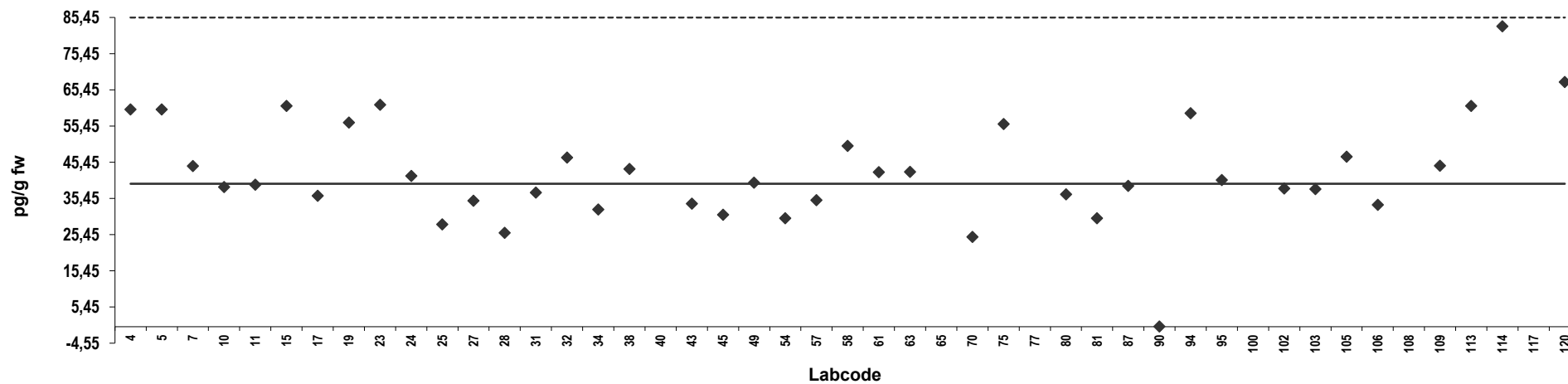
Z-score: PCB 52
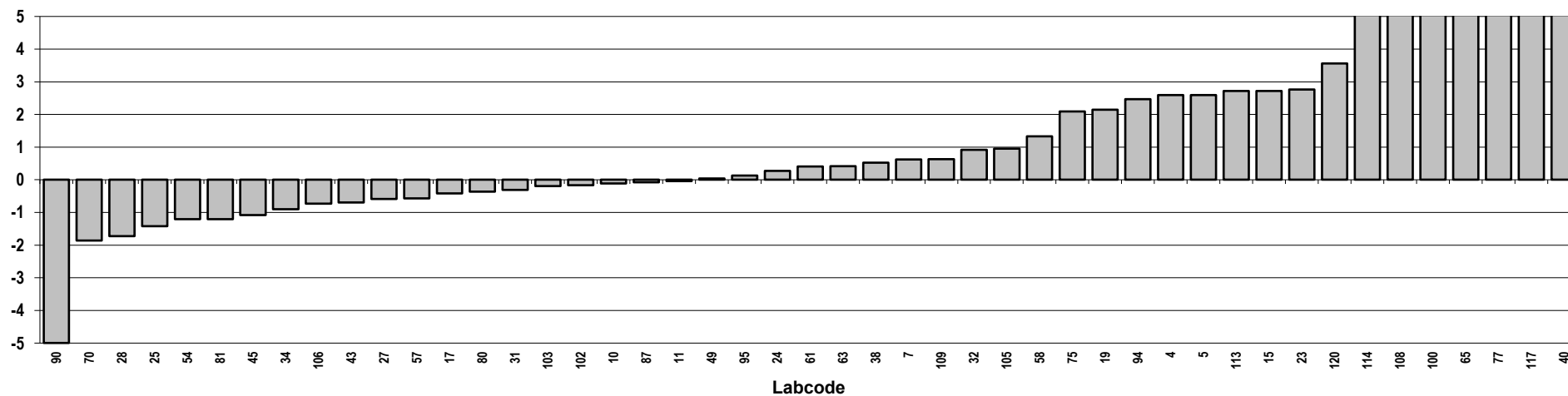
Brown meat
Congener: PCB 101

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	300	1,3		117	491	5,3	Outlier
5	300	1,3		120	267	0,62	
7	173	-1,4					
10	228	-0,21					
11	213	-0,52					
15	285	0,99					
17	258	0,42					
19	248	0,21					
23	344	2,2					
24	230	-0,16					
25	175	-1,3					
27	218	-0,43					
28	67	-3,6					
31	246	0,18					
32	226	-0,26					
34	237	-0,025					
38	250	0,26					
40	617	8,0	Outlier				
43	188	-1,0					
45	200	-0,80					
49	210	-0,58					
54	202	-0,75					
57	255	0,35					
58	263	0,53					
61	293	1,2					
63	248	0,22					
65	416	3,7					
70	178	-1,3					
75	279	0,87					
77	590	7,4	Outlier,ND				
80	242	0,088					
81	180	-1,2					
87	217	-0,44					
90	0,23	-5,0					
94	239	0,025					
95	232	-0,12					
100	390	3,2					
102	264	0,55					
103	229	-0,19					
105	130	-2,3					
106	187	-1,1					
108	375	2,9					
109	215	-0,47					
113	304	1,4					
114	250	0,26					

Consenus statistics

Consensus median, pg/g	238
Median all values pg/g	242
Consensus mean, pg/g	238
Standard deviation, pg/g	73
Relative standard deviation, %	31
No. of values reported	47
No. of values removed	3
No. of reported non-detects	1

PCB 101

Z-score: PCB 101
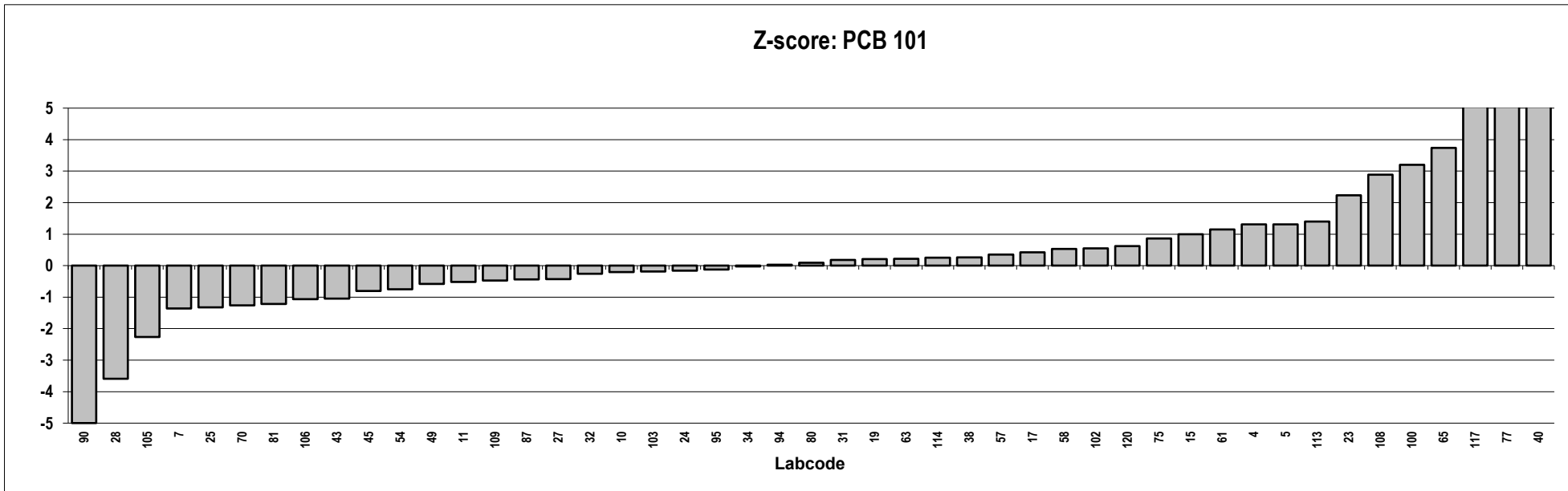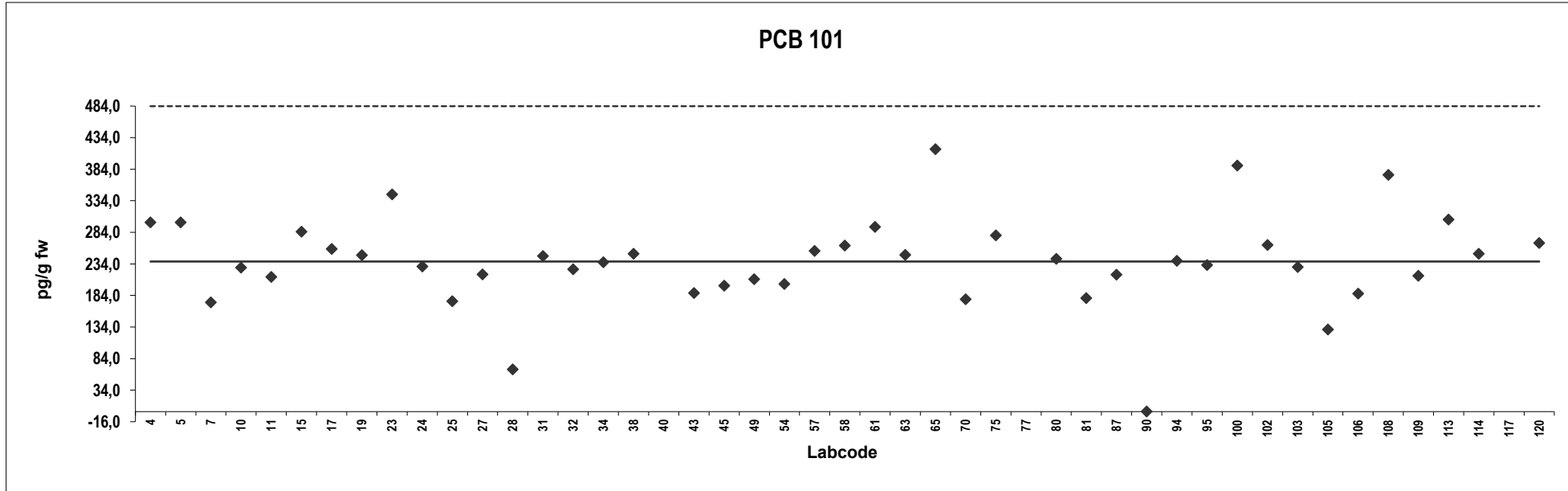
Brown meat

Congener: PCB 138

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	2130	0,96		117	1705	-0,23	
5	2130	0,96		120	1631	-0,44	
7	1012	-2,2					
10	1844	0,16					
11	1933	0,41					
15	1970	0,51					
17	3200	4,0					
19	1548	-0,67					
23	1810	0,064					
24	1514	-0,76					
25	1350	-1,2					
27	1595	-0,54					
28	1890	0,29					
31	1727	-0,17					
32	1401	-1,1					
34	1725	-0,17					
38	2265	1,3					
40	2240	1,3					
43	2793	2,8					
45	1495	-0,82					
49	1500	-0,80					
54	1757	-0,084					
57	2426	1,8					
58	1831	0,12					
61	2257	1,3					
63	2069	0,79					
65	1648	-0,39					
70	2390	1,7					
75	1900	0,32					
77	1787	0,00					
80	1672	-0,32					
81	1470	-0,89					
87	2054	0,75					
90	1,8	-5,0					
94	1635	-0,43					
95	1570	-0,61					
100	2550	2,1					
102	1900	0,32					
103	1816	0,081					
105	890	-2,5					
106	1590	-0,55					
108	1690	-0,27					
109	1625	-0,45					
113	2087	0,84					
114	2200	1,2					

Consensus statistics

Consensus median, pg/g	1787
Median all values pg/g	1787
Consensus mean, pg/g	1813
Standard deviation, pg/g	496
Relative standard deviation, %	27
No. of values reported	47
No. of values removed	0
No. of reported non-detects	0

PCB 138

Z-score: PCB 138
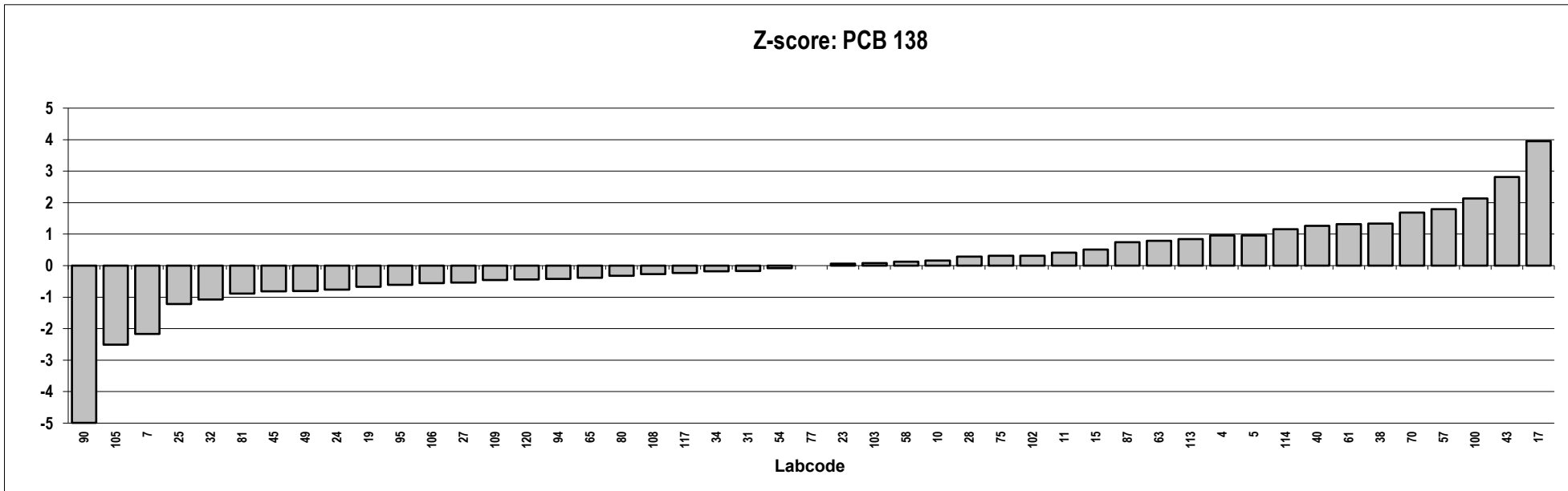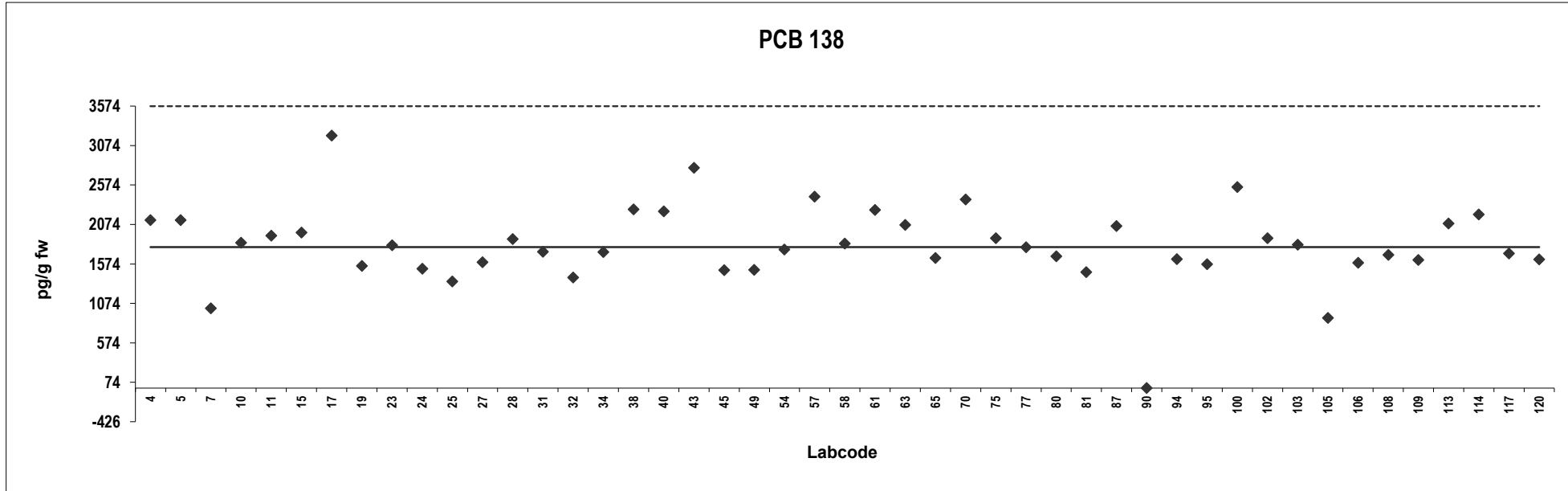
Brown meat
Congener: PCB 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	3710	1,1		117	2870	-0,31	
5	3710	1,1		120	2878	-0,3	
7	2189	-1,4					
10	3842	1,3					
11	3119	0,095					
15	3440	0,62					
17	3432	0,61					
19	2789	-0,44					
23	3270	0,34					
24	3088	0,045					
25	2210	-1,4					
27	2817	-0,40					
28	2780	-0,46					
31	2979	-0,13					
32	3120	0,097					
34	3004	-0,093					
38	2780	-0,46					
40	3771	1,2					
43	2606	-0,74					
45	2491	-0,93					
49	2630	-0,70					
54	3275	0,35					
57	3273	0,35					
58	3069	0,013					
61	3878	1,3					
63	3061	0,00					
65	3324	0,43					
70	2690	-0,61					
75	3410	0,57					
77	3236	0,29					
80	2854	-0,34					
81	2090	-1,6					
87	3009	-0,084					
90	3,1	-5,0					
94	2700	-0,59					
95	3040	-0,034					
100	3220	0,26					
102	3180	0,19					
103	2697	-0,59					
105	1900	-1,9					
106	2720	-0,56					
108	3120	0,097					
109	3293	0,38					
113	4065	1,6					
114	3200	0,23					

Consenus statistics

Consensus median, pg/g	3061
Median all values pg/g	3061
Consensus mean, pg/g	2975
Standard deviation, pg/g	640
Relative standard deviation, %	22
No. of values reported	47
No. of values removed	0
No. of reported non-detects	0

