

**REPORT**

2024

# Interlaboratory Comparison on POPs in Food 2024

The twenty-fifth round of an international study

# **Interlaboratory Comparison on POPs in Food 2024**

The twenty-fifth round of an international study

Mahin Karimi, Inger-Lise Steffensen and Cathrine Thomsen

Published by the Norwegian Institute of Public Health  
Division of Climate and Environmental Health  
Department of Food Safety  
December 2024

**Title:**

Interlaboratory Study on POPs in Food  
The twenty-fourth round of an international study

**Authors:**

Mahin Karimi  
Inger-Lise Steffensen  
Cathrine Thomsen

**Order:**

The report may be downloaded as a pdf-file  
from the webpage: [www.fhi.no/ILC](http://www.fhi.no/ILC)

**Cover graphic design:**

Fete Typer

**Keywords (MeSH):** Interlaboratory Comparison, POPs, Dioxins, PCBs, PBDEs, PFASs

**Citation:** Karimi M, Steffensen I-L, Thomsen C. Interlaboratory Comparison on POPs in Food 2024. Oslo:  
The Norwegian Institute of Public Health

## Contents

<b>Summary</b>	<b>5</b>
<b>Introduction</b>	<b>8</b>
<b>Design and practical implementation</b>	<b>11</b>
Study design and reporting of results: PCDDs/PCDFs, non-ortho substituted PCBs, mono-ortho substituted PCBs, indicator PCBs, PBDEs and HBCDs	11
Study design and reporting of results: PFASs	11
Confidentiality	12
Collection, preparation and distribution of samples	12
Statistical analysis	12
The final report and certificate	13
Coordination	13
<b>Results</b>	<b>15</b>
Presentations in the report	15
Summary of the results	15
<i>PCDDs/PCDFs</i>	15
Analyte solution-2024	15
Mackerel-2024	15
Cream-2024	15
Egg yolk-2024	16
<i>Dioxin-like PCBs</i>	16
Analyte solution-2024	16
Mackerel-2024	16
Cream-2024	16
Egg yolk-2024	16
<i>Total TEQ</i>	16
<i>Indicator PCBs</i>	18
Analyte solution-2024	18
Mackerel-2024	18
Cream-2024	18
Egg yolk-2024	18
<i>PBDEs</i>	18
Analyte solution-2024	18
Mackerel-2024	18
Cream-2024	18
Egg yolk-2024	19
<i>HBCD</i>	19
<i>PFASs</i>	19
<i>Lipid content</i>	19
<b>Acknowledgements</b>	<b>20</b>
<b>Appendix A: Participants' affiliations and addresses</b>	
<b>Appendix B: Study announcement and instructions for participants</b>	
<b>Appendix C: WHO TEFs for human risk assessment</b>	
<b>Appendix D: Homogeneity testing</b>	
<b>Appendix E: Summary of results</b>	
Consensus of congener concentrations	
Consensus of TEQ values	
Consensus statistics	
Laboratories' reported TEQs	
Laboratories' Z-scores	

Z-score plots

**Appendix 1: Presentation of results for Analyte solutions-2024**

**Appendix 2: Presentation of results for Mackerel-2024**

**Appendix 3: Presentation of results for Cream-2024**

**Appendix 4: Presentation of results for Egg yolk-2024**

**Appendix 5: Presentation of results for PFAS Mackerel-2024**

**Appendix 6: Presentation of results for lipid determination-2024**

## Summary

The 25<sup>th</sup> round of the Interlaboratory Comparison on POPs in Food was conducted in 2024 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.

This year the fish sample for determination of poly- and perfluoroalkyl substances (PFAS) was the Mackerel sample, shared for both persistent organic pollutants (POPs) and PFAS, 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  $\alpha$ -HBCD, the 2024 round of this study was performed on unfortified homogenates of Mackerel, Cream and Egg yolk. The unfortified Mackerel homogenate was offered also 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  $\alpha$ -HBCD in standard solutions from Cambridge Isotope Laboratories, provided by NIPH. The results for these Analytes are reported in Appendix 1.

The test materials were sent to 53 laboratories worldwide in March 2024 and results were returned from 52 of these.