PCB 153

Z-score: PCB 153
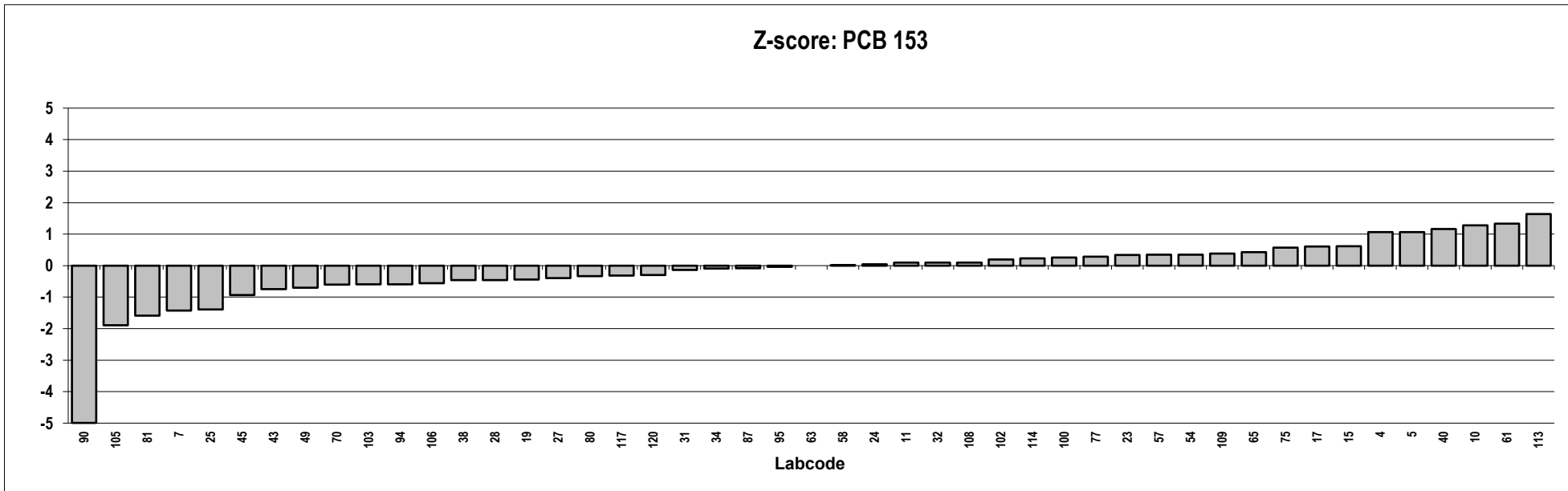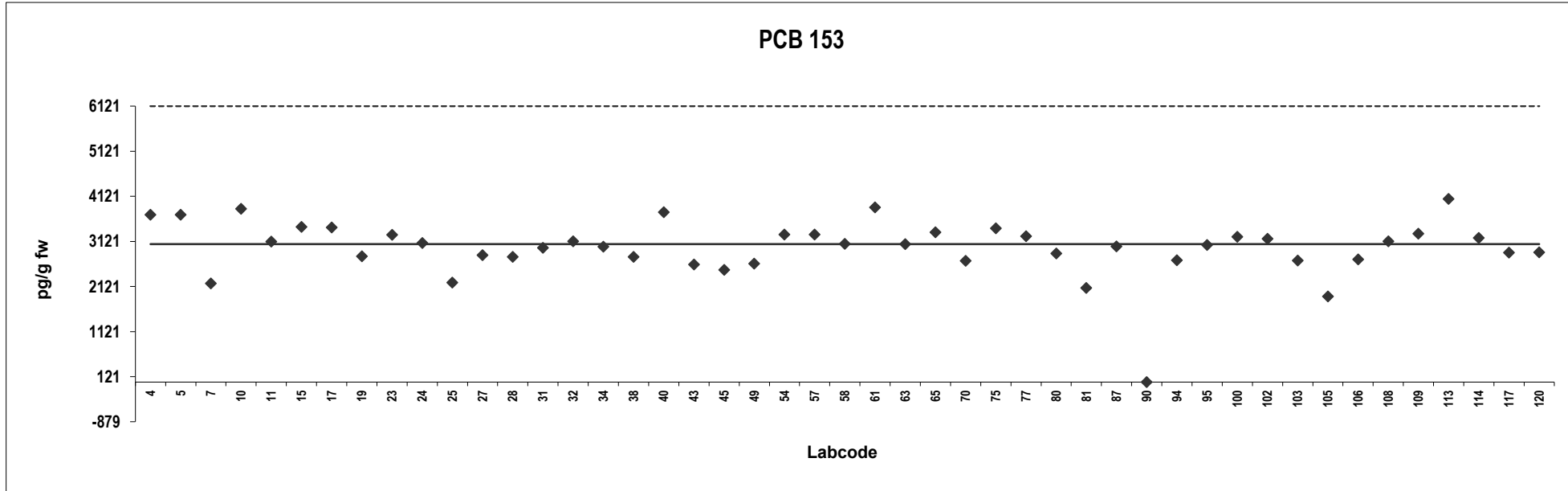
Brown meat
Congener: PCB 180

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
4	630	0,53		117	581	0,099	
5	630	0,53		120	752	1,6	
7	374	-1,7					
10	671	0,89					
11	644	0,64					
15	654	0,74					
17	624	0,48					
19	497	-0,64					
23	639	0,61					
24	575	0,041					
25	456	-1,0					
27	531	-0,35					
28	567	-0,026					
31	525	-0,39					
32	724	1,4					
34	546	-0,21					
38	481	-0,78					
40	771	1,8					
43	919	3,1					
45	512	-0,51					
49	544	-0,23					
54	629	0,52					
57	529	-0,36					
58	687	1,0					
61	976	3,6					
63	555	-0,13					
65	510	-0,53					
70	434	-1,2					
75	645	0,66					
77	625	0,48					
80	542	-0,25					
81	410	-1,4					
87	514	-0,49					
90	0,61	-5,0					
94	570	0,00					
95	563	-0,061					
100	534	-0,32					
102	588	0,16					
103	637	0,59					
105	250	-2,8					
106	461	-0,96					
108	586	0,14					
109	553	-0,15					
113	774	1,8					
114	600	0,26					

Consenus statistics

Consensus median, pg/g	570
Median all values pg/g	570
Consensus mean, pg/g	575
Standard deviation, pg/g	152
Relative standard deviation, %	26
No. of values reported	47
No. of values removed	0
No. of reported non-detects	0

PCB 180

Z-score: PCB 180
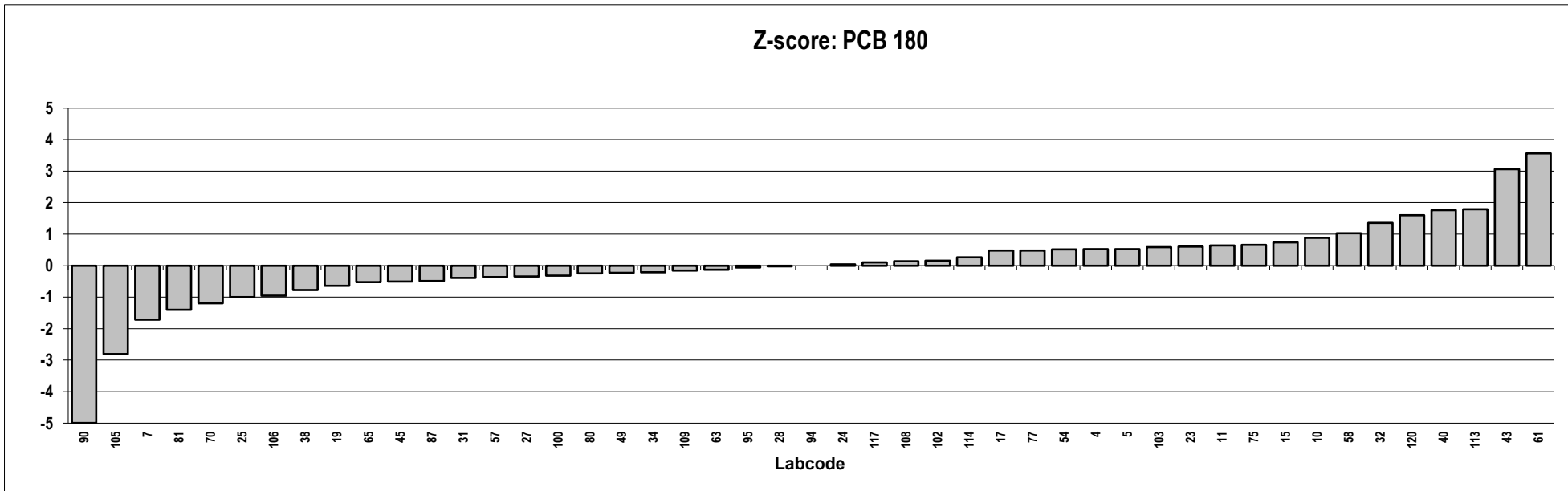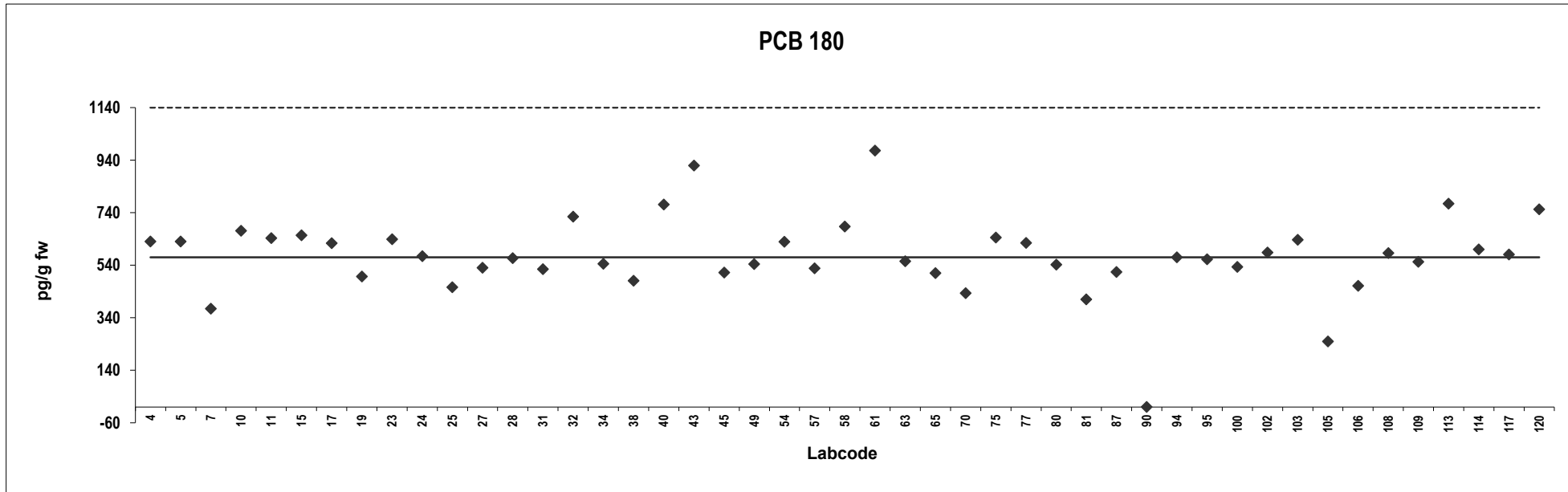
Brown meat
Congener: PBDE 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	5,0	1,6					
19	3,9	0,10					
23	8,9	6,7	Outlier				
25	3,4	-0,50					
31	3,5	-0,43					
36	3,6	-0,26					
40	4,9	1,4					
43	4,6	1,0					
49	2,8	-1,4					
54	3,8	0,015					
57	3,2	-0,77					
63	4,6	1,1					
65	4,3	0,59					
77	9,6	7,6	Outlier				
81	2,0	-2,4					
90	2,7	-1,5					
94	3,7	-0,21					
95	3,0	-1,1					
102	4,2	0,51					
108	2,5	-1,7	ND				
113	6,6	3,6					
116	3,8	0,00					

Consenus statistics

Consensus median, pg/g	3,8
Median all values pg/g	3,8
Consensus mean, pg/g	3,8
Standard deviation, pg/g	1,0
Relative standard deviation, %	27
No. of values reported	22
No. of values removed	2
No. of reported non-detects	1

PBDE 28

pg/g fw

Labcode

Z-score: PBDE 28
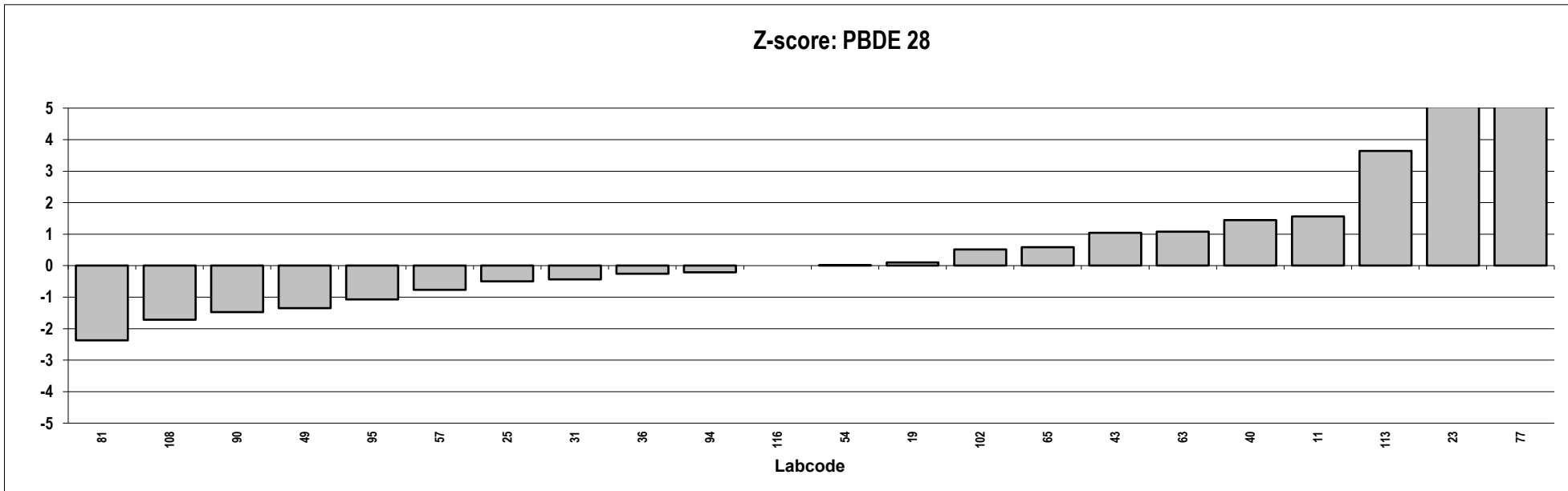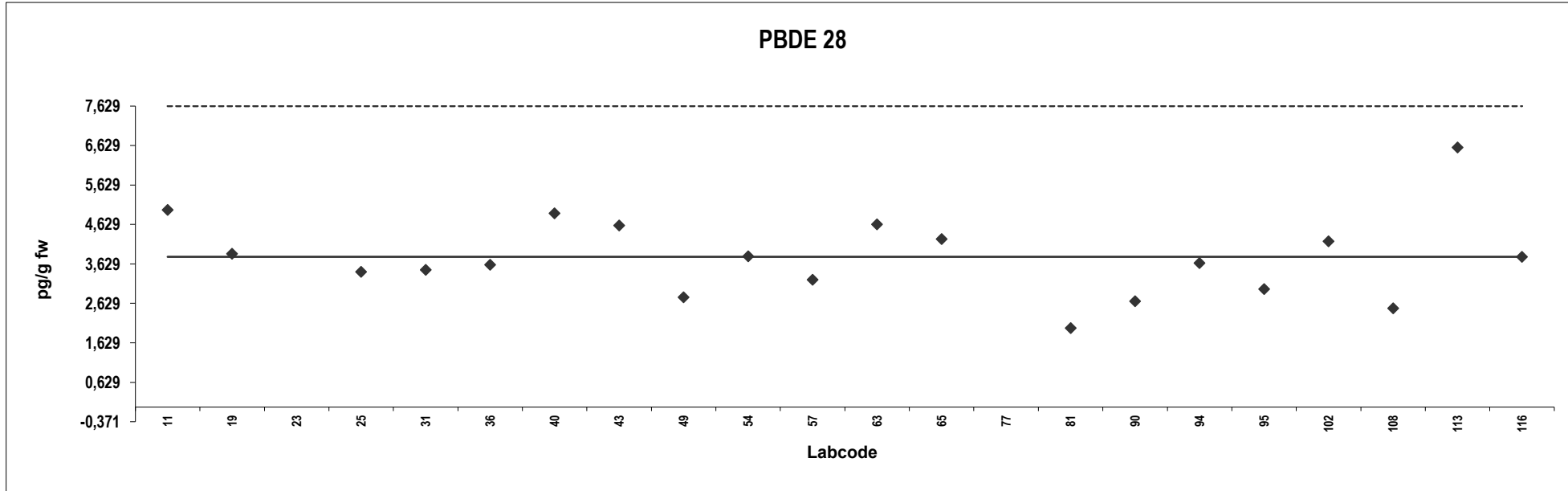
Labcode

Brown meat
Congener: PBDE 47

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	52	0,20					
19	51	0,053					
23	111	6,1	Outlier				
25	55	0,55					
31	49	-0,066					
36	49	-0,11					
40	64	1,4					
43	71	2,1					
49	41	-0,94					
54	48	-0,25					
57	45	-0,51					
63	59	0,93					
65	50	-0,011					
77	52	0,16					
81	34	-1,6					
90	41	-0,88					
94	50	0,00					
95	48	-0,22					
102	48	-0,18					
108	64	1,4					
113	69	1,90					
116	50	0,013					

Consenus statistics

Consensus median, pg/g	50
Median all values pg/g	50
Consensus mean, pg/g	52
Standard deviation, pg/g	9,3
Relative standard deviation, %	18
No. of values reported	22
No. of values removed	1
No. of reported non-detects	0

PBDE 47

Z-score: PBDE 47
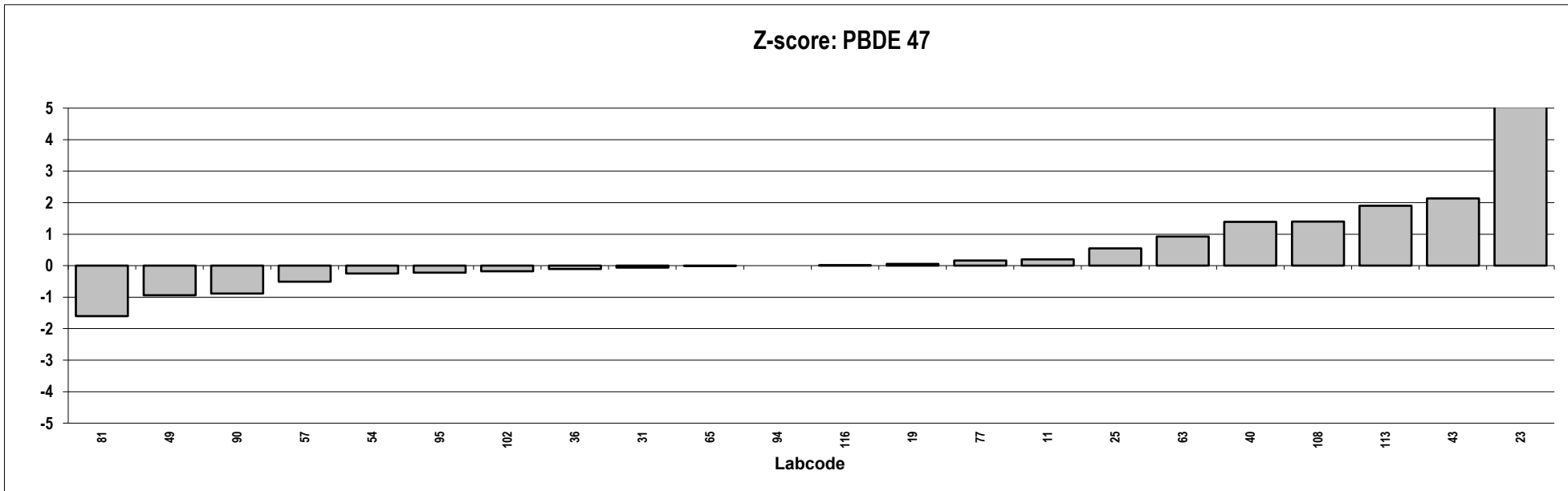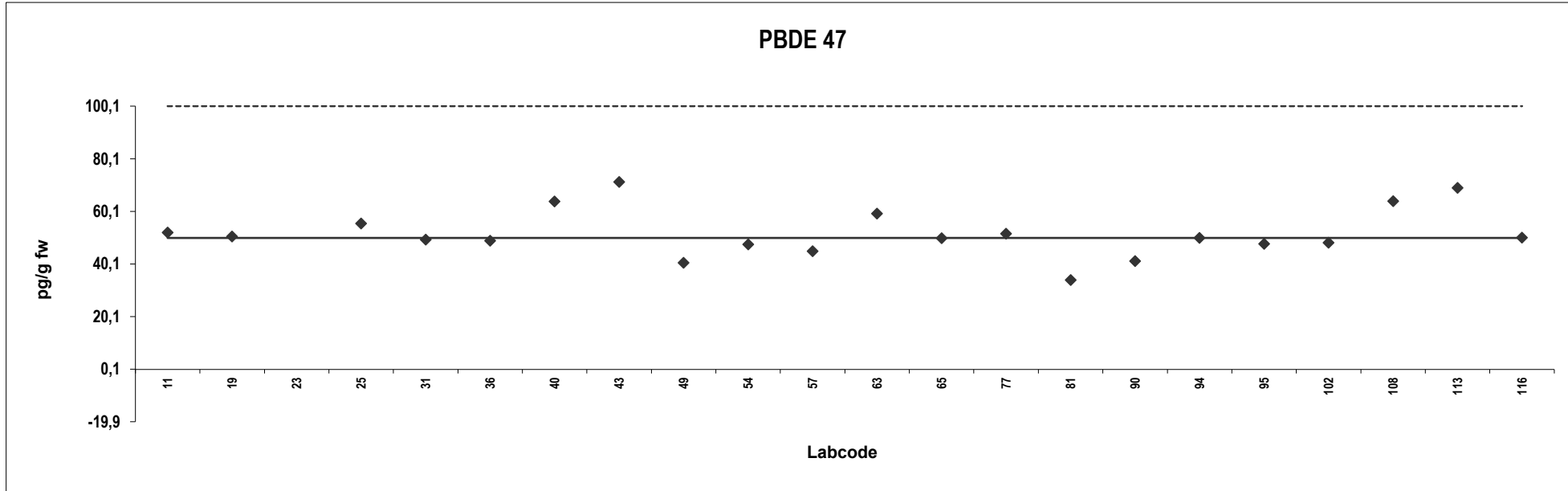
Brown meat
Congener: PBDE 99

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	7,0	-0,37					
19	7,6	0,015					
23	26	12	Outlier				
25	9,7	1,4					
31	6,2	-0,88					
36	7,5	-0,015					
40	8,5	0,64					
43	9,1	1,0					
49	8,2	0,40					
54	5,3	-1,5					
57	7,0	-0,37					
63	8,5	0,60					
65	6,8	-0,52					
77	7,7	0,12					
81	5,0	-1,7					
90	4,3	-2,2					
94	6,2	-0,90					
95	7,4	-0,10					
102	8,7	0,75					
108	33	17	Outlier				
113	9,8	1,5					
116	8,6	0,69					

Consenus statistics

Consensus median, pg/g	7,6
Median all values pg/g	7,7
Consensus mean, pg/g	7,5
Standard deviation, pg/g	1,5
Relative standard deviation, %	20
No. of values reported	22
No. of values removed	2
No. of reported non-detects	0

PBDE 99

Z-score: PBDE 99
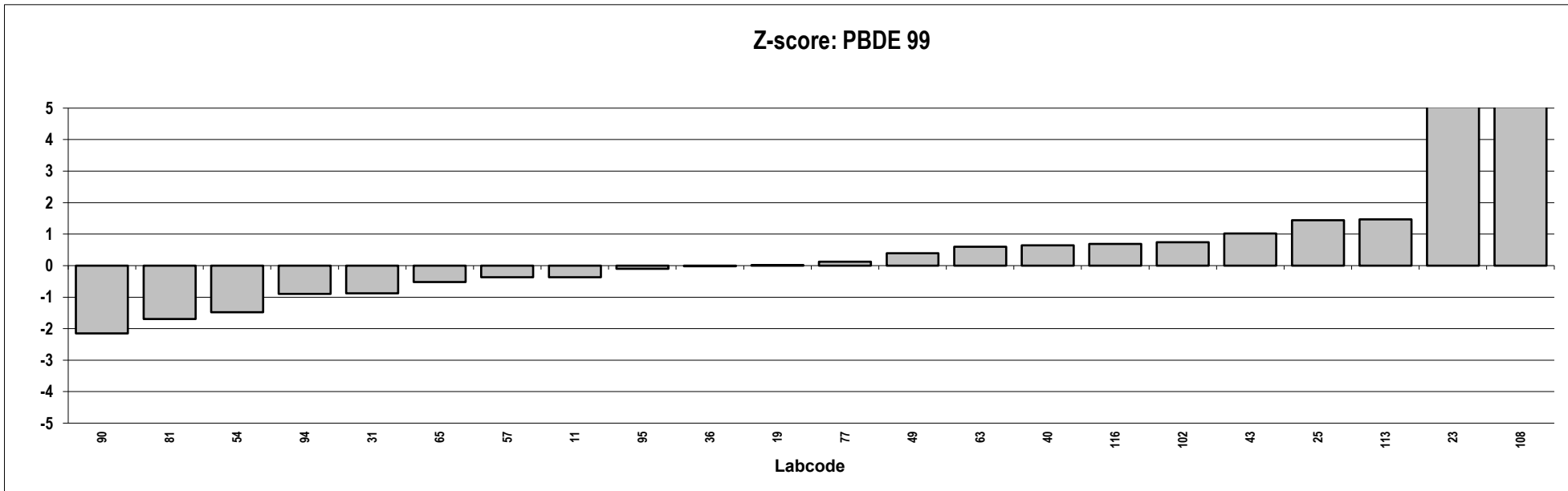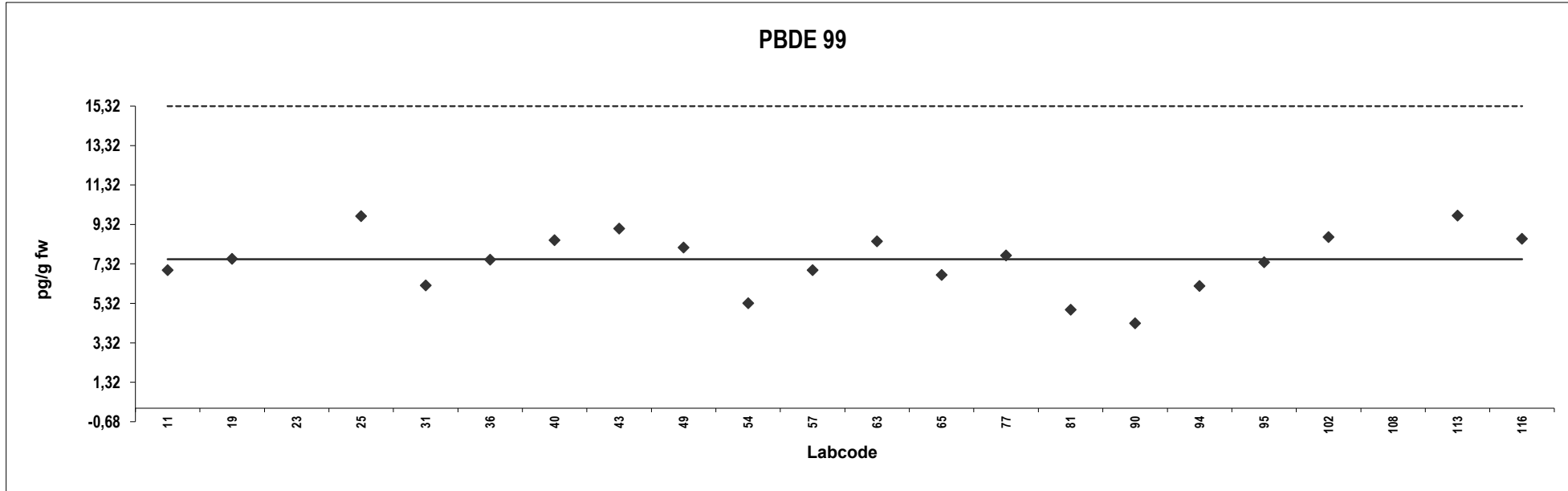
Brown meat
Congener: PBDE 100

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	14	-0,12					
19	13	-0,55					
23	19	1,5					
25	15	0,35					
31	14	-0,16					
36	15	0,087					
40	18	1,1					
43	22	2,6					
49	12	-0,82					
54	2,4	-4,2					
57	13	-0,58					
63	17	0,76					
65	14	-0,16					
77	20	1,8					
81	8,0	-2,2					
90	12	-0,93					
94	14	-0,30					
95	15	0,19					
102	14	-0,09					
108	19	1,5					
113	20	1,9					
116	16	0,42					

Consenus statistics

Consensus median, pg/g	14
Median all values pg/g	14
Consensus mean, pg/g	15
Standard deviation, pg/g	4,2
Relative standard deviation, %	29
No. of values reported	22
No. of values removed	0
No. of reported non-detects	0

PBDE 100

pg/g fw

Labcode: 11, 19, 23, 25, 31, 36, 40, 43, 49, 54, 57, 63, 65, 77, 81, 90, 94, 95, 102, 108, 113, 116

Z-score: PBDE 100

Labcode: 54, 81, 90, 49, 57, 19, 94, 65, 31, 11, 102, 36, 95, 25, 116, 63, 40, 23, 108, 77, 113, 43
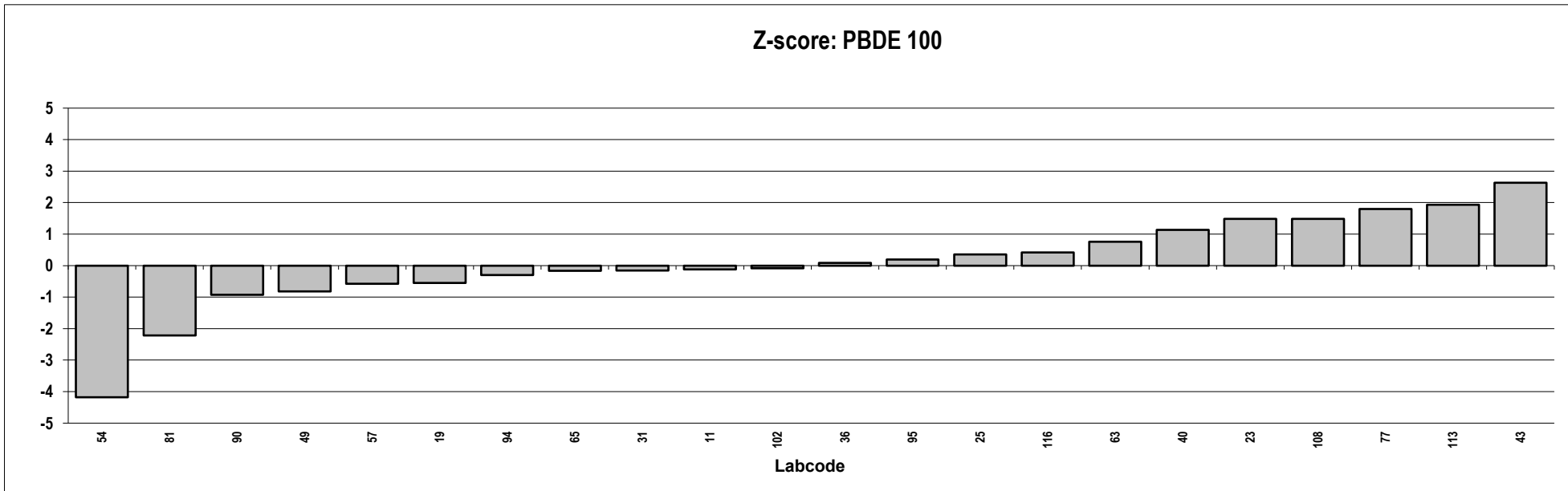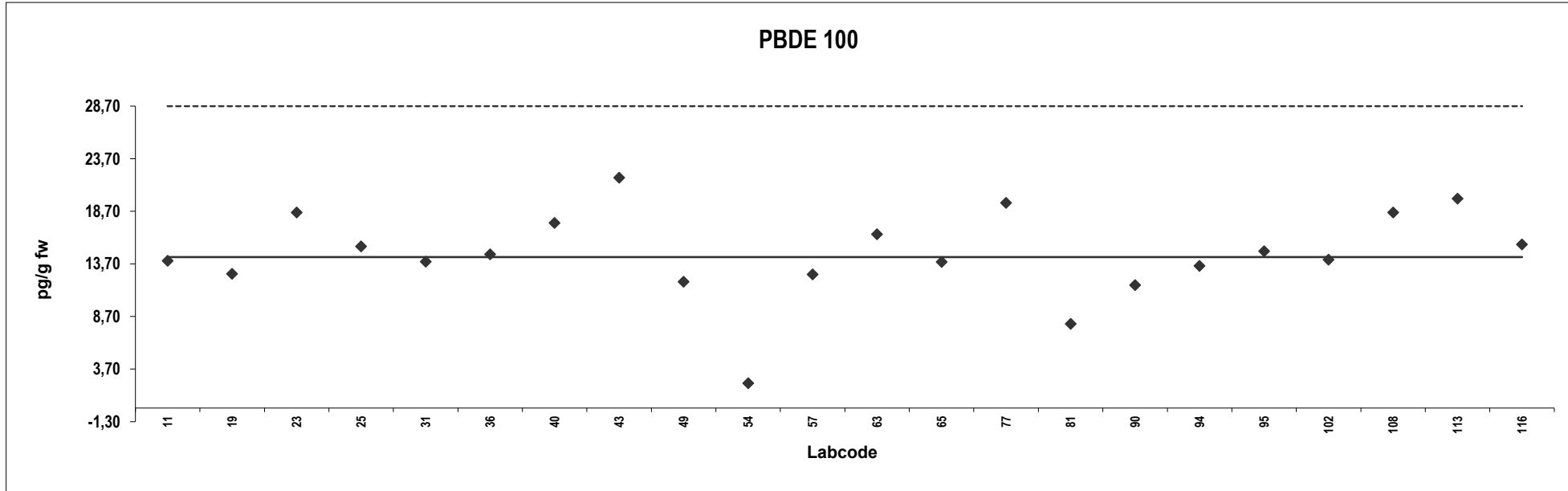
Brown meat

Congener: PBDE 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	7,0	1,5					
19	4,1	-1,2					
23	5,8	0,38					
25	6,5	1,0					
31	4,4	-0,89					
36	4,2	-1,1					
40	7,3	1,8					
43	6,7	1,2					
49	4,0	-1,3					
54	5,2	-0,15					
57	4,5	-0,80					
63	6,1	0,67					
65	5,4	0,00					
77	5,9	0,44					
81	2,0	-3,1					
90	4,5	-0,82					
94	5,1	-0,27					
95	5,2	-0,15					
102	5,8	0,35					
108	16	10	Outlier				
113	5,7	0,32					
116	6,2	0,73					

Consenus statistics	
Consensus median, pg/g	5,4
Median all values pg/g	5,6
Consensus mean, pg/g	5,3
Standard deviation, pg/g	1,2
Relative standard deviation, %	23
No. of values reported	22
No. of values removed	1
No. of reported non-detects	0
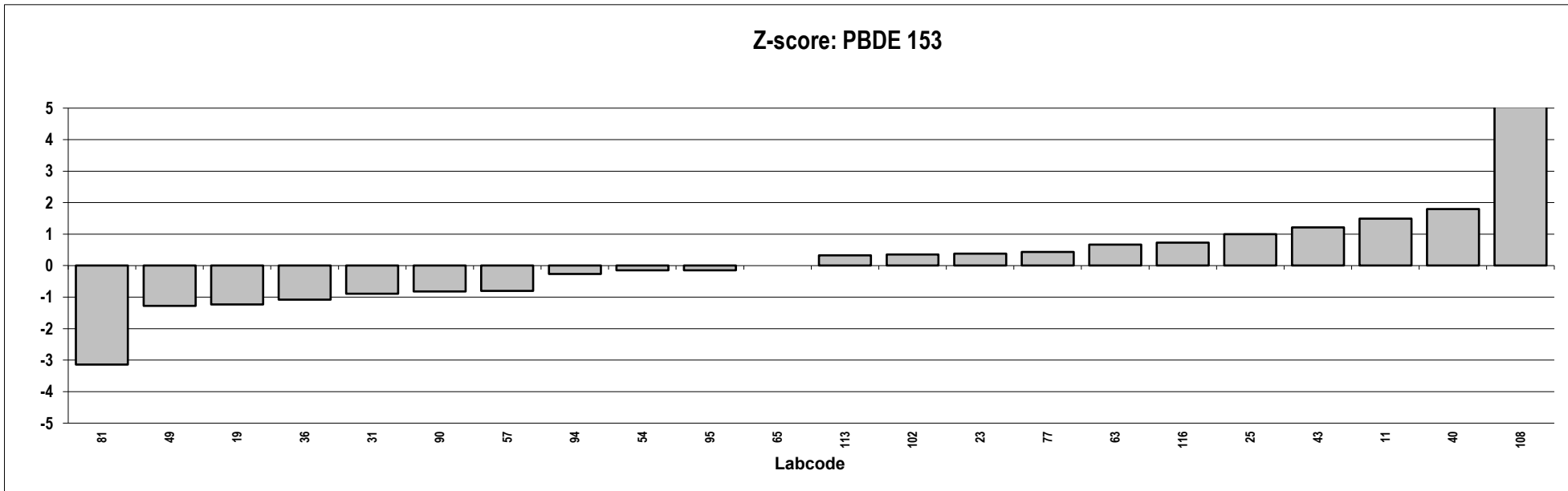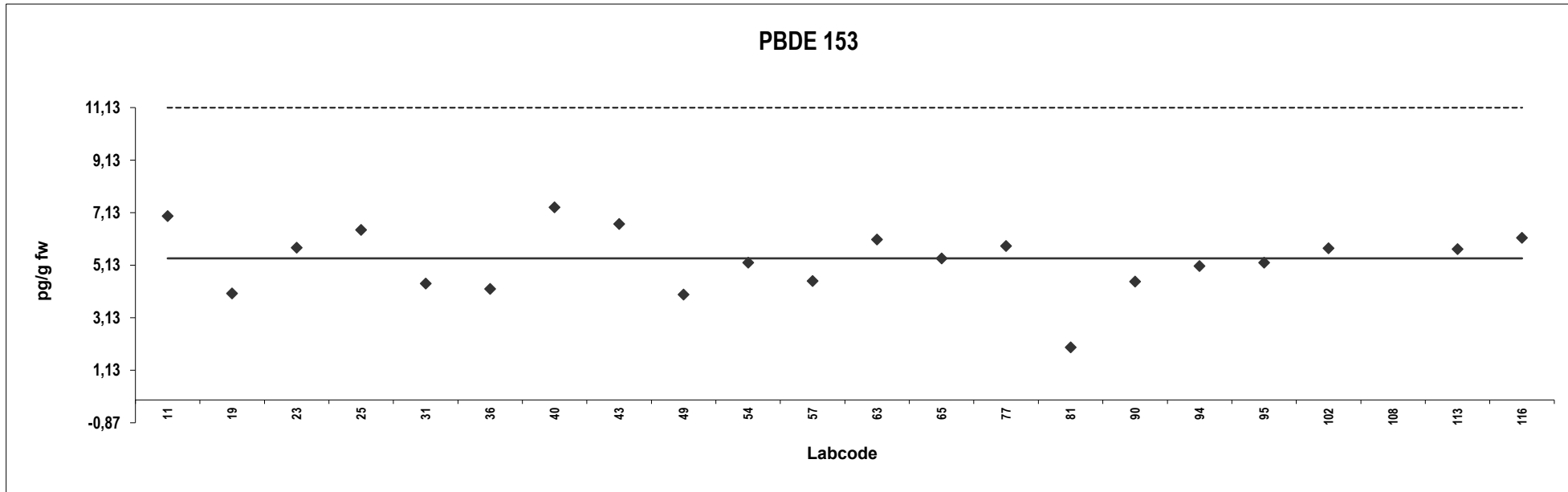
Brown meat
Congener: PBDE 154