A draft report was made available on our webpage [www.fhi.no/ILC](http://www.fhi.no/ILC) November 5<sup>th</sup>, 2024, and the deadline for commenting on the published results was set to November 25<sup>th</sup>, 2024.

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

The results of PFOS (for all reported PFOS, sum of branched and linear PFOS, and only linear PFOS), and PFHxS, PFOA, PFNA, PFDA and PFUnDA, without distinguishing between these branched and linear PFAS, in a sample of Mackerel are also included.

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 calculations. 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 Mackerel, we adopted the same approach as we used for the indicator PCBs and PBDEs.

Toxic equivalents (TEQs) were calculated from the consensus medians of individual congeners using the toxic equivalency factors (TEFs) derived by WHO in 1997, published in 1998, and later updated in 2005, published in 2006 (see Appendix C). From 2012: WHO2005TEQs as well as WHO1998TEQs were used, as opposed to only WHO1998TEQs in the reports published before 2012. From 2024, the WHO1998TEQs were no longer calculated, only WHO2006TEQs, as well as the new TEQs from WHO in 2022, published in 2024 (WHO2024TEQs).

Z-scores for the PCDD/PCDF TEQs were calculated for each laboratory using  $\pm 20\%$  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 TEQs, 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 individual congener in all three matrices of Mackerel, Cream and Egg yolk ( $\sigma=0.2$ , 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 basis only.

The consensus values of the standard solutions were calculated as mentioned above except for the removal of all values exceeding  $\pm 50\%$  of the median prior to the final calculations 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 Mackerel was the sample in this study with the highest total TEQ (0.39 pg TE/g fresh weight, WHO<sub>2024</sub>TEFs). For this sample, Z-scores within  $\pm 1$  were obtained by 68% of the participating laboratories and Z-scores within  $\pm 2$  were achieved by 86% of the participants (Z scores within  $\pm 1$  and  $\pm 2$ , corresponds to a trueness of  $\pm 20\%$  and  $\pm 40\%$ , respectively). The Mackerel sample was followed by the sample of Cream, with a consensus total TEQ of 0.040 pg TE/g fresh weight (WHO<sub>2024</sub>TEFs). For this sample, 30% of the participants achieved Z-scores within  $\pm 1$  and 50% achieved Z-scores within  $\pm 2$ . For the sample of Egg yolk, total TEQ was 0.036 pg TE/g fresh weight (WHO<sub>2024</sub>TEFs) and Z-scores within  $\pm 1$  were obtained by 38% of the reporting participants and Z-scores within  $\pm 2$  were achieved by 55% of the participants.

The relative standard deviation (RSD) calculated for the total TEQ (fresh weight) after removal of outliers was 16% for the sample that had the highest levels of contaminants (Mackerel). For the less contaminated Cream and Egg yolk samples, the corresponding RSD values were 17% and 16%, respectively. This year the levels of contamination in the three unfortified food samples were very low, and this is reflected in the z-scores and the variability (RSD).

Across the three food samples, 37-47 laboratories reported results for the six indicator PCBs. The total consensus concentrations (median) on fresh weight basis for six indicator PCBs were 4259 pg/g (15%) in Mackerel, 182 pg/g (17%) in Cream and 764 pg/g (12%) in Egg yolk, with % of total RSDs given in parentheses.

For the three food samples, 14-20 laboratories reported concentrations for all seven of the tetra- to hepta-PBDEs and 10-16 laboratories reported concentrations for PBDE-209. The consensus concentrations of the sum of the PBDEs without PBDE-209 were on fresh weight basis 395 (13%), 11 (25%) and 22 (19%) pg/g in Mackerel, Cream and Egg yolk, respectively, with total RSDs given in parentheses. The consensus concentrations for PBDE-209 were 11 (n=16, RSD=66%), 10 (n=10, RSD=66%) and 69 (n=14, RSD=44%) pg/g fresh weight in Mackerel, Cream and Egg yolk, respectively.

The consensus concentrations calculated for HBCDs are only indicative, as only a few laboratories reported results across the three food samples (n=2-4, including  $\alpha$ -,  $\beta$ - and  $\gamma$ -HBCD).