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	20	-0,10					
19	20	0,00					
23	27	1,6					
25	20	-0,14					
31	20	-0,074					
36	20	-0,10	ND				
40	22	0,29					
43	29	2,2					
49	19	-0,37					
54	23	0,71					
57	23	0,66					
63	27	1,7					
65	20	-0,050					
77	25	1,0					
81	10	-2,6					
90	19	-0,23					
94	14	-1,7					
95	22	0,29					
102	24	0,83					
108	31	2,6					
113	0,50	-4,9					
116	19	-0,28					

Consenus statistics

Consensus median, pg/g	20
Median all values pg/g	20
Consensus mean, pg/g	21
Standard deviation, pg/g	6,5
Relative standard deviation, %	31
No. of values reported	22
No. of values removed	0
No. of reported non-detects	1

PBDE 154

Z-score: PBDE 154
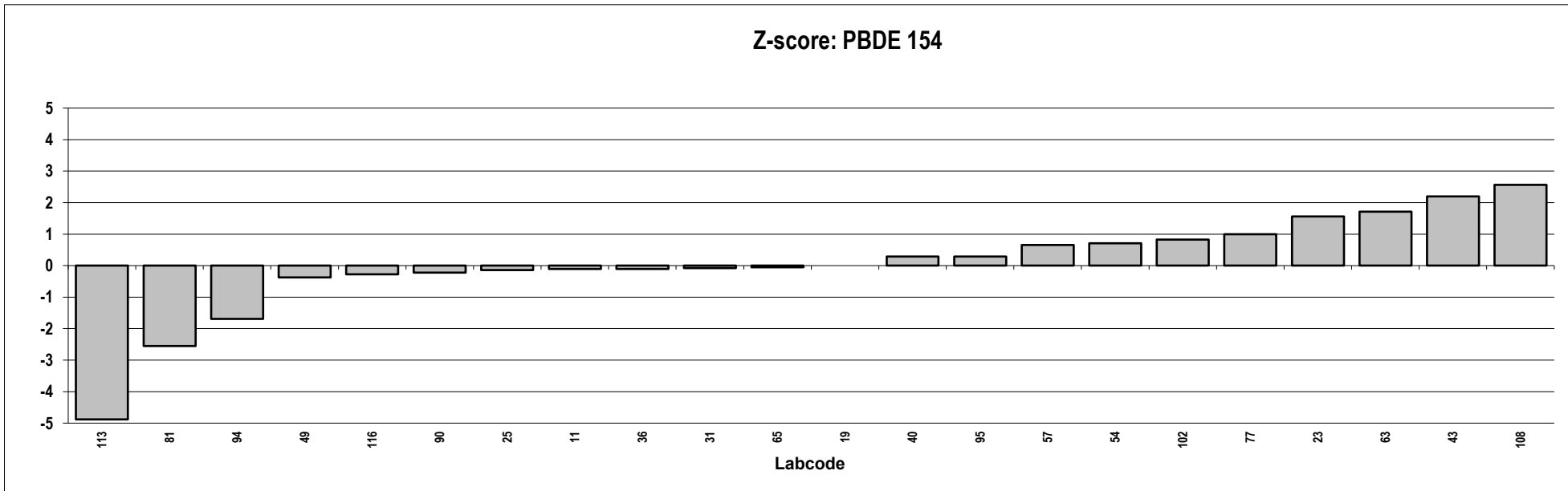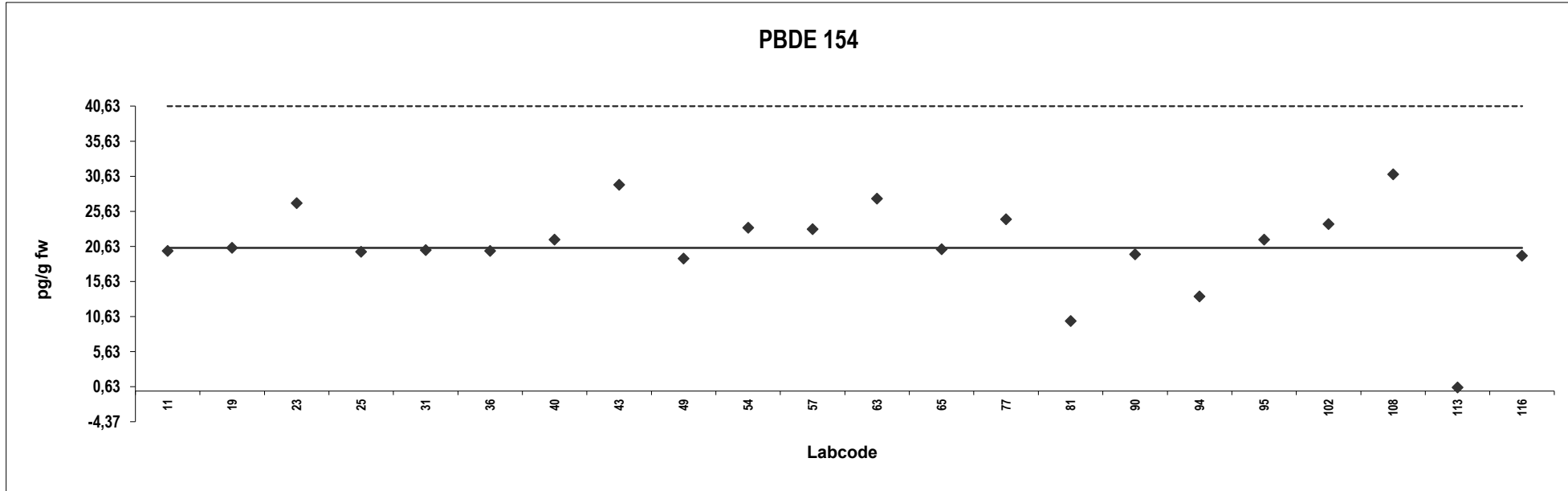
Brown meat
Congener: PBDE 183

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	8,9	54	Outlier,ND				
19	2,3	10	ND				
23	1,9	7,6					
25	0,49	-1,8	ND				
31	0,90	0,95	ND				
36	0,49	-1,8					
40	2,1	8,7					
43	1,2	2,9					
49	0,42	-2,2					
54	1,2	2,9					
57	0,44	-2,1					
63	3,2	16	Outlier,ND				
65	0,49	-1,7					
77	10	61	Outlier,ND				
81	2,0	8,2	ND				
90	0,72	-0,23					
94	8,00	48	Outlier,ND				
95	0,79	0,23					
102	3,8	20	Outlier				
108	8,8	53	Outlier				
113	3,1	15					
116	0,42	-2,2					

Consenus statistics	
Consensus median, pg/g	0,76
Median all values pg/g	1,6
Consensus mean, pg/g	1,2
Standard deviation, pg/g	0,84
Relative standard deviation, %	71
No. of values reported	22
No. of values removed	6
No. of reported non-detects	8

PBDE 183

Z-score: PBDE 183
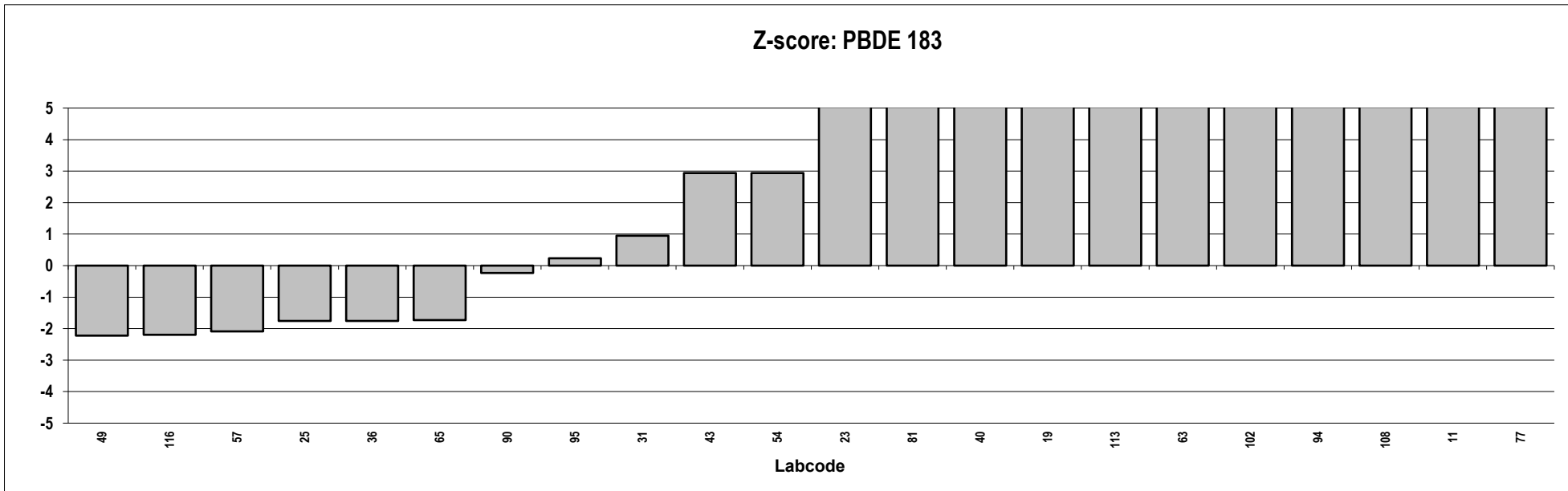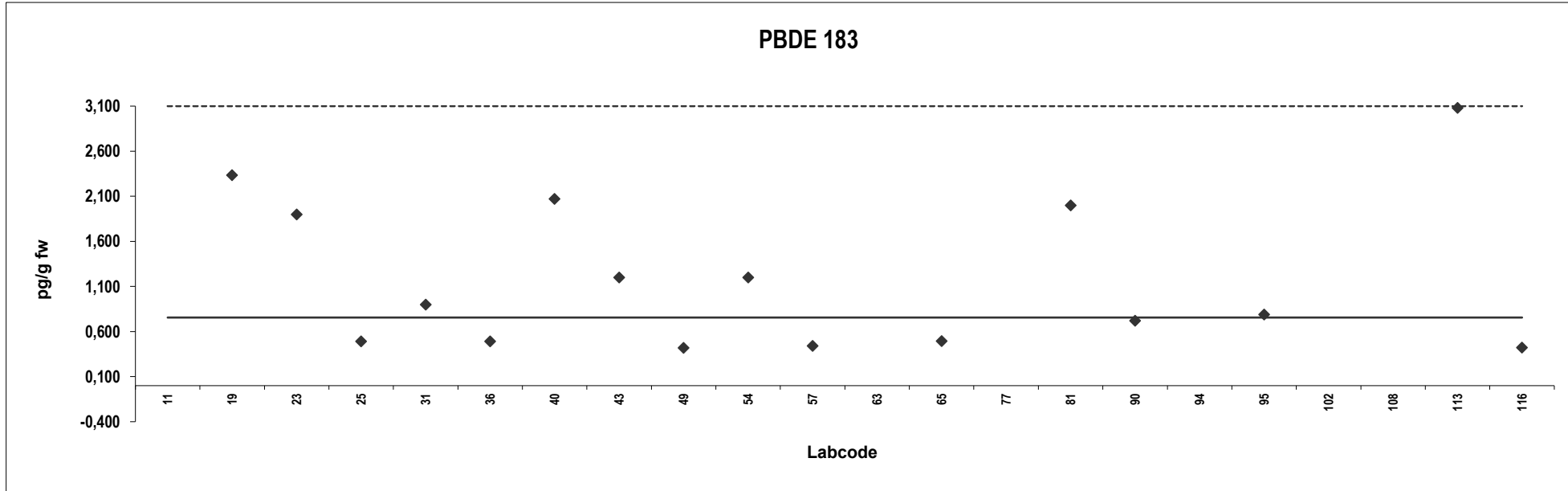
Brown meat
Congener: PBDE 209

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	236	80	Outlier				
23	24	3,8					
25	3	-3,8					
31	72	21	Outlier,ND				
36	10	-1,4	ND				
43	23	3,3					
57	5,7	-3,0					
63	242	82	Outlier				
65	14	0,035					
77	200	67	Outlier,ND				
90	171	57	Outlier				
94	83	25	Outlier,ND				
95	13	-0,24					
102	798	283	Outlier				
108	24	3,8					
113	138	45	Outlier				
116	14	-0,035					

Consenus statistics

Consensus median, pg/g	14
Median all values pg/g	24
Consensus mean, pg/g	15
Standard deviation, pg/g	7,9
Relative standard deviation, %	54
No. of values reported	17
No. of values removed	8
No. of reported non-detects	4

PBDE 209

pg/g fw
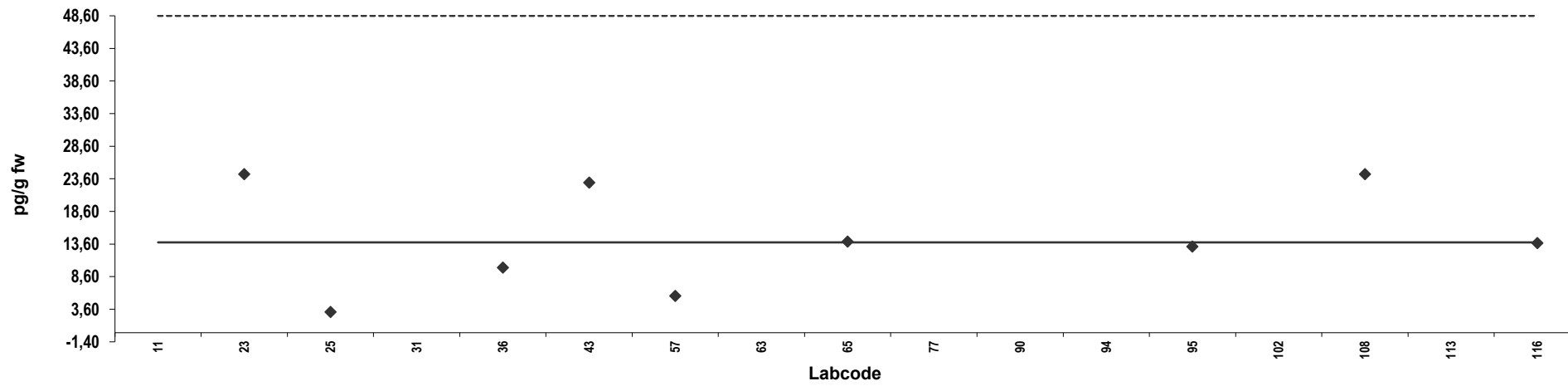
Labcode

Z-score: PBDE 209
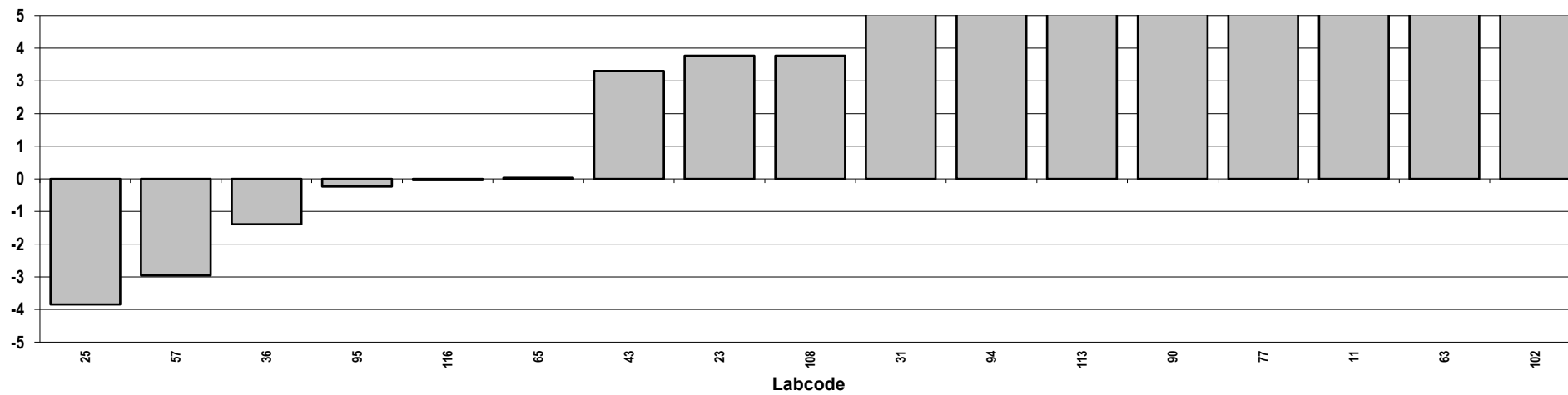
Labcode

Brown meat

Congener: α-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	6,0	-2,4	ND				
17	15	1,5					
49	15	1,6	ND				
65	8,0	-1,5					
95	10	-0,59	ND				

Consenus statistics

Consensus median, pg/g	11
Median all values pg/g	10
Consensus mean, pg/g	11
Standard deviation, pg/g	4,0
Relative standard deviation, %	37
No. of values reported	5
No. of values removed	0
No. of reported non-detects	3

α-HBCD

Z-score: α-HBCD
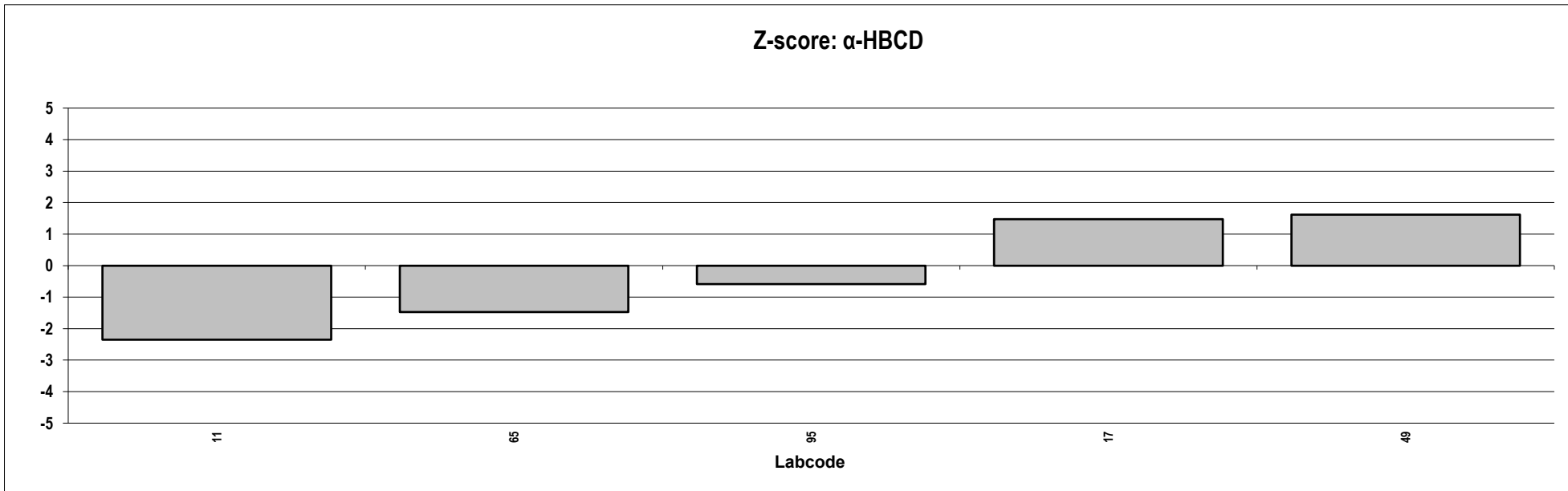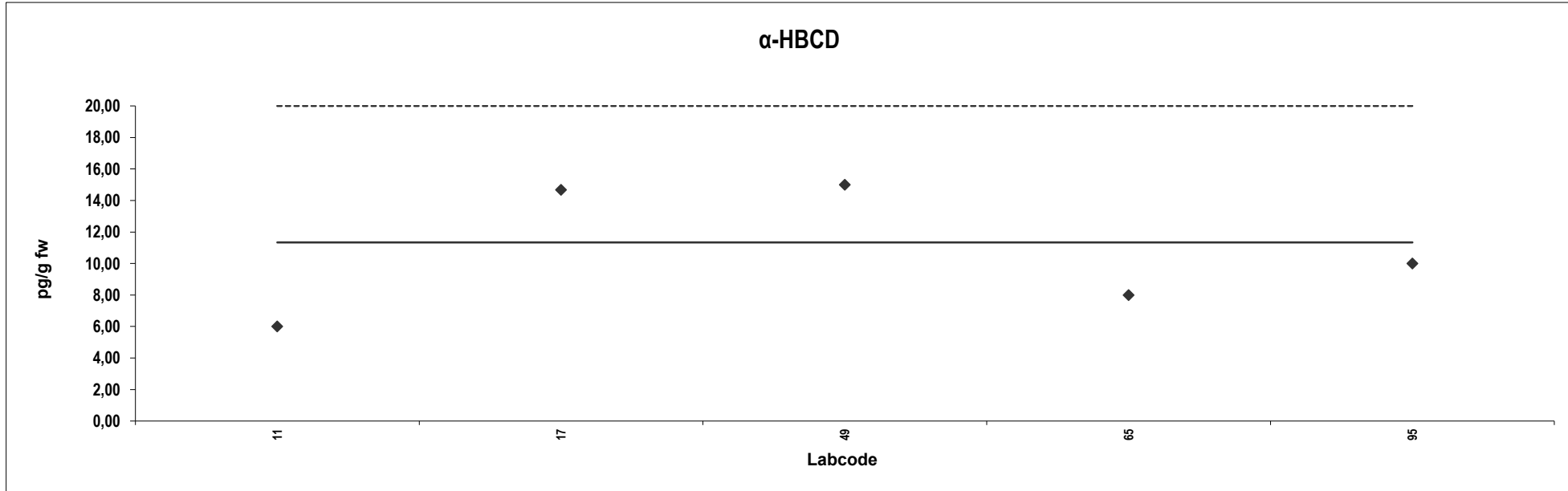
Brown meat
Congener: β-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	6,0	2,9	ND				
17	6,1	3,0					
49	15	15	Outlier,ND				
65	1,5	-3,0					
95	5,0	1,6	ND				

Consenus statistics

Consensus median, pg/g	3,8
Median all values pg/g	6,0
Consensus mean, pg/g	4,7
Standard deviation, pg/g	2,2
Relative standard deviation, %	46
No. of values reported	5
No. of values removed	1
No. of reported non-detects	3
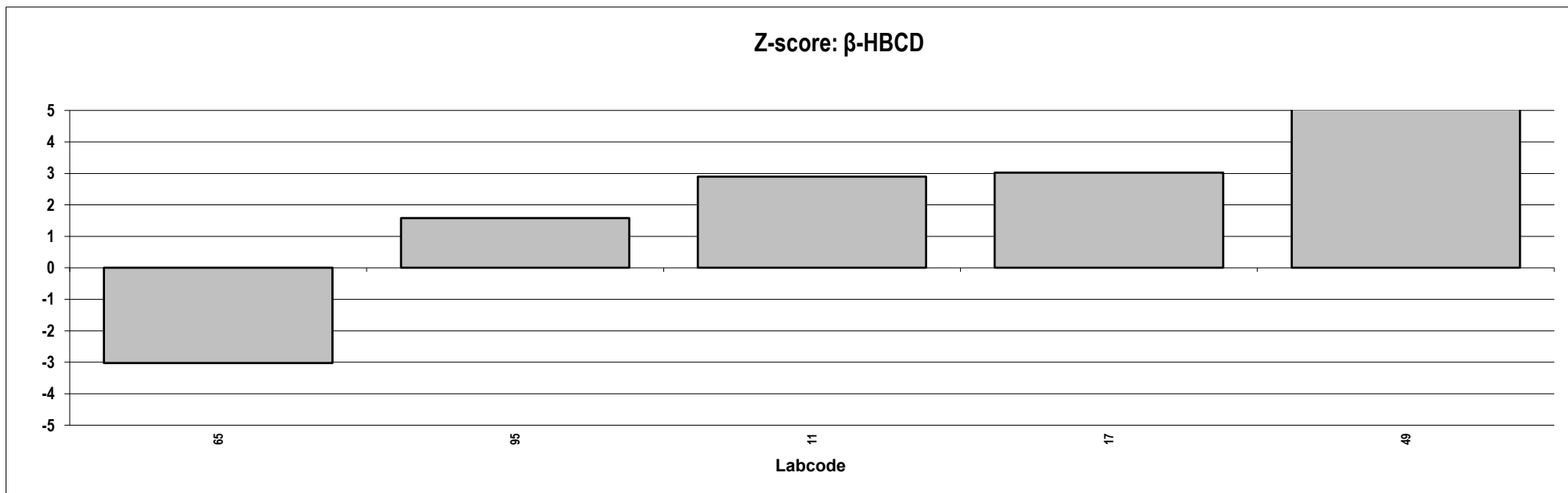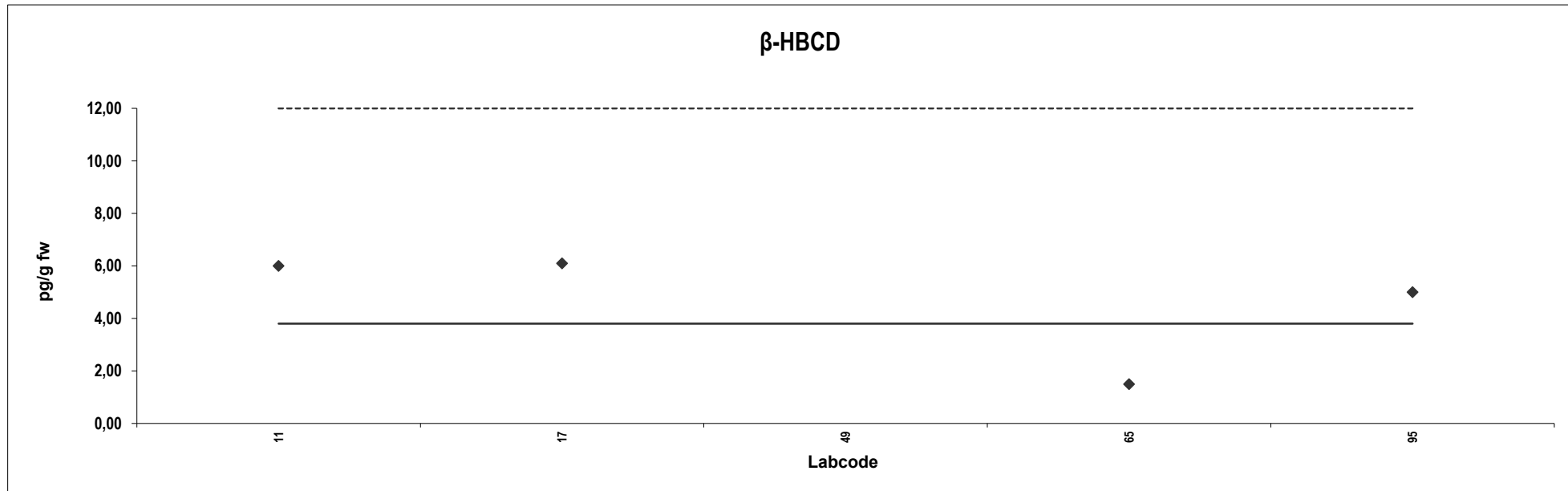
β-HBCD

Z-score: β-HBCD

Brown meat

Congener: γ-HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
11	6,0	-0,39	ND				
17	12	4,2					
49	15	6,5	ND				
65	1,1	-4,2					
95	10	2,7	ND				

Consensus statistics

Consensus median, pg/g	6,5
Median all values pg/g	10
Consensus mean, pg/g	8,8
Standard deviation, pg/g	5,4
Relative standard deviation, %	61
No. of values reported	5
No. of values removed	0
No. of reported non-detects	3

γ-HBCD

Z-score: γ-HBCD
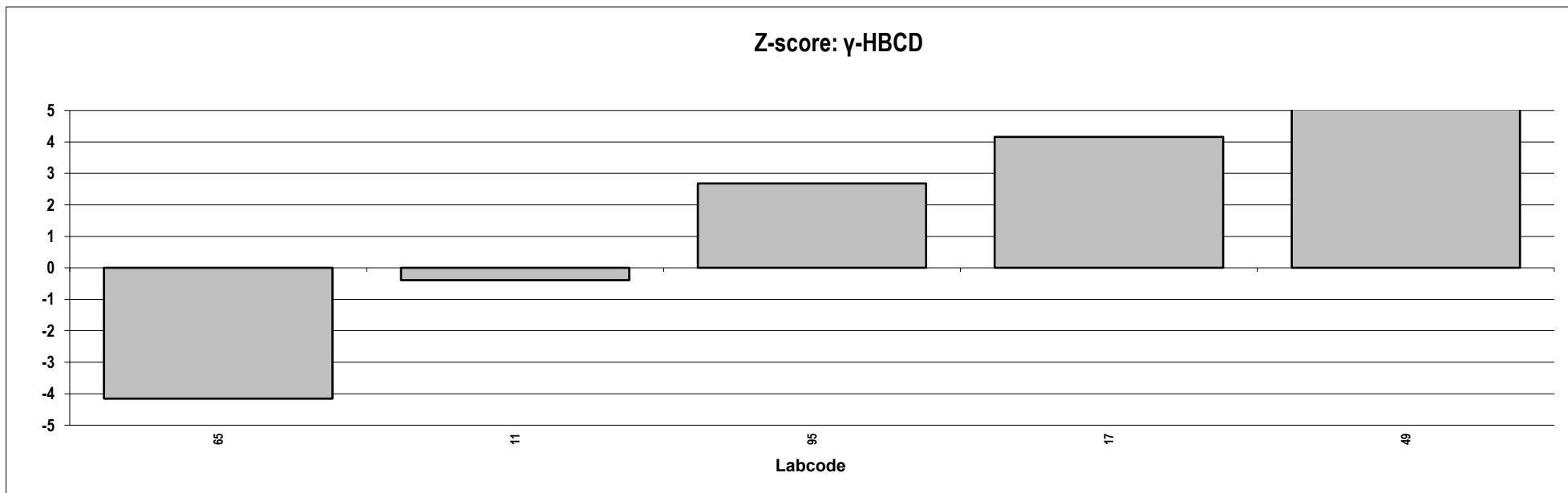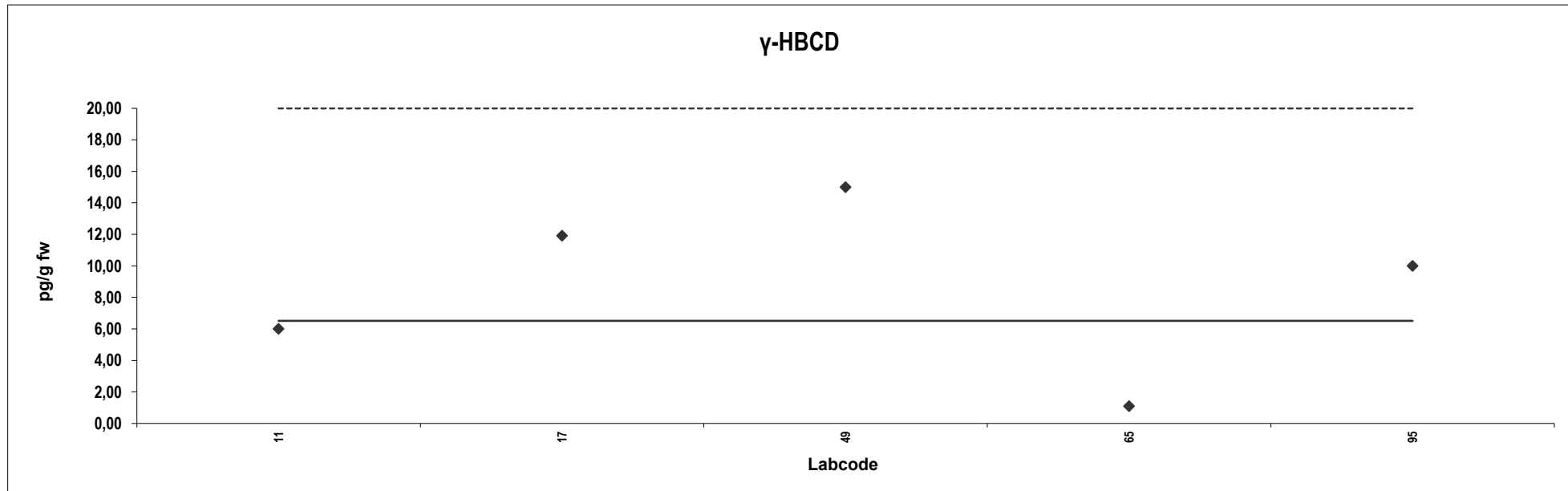
Brown meat

Congener: total HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
17	33	8,2	Outlier				
65	11	-0,55					
108	14	0,55					

Consenus statistics

Consensus median, pg/g	12
Median all values pg/g	14
Consensus mean, pg/g	12
Standard deviation, pg/g	1,9
Relative standard deviation, %	15
No. of values reported	3
No. of values removed	1
No. of reported non-detects	0

total HBCD

Z-score: total HBCD
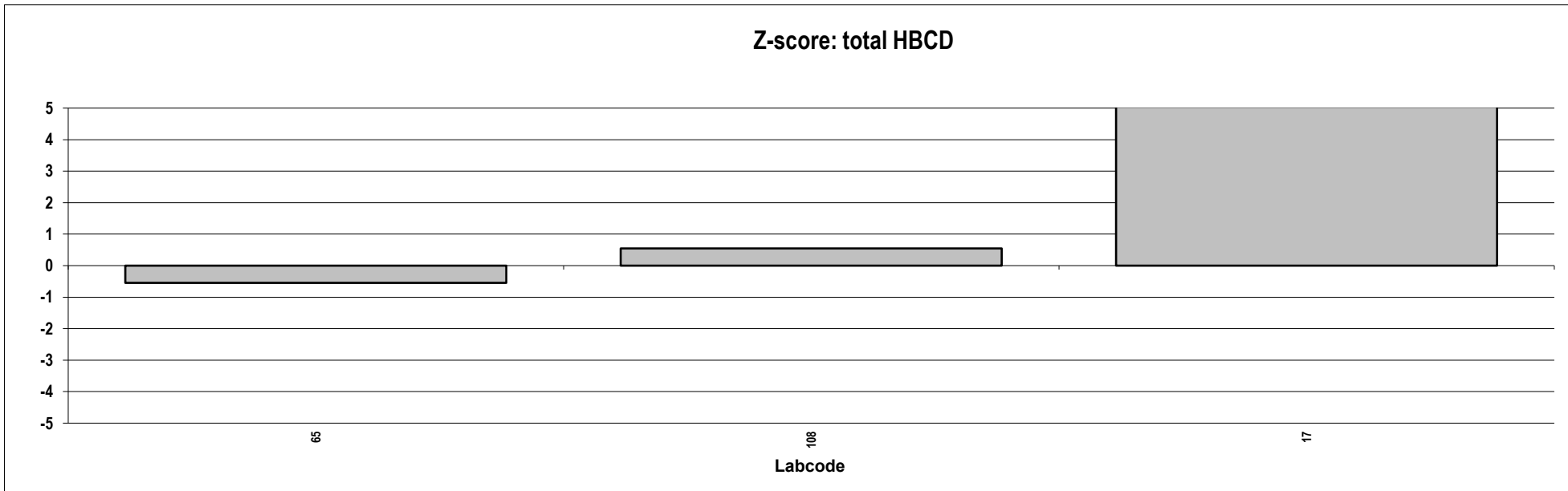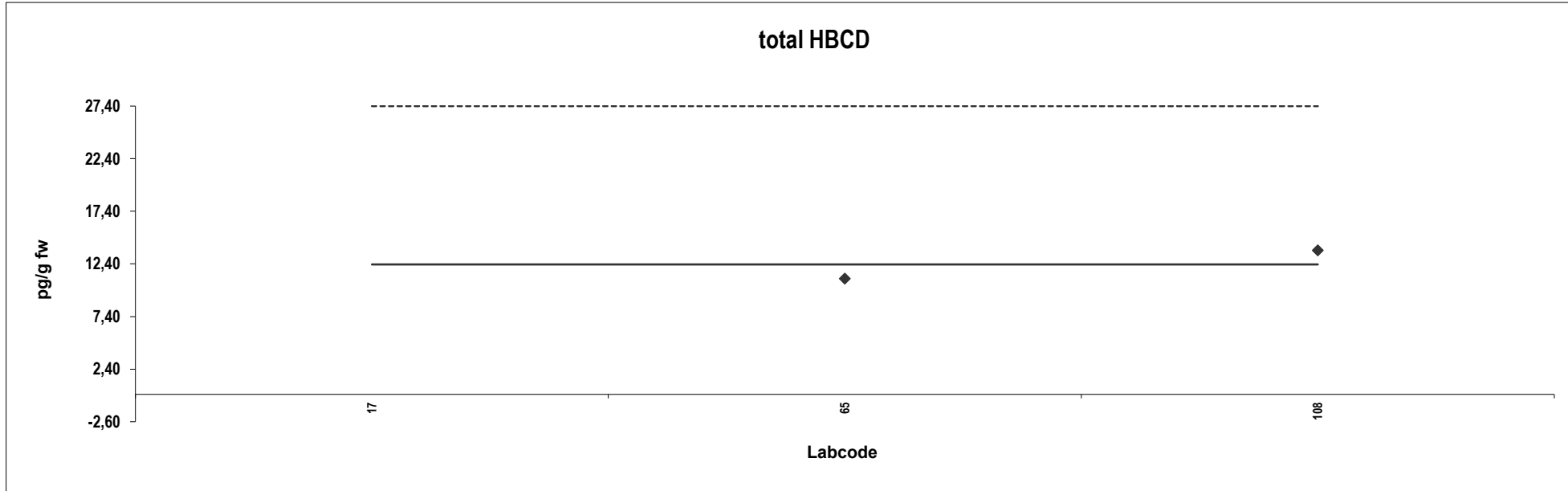
Appendix 5:

Presentation of results for
Perch-2019

Appendix 5: Presentation of results: Perch-2019

Statistic calculations for PFASs

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 × this median were defined as outliers and removed from the data set. The NDs were also removed.
3. As the number of reported results were limited, we also choose to remove low outliers.
4. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
5. For comparison, median, mean and standard deviation were also calculated without removing NDs.
6.