Among the laboratories, 6-15 reported results for the different PFASs in the sample of Mackerel. The consensus concentrations for all reported PFOS, sum (i.e. branched and linear PFOS) and only linear PFOS were 261, 272 and 252 pg/g fresh weight, respectively, for which 67%, 78% and 67% of the laboratories obtained a Z-score within  $\pm 2$ . For PFUnDA (consensus concentration 98 pg/g fresh weight), 64% of the laboratories obtained z-scores  $\pm 2$ , and for PFDA (consensus concentration 30 pg/g fresh weight), 43% of the participants obtained z-scores  $\pm 2$ . For PFNA (consensus concentration 20 pg/g fresh weight), 40% obtained z-scores  $\pm 2$ . The consensus concentrations for PFHxS and PFOA were 17 and 11 pg/g fresh weight, respectively, for which 27% and 20% of the laboratories had z-scores  $\pm 2$ . All these consensus concentrations, except for all reported PFOS and PFUnDA are only indicative due to few reported results (many NDs), i.e.  $\leq 7$ .

## Introduction

Maximum residue limits and official food control systems are established in many countries for the monitoring of 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. New tolerable daily intakes (TDIs) for dioxins were introduced by EFSA in 2018 and for PFASs (more specifically; PFOS, PFOA, PFHxS and PFNA), tolerable weekly intakes (TWIs) were established in 2020. 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.

Additionally, it is usually required by the authorities that laboratories performing such measurements are accredited according to ISO standards and/or prove their competence by successful participation in interlaboratory studies.

This is the 25<sup>th</sup> round of the world-wide interlaboratory comparison study on dioxin-like compounds, eight PBDEs, six indicator PCBs and HBCD in food, organized by the Department of Food Safety at the Norwegian Institute of Public Health (NIPH), Oslo, Norway. From 2019, a food sample designated for the determination of six selected PFASs was also added. This year, the same sample (Mackerel) was offered for analysis of both POPs and PFAS.

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

The exercise took place from March 2024, when the samples were shipped to the laboratories for analysis, until the reporting deadline 30<sup>th</sup> July, 2024, 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>) on November 5<sup>th</sup>, 2024.

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

**Table 1. Participants that reported results in the 25<sup>th</sup> round of the Interlaboratory Comparison on POPs in Food 2024**

<p><b>Additives, Contaminants and Composition Section</b> Hong Kong, P.R. China</p>	<p><b>ALS Czech Republic, s.r.o.</b> Pardubice, Czech Republic</p>
<p><b>Arkansas Human and Animal Food Laboratory</b> Jefferson, AR, USA</p>	<p><b>AsureQuality Ltd-Wellington Laboratory</b> Wellington, New Zealand</p>
<p><b>Australian Ultra Trace Laboratory</b> Sydney, Australia</p>	<p><b>BC Food Laboratory, Regulatory Operations and Enforcement Branch, Health Canada</b> Burnaby, Canada</p>
<p><b>Biodetection Systems</b> Amsterdam, The Netherlands</p>	<p><b>Bureau Veritas Canada (2019) Inc.</b> Mississauga, Canada</p>
<p><b>Canadian Food Inspection Agency (CFIA)</b> Calgary, Alberta, Canada</p>	<p><b>CARSO-LSEHL</b> Vénissieux, France</p>
<p><b>Central Laboratory of Residue Analysis of Pesticides and Heavy Metals in Foods</b> Giza, Arabic Republic of Egypt (ARE)</p>	<p><b>Chemisches und Veterinäruntersuchungsamt (CVUA) Freiburg</b> Freiburg, Germany</p>
<p><b>China National Center for Food Safety Risk Assessment</b> Beijing, P.R. China</p>	<p><b>CSIR-National Institute for Interdisciplinary Science &amp; Technology (CSIR-NIIST)</b> Thiruvananthapuram, India</p>
<p><b>CVUA MEL</b> Münster; Germany</p>	<p><b>Danish Veterinary and Food Administration</b> Ringsted, Denmark</p>
<p><b>Eurofins Lab Zeeuws Vlaanderen (CNL027)</b> Graauw, The Netherlands</p>	<p><b>Eurofins GfA Lab Service GmbH</b> Hamburg, Germany</p>
<p><b>Havforskningsinstituttet (Institute of Marine Research)</b> Bergen, Norway</p>	<p><b>Hubei Provincial Center for Disease Control and Prevention</b> Wuhan, P.R. China</p>
<p><b>Japan Food Research Laboratories</b> Tokyo, Japan</p>	<p><b>Laboratoire de l'Environnement et de l'Alimentation de la Vendée</b> Roche sur Yon, France</p>
<p><b>Laboratory of SGS Bulgaria</b> Varna, Bulgaria</p>	<p><b>Landesamt für Umweltschutz Sachsen-Anhalt</b> Halle/Saale, Germany</p>
<p><b>Landesuntersuchungsamt</b> Speyer, Germany</p>	<p><b>Marchwood Scientific Services</b> Southampton, United Kingdom</p>