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

Z-Scores of individual congeners

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

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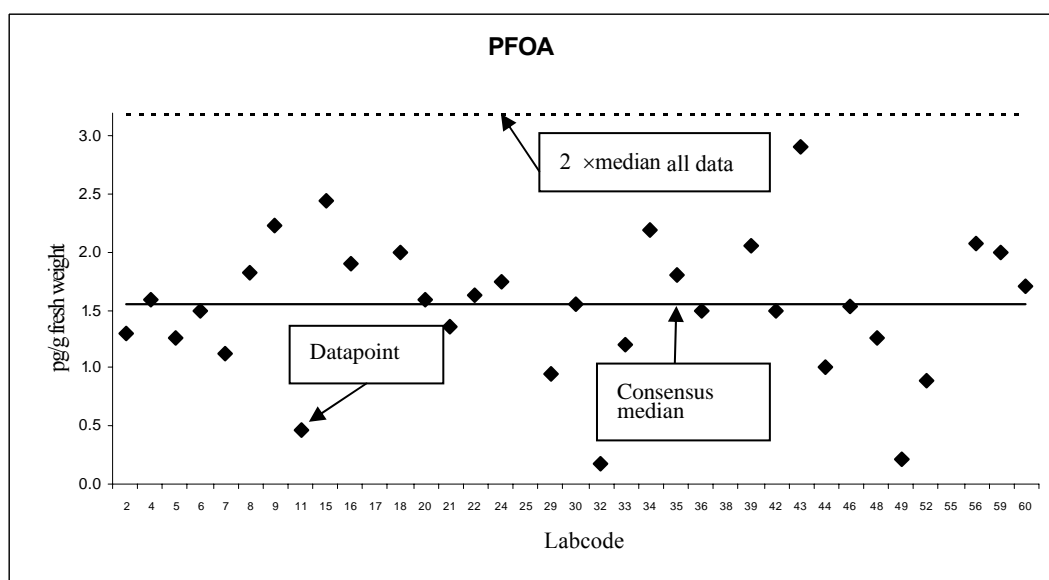
where x = reported value; X = assigned value (consensus); σ = target value for standard deviation. A σ of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of ± 20% from the consensus value.

Perch

PFOS

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
11	198675	2,9				
19	92780	-1,3				
36	131000	0,22				
43	125393	0,00				
49	141000	0,62				
56	125348	-0,0018				
61	79569	-1,8				
70	120000	-0,22				
94	147	-5,0	Outlier			
113	132550	0,29				

Consensus statistics

Consensus median, pg/g	125393
Median all values pg/g	125371
Consensus mean, pg/g	127368
Standard deviation, pg/g	33268
Relative standard deviation, %	26
No. of values reported	10
No. of values removed	1
No. of reported non-detects	0

PFOA

Z-score: PFOA
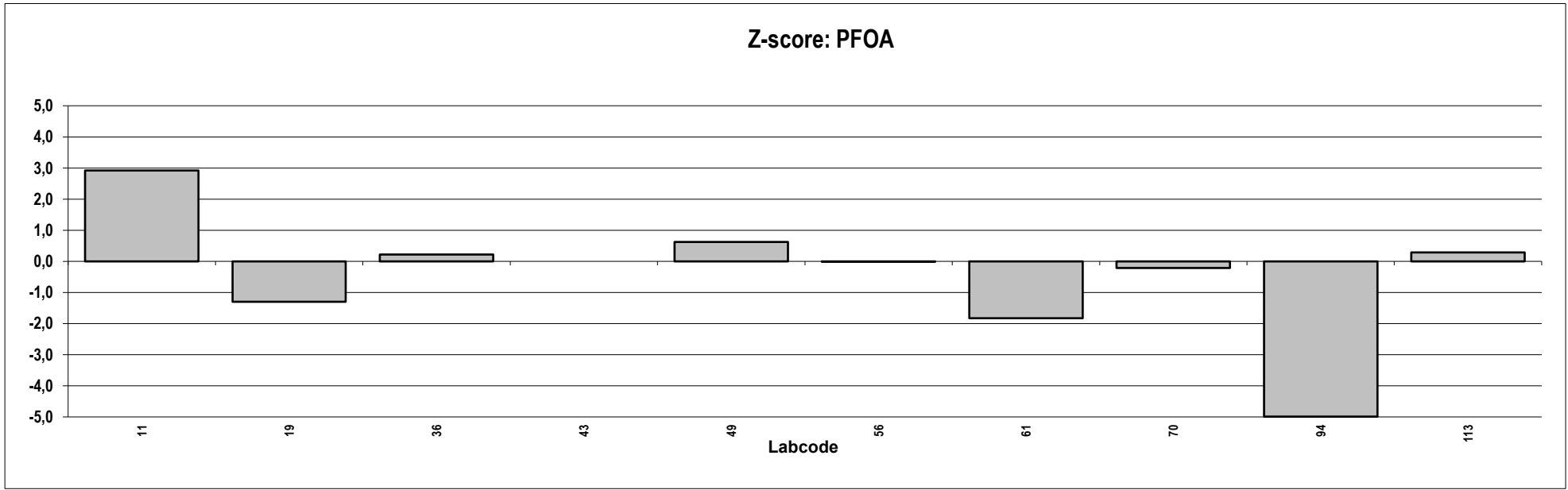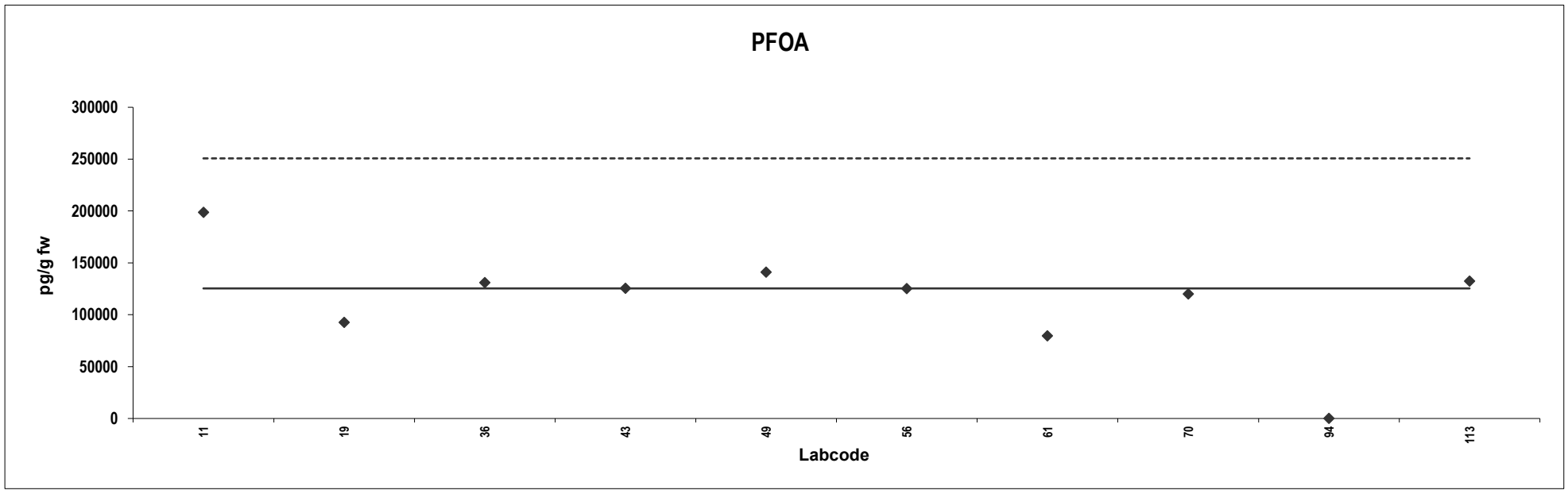
Perch

PFHxS

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
11	319	7,4	Outlier			
19	333	7,9	ND, Outlier			
36	200	2,8	ND			
43	200	2,8	ND			
49	2000	73	ND, outlier			
56	147	0,70				
70	499	14	ND, outlier			
81	260	5,1				
94	0,084	-5,0	Outlier			
113	110	-0,74				

Consensus statistics	
Consensus median, pg/g	147
Median all values pg/g	230
Consensus mean, pg/g	172
Standard deviation, pg/g	78
Relative standard deviation, %	45
No. of values reported	10
No. of values removed	7
No. of reported non-detects	5

PFHxS

pg/g fw

Labcode

Z-score: PFHxS
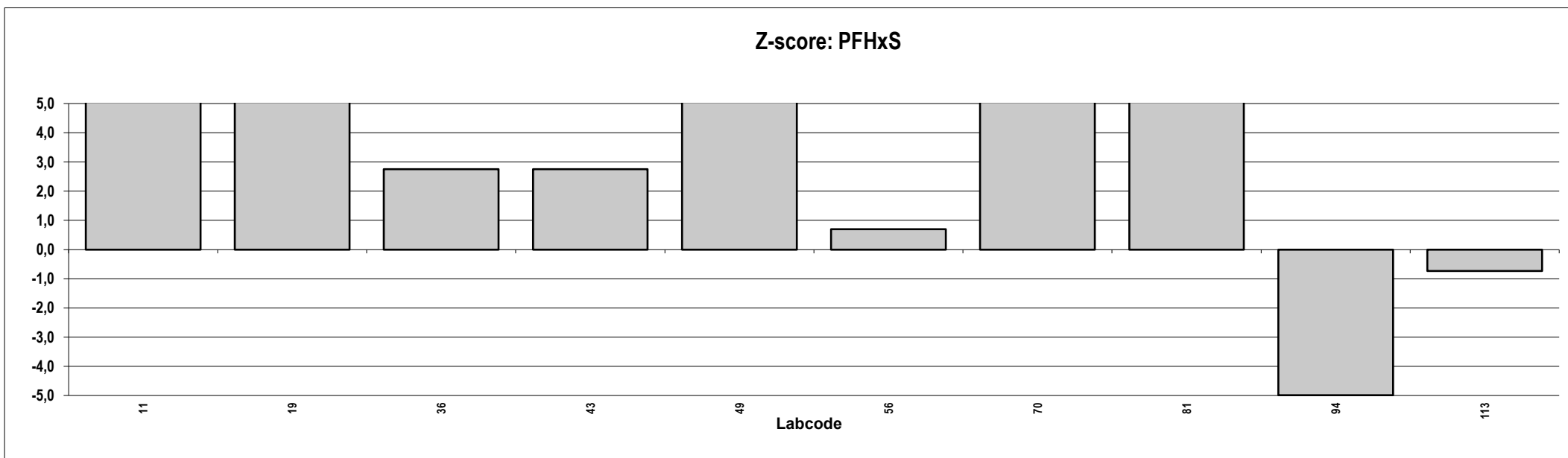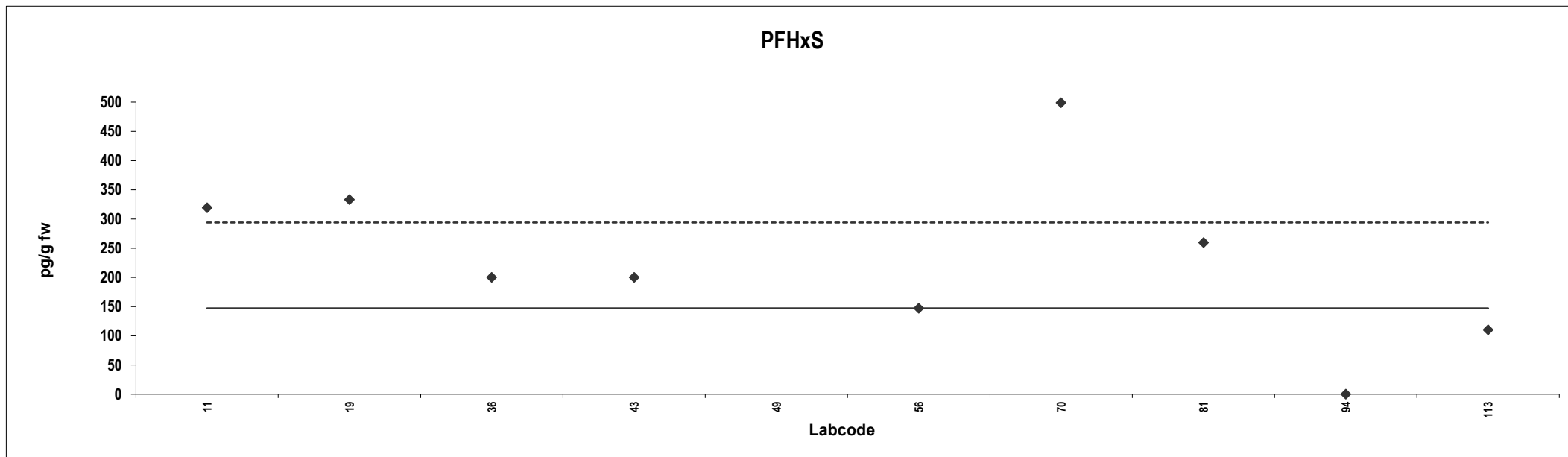
Labcode

Perch

PFOA

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
11	34	-2,05				
19	1333	112	ND			
36	200	13	ND			
43	200	13	ND			
49	2000	171	ND, Outlier			
56	100	3,8	ND			
61	150	8	ND			
70	251	17	ND			
81	667	54	Outlier			
94	0,014	-5,0	Outlier			
113	80	2,0				

Consensus statistics	
Consensus median, pg/g	57
Median all values pg/g	200
Consensus mean, pg/g	57
Standard deviation, pg/g	33
Relative standard deviation, %	58
No. of values reported	11
No. of values removed	9
No. of reported non-detects	7

PFOA

Z-score: PFOA
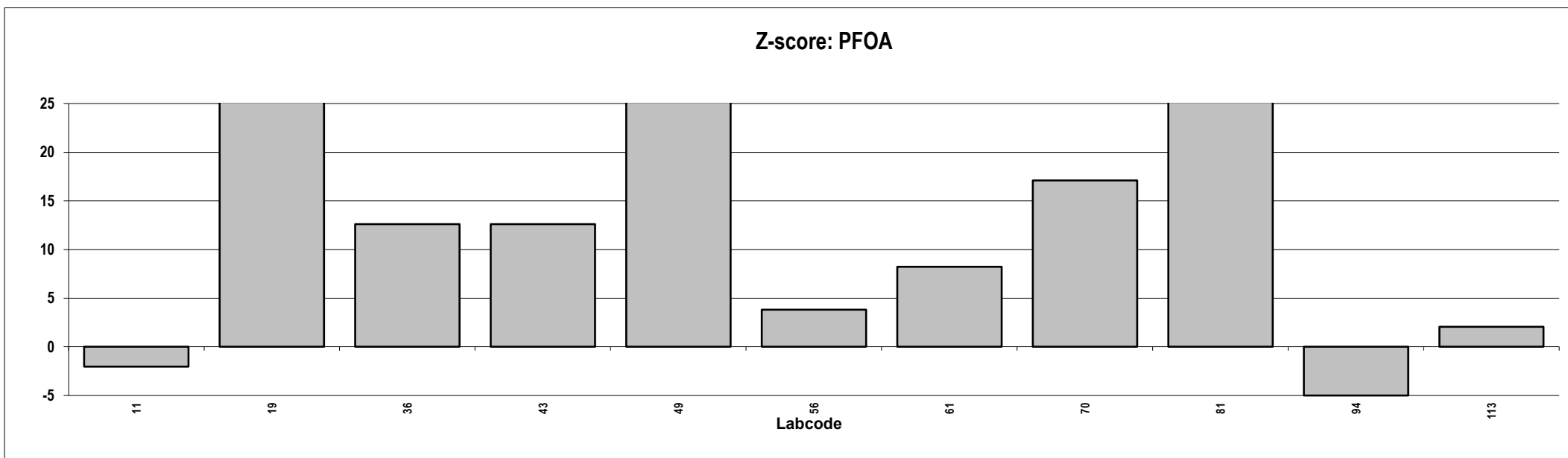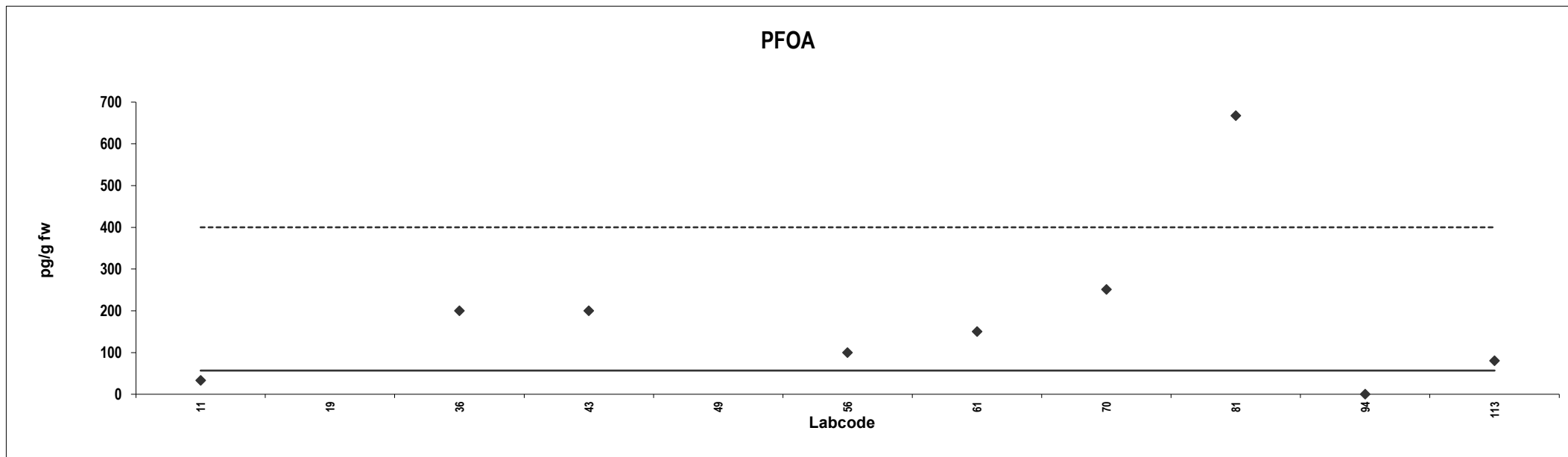
Perch

PFNA

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
11	247	-0,14				
19	67	-3,7	ND			
36	255	0,040				
43	2266	40	Outlier			
49	2000	35	ND, Outlier			
56	253	0,00				
70	609	7,0	ND			
81	1671	28	Outlier			
94	0,20	-5,0	Outlier			
113	350	1,9				

Consensus statistics	
Consensus median, pg/g	254
Median all values pg/g	303
Consensus mean, pg/g	276
Standard deviation, pg/g	49
Relative standard deviation, %	18
No. of values reported	10
No. of values removed	6
No. of reported non-detects	3
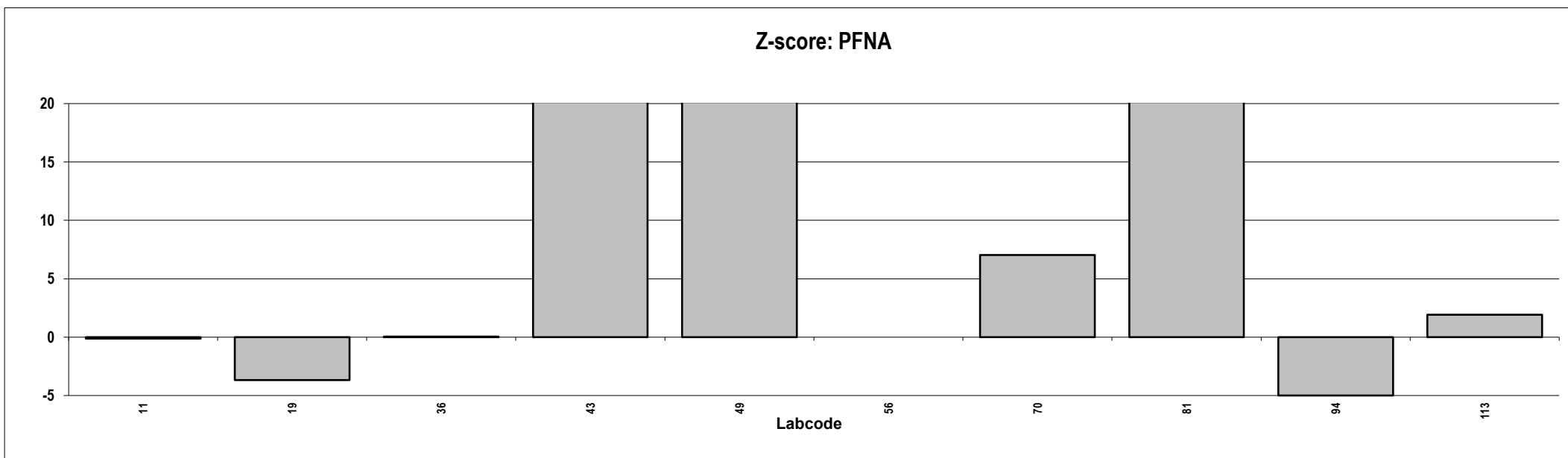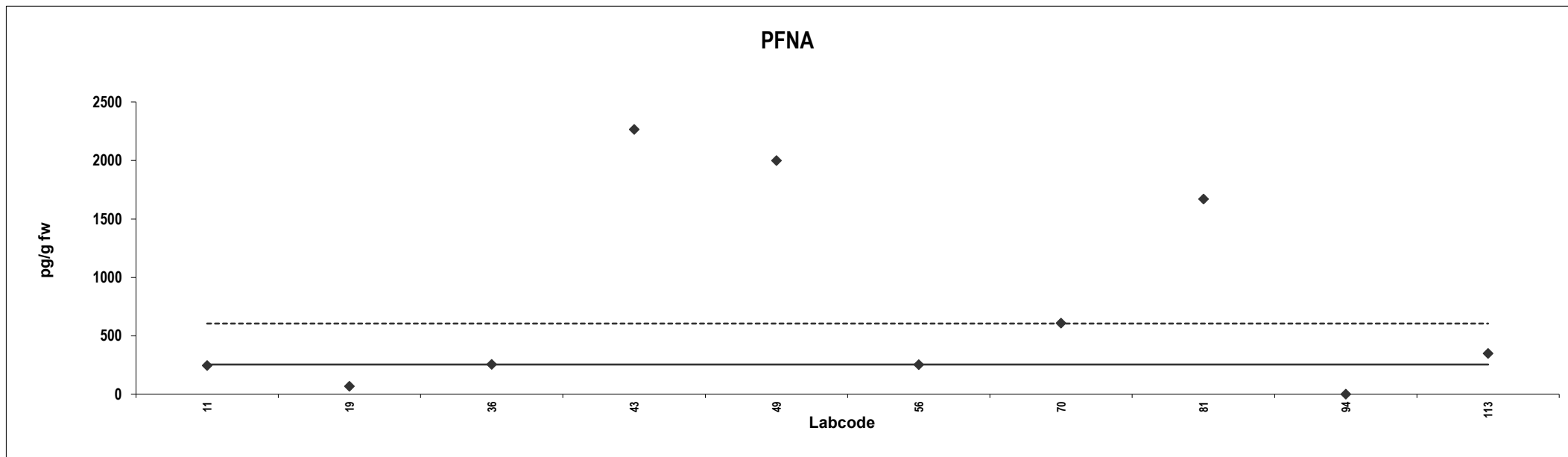
Perch

PFDA

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
11	676	-0,20				
19	590	-0,81				
36	801	0,68				
43	733	0,20				
49	2000	9,2	ND, Outlier			
56	768	0,45				
70	401	-2,2	ND			
81	4263	25	Outlier			
94	0,65	-5,0	Outlier			
113	660	-0,32				

Consensus statistics	
Consensus median, pg/g	705
Median all values pg/g	705
Consensus mean, pg/g	705
Standard deviation, pg/g	78
Relative standard deviation, %	11
No. of values reported	10
No. of values removed	4
No. of reported non-detects	2

PFDA

Z-score: PFDA
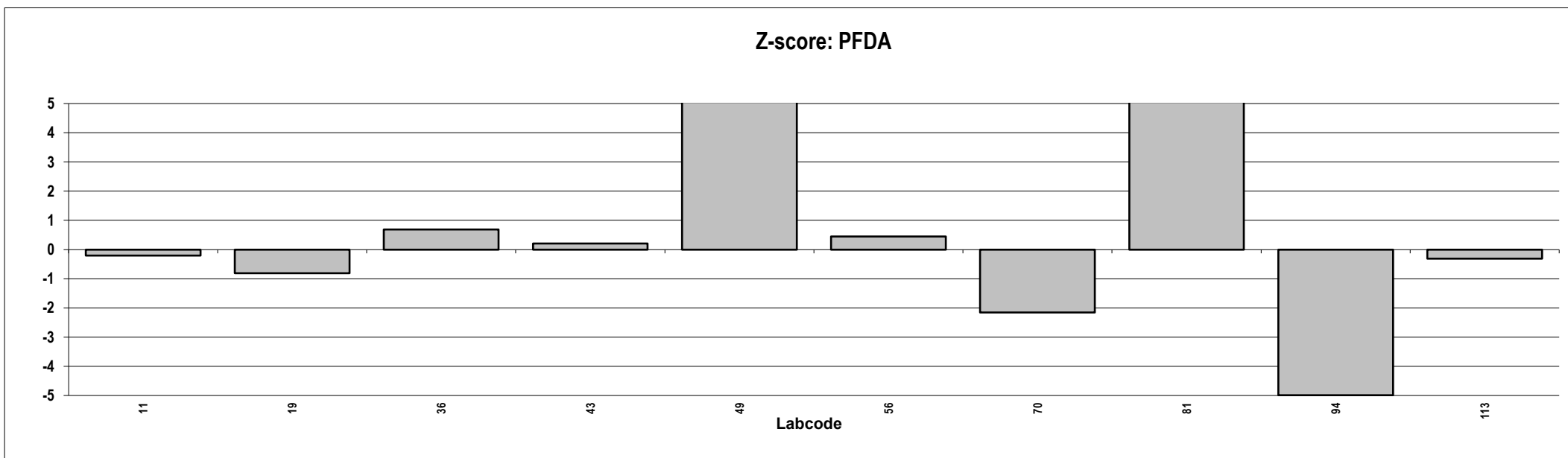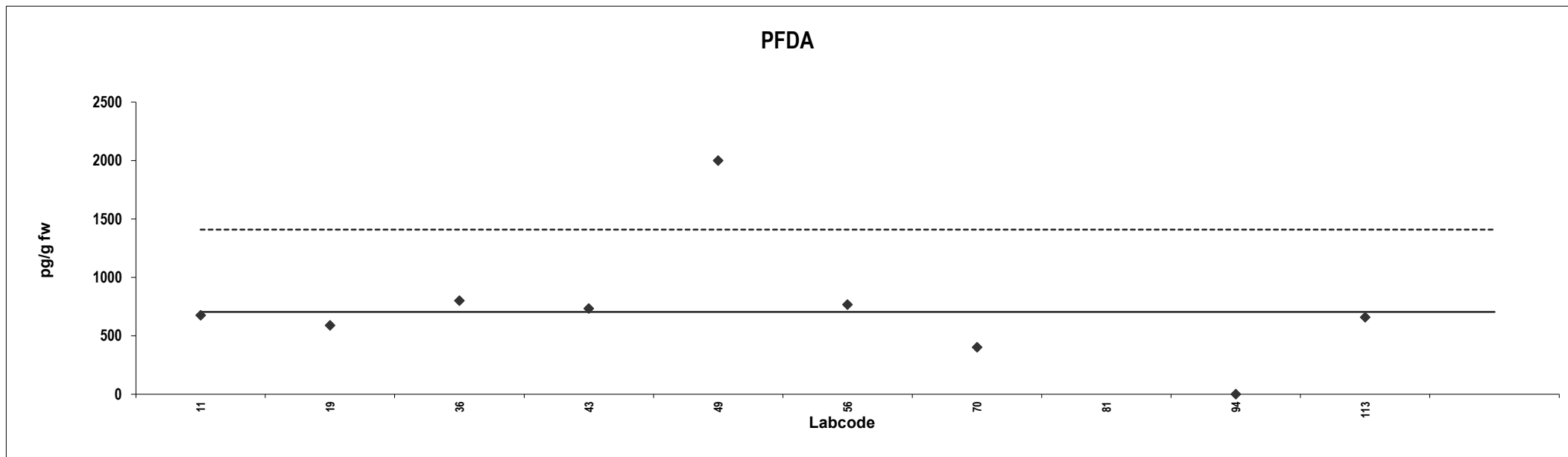
Perch

PFUnDA

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
11	951	-0,024				
19	960	0,024				
36	907	-0,25				
43	1753	4,2				
49	2000	5,5	ND			
56	1003	0,25				
70	456	-2,6	ND			
94	0,88	-5,0	Outlier			
113	950	-0,029				

| Consensus statistics	
Consensus median, pg/g	956
Median all values pg/g	951
Consensus mean, pg/g	1087
Standard deviation, pg/g	328
Relative standard deviation, %	30
No. of values reported	9
No. of values removed	3
No. of reported non-detects	2

PFUnDA

Z-score: PFUnDA
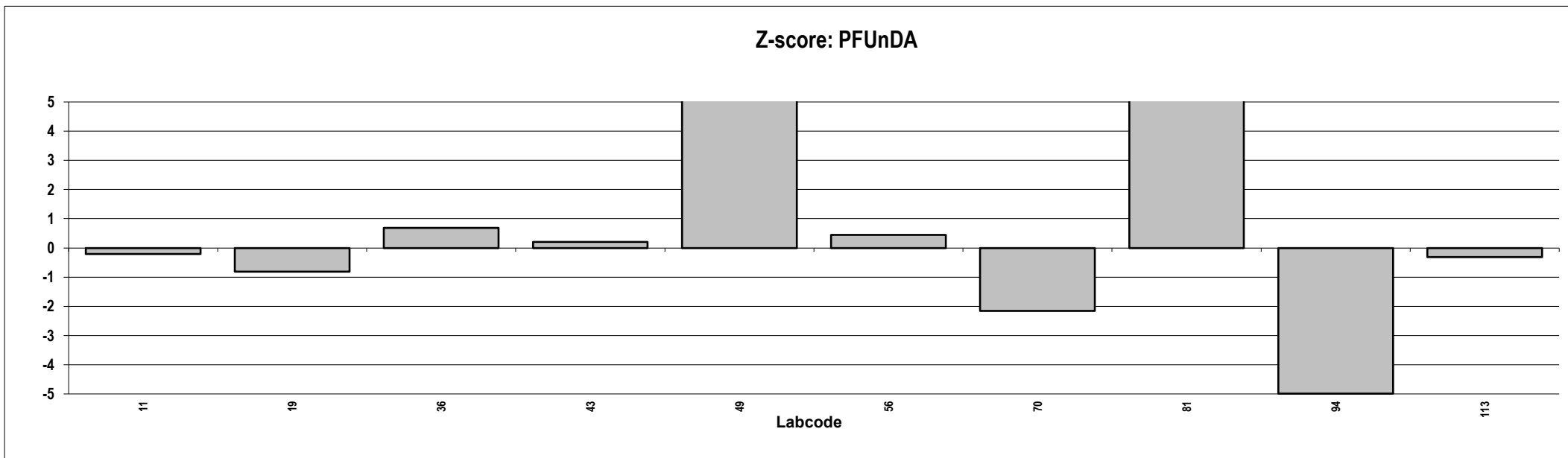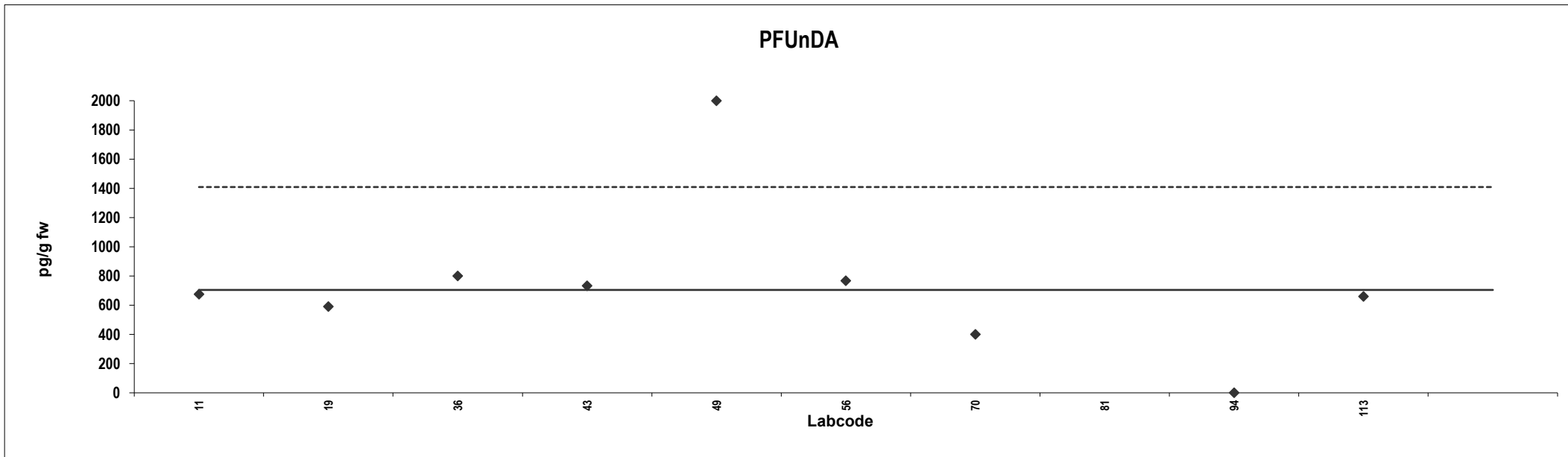
Appendix 6:

Presentation of results
for lipid determination

Presentation of results for lipid determination

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

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

The diagram shows the reported data with consensus and consensus $\pm$ the new standard deviation $\times 2$.
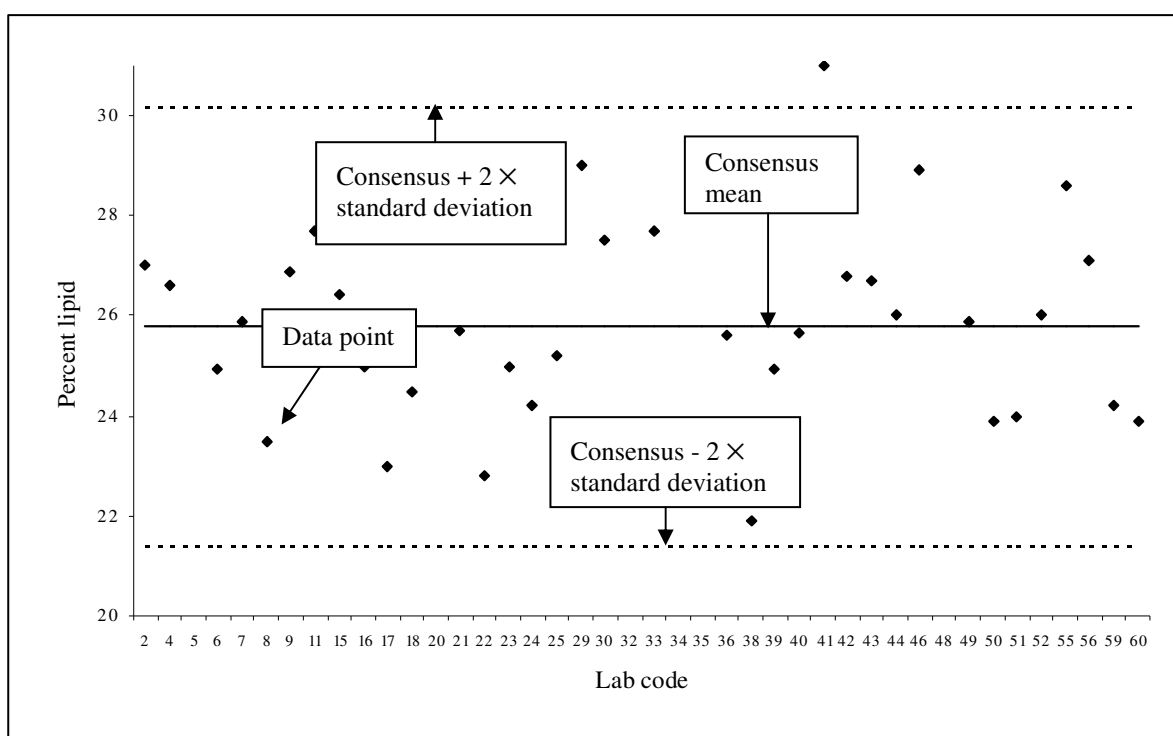
Z-Scores of lipid content

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

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

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

Lipid determination for Veal

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
4	8,9		113	9,0				
5	8,5		114	3,2	outlier			
7	9,4		115	7,5				
10	9,0		116	8,7				
11	11	outlier	117	7,4				
15	8,0		118	8,1				
17	8,4		120	8,4				
20	8,9							
23	8,5							
24	6,6							
27	7,8							
28	8,4							
31	7,9							
32	7,8							
33	8,4							
34	6,5							
36	8,0							
37	7,6							
40	8,1							
43	8,5							
44	9,5							
45	8,9							
49	7,6							
54	8,1							
56	7,5							
57	8,2							
58	6,7							
61	9,5							
63	8,5							
64	8,6							
65	7,4							
70	8,0							
73	7,9							
75	8,2							
76	9,6							
80	8,1							
87	8,3							
88	7,1							
89	7,6							
95	9,3							
100	8,6							
103	8,0							
105	6,4							
106	7,0							
108	8,1							
109	8,0							

Mean	Standard deviation	Relative standard deviation	Median
8,1	0,77	9,4	8,1

Lipid determination for Herring

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
4	7,2		102	6,6				
5	7,5		103	6,9				
7	8,4		105	5,3				
11	9,2		106	7,0				
12	6,7		108	6,5				
15	7,0		109	7,5				
17	7,6		110	29	**outlier**			
24	6,1		113	8,1				
25	6,7		114	1,4				
27	7,4		115	7,1				
28	7,2		116	5,7				
30	6,3		117	6,9				
31	6,9		118	7,7				
32	7,0		119	4,8				
33	8,1		120	6,6				
34	6,9							
36	6,6							
37	7,0							
40	7,8							
42	14	**outlier**						
43	6,4							
45	7,3							
48	7,2							
49	6,9							
54	7,4							
56	6,8							
57	6,8							
58	6,0							
61	7,8							
63	7,4							
64	6,5							
65	7,0							
71	10							
73	6,8							
75	7,1							
78	8,3							
80	6,8							
81	7,6							
84	7,1							
87	7,4							
88	5,3							
89	7,3							
90	6,5							
92	7,5							
95	7,0							
100	6,8							

Mean	Standard deviation	Relative standard deviation	Median
7,0	1,1	16	7,0

Lipid determination for Brown meat

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
4	7,3		103	7,5				
5	8,8		105	9,0				
7	9,3		106	7,6				
10	9,2		108	8,1				
11	8,9		109	9,1				
15	6,4		113	9,8				
17	8,7		114	1,8	**outlier**			
20	9,1		116	12	**outlier**			
23	8,6		117	7,5				
24	8,0		119	8,0				
25	7,7		120	8,8				
27	8,6							
28	9,3							
31	7,8							
32	8,2							
33	11							
34	7,4							
36	8,1							
40	8,7							
43	8,3							
45	8,0							
49	7,6							
54	8,0							
56	7,9							
57	7,3							
58	6,7							
61	9,4							
63	8,9							
65	8,3							
70	7,8							
73	6,9							
75	6,5							
76	9,6							
77	6,4							
80	7,8							
81	8,8							
87	8,9							
88	5,4	**outlier**						
89	8,3							
90	6,7							
91	8,4							
92	8,4							
94	9,4							
95	8,4							
100	8,9							
102	8,1							

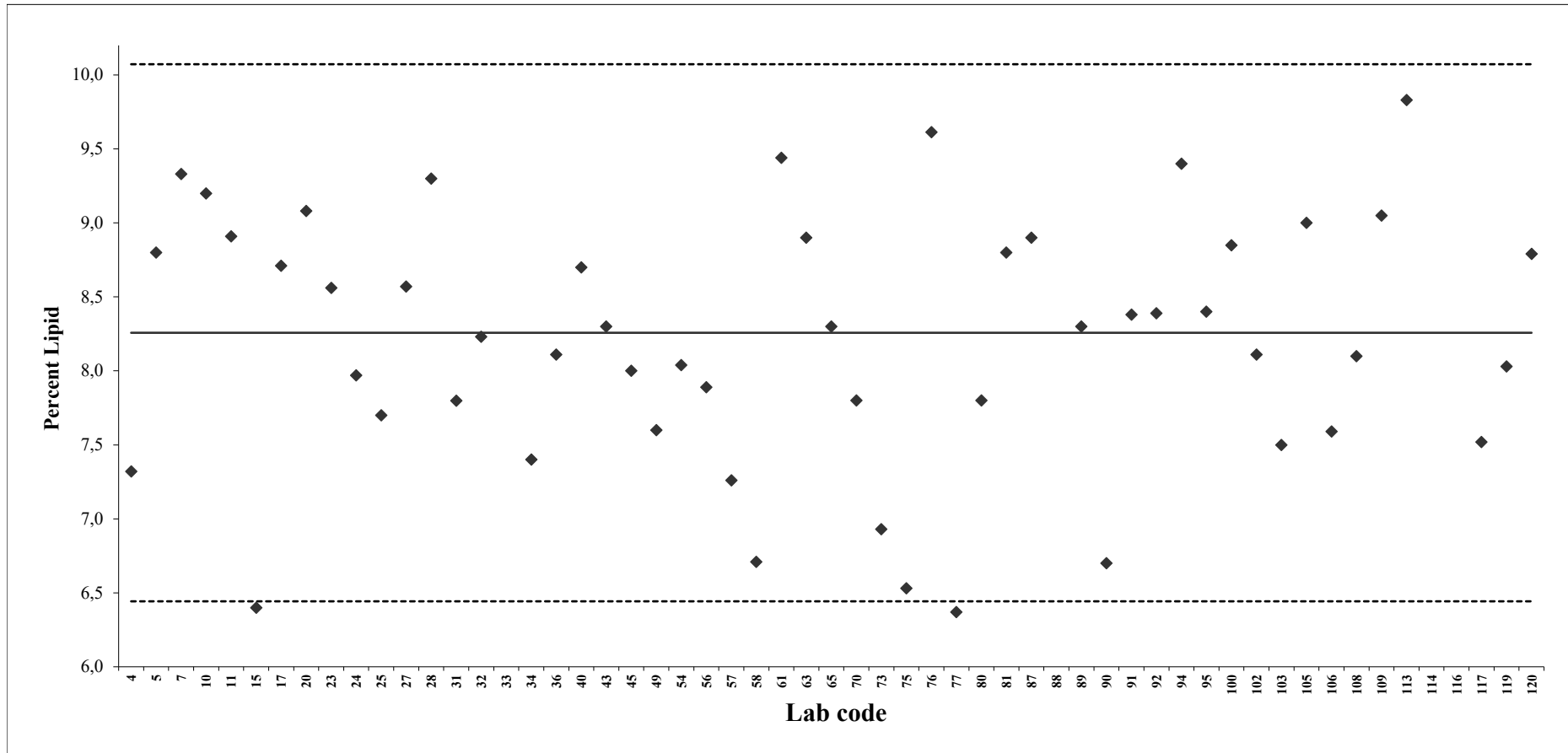| Mean	Standard deviation	Relative standard deviation	Median
8,3	0,91	11	8,3

Lipid determination; Veal
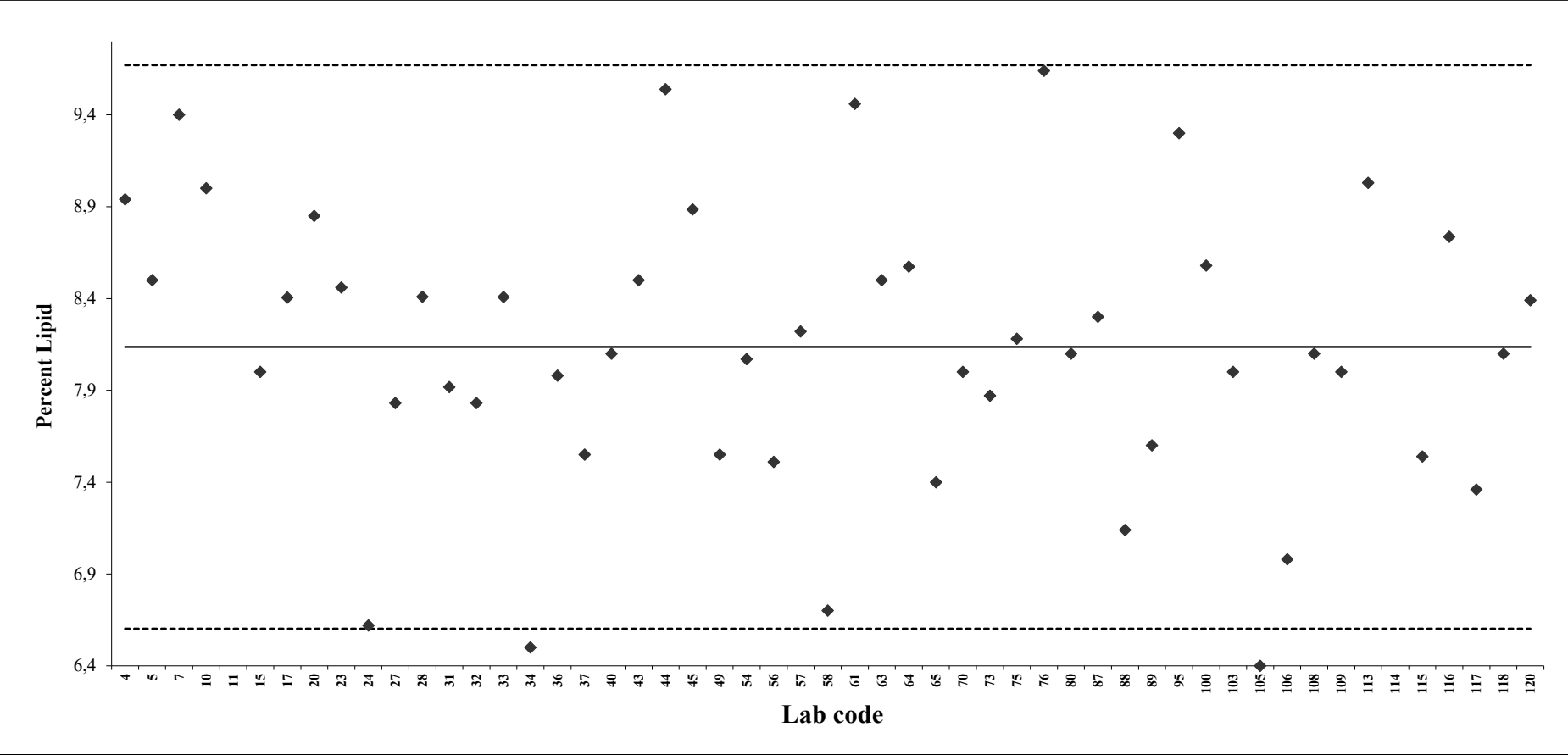
Lipid determination; Herring
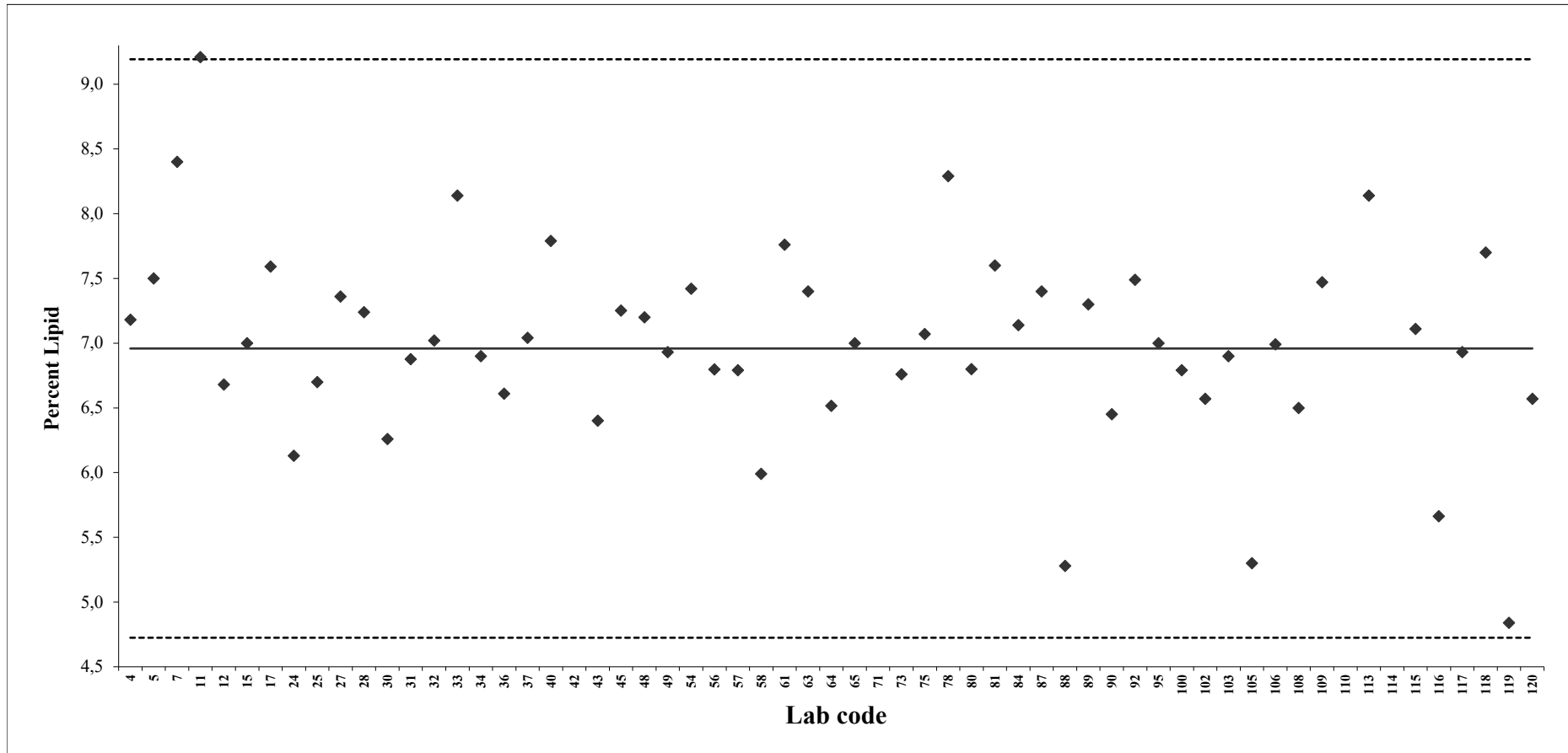
Lipid determination; Brown meat

Z-score lipid determination; Veal

Percent Lipid (y-axis)

Lab code (x-axis)
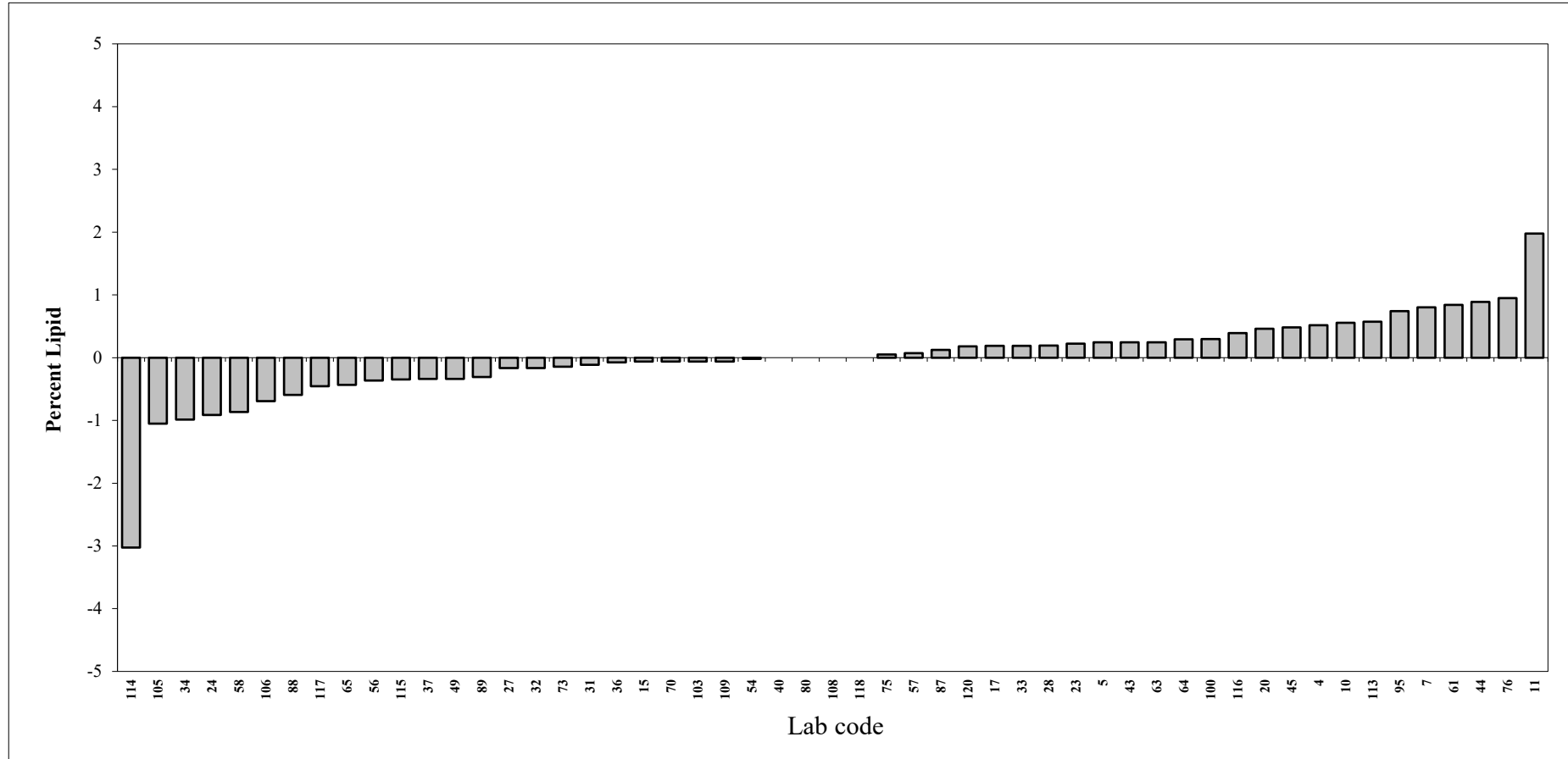
Z-score lipid determination; Herring

Z-score lipid determination; Brown meat