<b>MicroPolluants Technologie SAS</b> Saint Julien les Metz, France	<b>National Cheng Kung University</b> Tainan, Taiwan (R.O.C)
<b>Ningbo Customs District Technology Center</b> Shanghai, P.R. China	<b>NofaLab B.V.</b> Schiedam, The Netherlands
<b>Oekometric</b> Bayreuth, Germany	<b>Pacific Rim Laboratories Inc.</b> Surrey, Canada
<b>POP Lab, Shenzhen Center for Disease Control &amp; Prevention, Guangdong, PRC</b> Shanghai, P.R. China	<b>Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences</b> Beijing, P.R. China
<b>SGS Analytics Germany GmbH Jena</b> Jena, Germany	<b>SGS Institut Fresenius GmbH, Hamburg</b> Bayreuth, Germany
<b>SGS Institut Fresenius GmbH, Berlin</b> Berlin, Germany	<b>SGS Taiwan Ltd.</b> New Taipei City, Taiwan (R.O.C.)
<b>Shanghai Academy of Agricultural Sciences (Shanghai Co-Elite Agro-food Testing Technical Service Co., Ltd.)</b> Shanghai, P.R. China	<b>Shanghai Municipal Center for Disease Control and Prevention</b> Shanghai, P.R. China
<b>Shimadzu Techno-Research, Inc.</b> Kyoto, Japan	<b>SINTEF Industri</b> Trondheim, Norway
<b>Stiftelsen NILU</b> Kjeller, Norway	<b>Super Micro Mass Research &amp; Technology Center, Cheng Shiu University</b> Kaohsiung City, Taiwan (R.O.C.)
<b>Swedish Food Agency</b> Uppsala, Sweden	<b>T.L.R. International Laboratories</b> Ridderkerk, The Netherlands
<b>Umeå University, Department of Chemistry</b> Umeå, Sweden	<b>Wellington Laboratories Inc.</b> Guelph, Canada
<b>Zhejiang Provincial Center for Disease Control and Prevention</b> Shanghai, P.R. China	<b>Wessling GmbH</b> Altenberge, Germany
<b>LMS Agrarberatung GmbH LUFA Rostock</b> Rostock, Germany	<b>TERANA</b> Valence, France

## Design and practical implementation

### Study design and reporting of results: PCDDs/PCDFs, non-ortho substituted 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 ( $\alpha$ -,  $\beta$ -,  $\gamma$ -HBCD). The six PCB congeners belong together with the mono-ortho PCB #118 to the selection of PCBs commonly referred to as ICES-7 (ICES-7: Report of the ICES Advisory Committee, 2010; Book 7).

The analysis should be performed using the laboratories' own methods for sample preparation and instrumental analysis, their own 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 Mackerel, Cream and Egg yolk.

The laboratories were to report the concentration of each detected congener (e.g.  $S/N \geq 3$ ) 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 analysed, 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/ $\mu$ l for tetra:penta-hexa-hepta:octa chlorinated dibenzo-p-dioxins/-dibenzo furans, respectively)
- 2) Four non-ortho PCBs (10 pg/ $\mu$ l)
- 3) Eight mono-ortho PCBs (100 pg/ $\mu$ l)
- 4) Eight PBDEs (100 pg/ $\mu$ l)
- 5) Six indicator PCBs (100 pg/ $\mu$ l)
- 6)  $\alpha$ -HBCD (500 pg/ $\mu$ l)

The test materials consisted of homogenates of Mackerel, Cream and Egg yolk. The laboratories could choose to analyse one, two or all three food samples.

### Study design and reporting of results: PFASs

For the 25<sup>th</sup> round of the Norwegian POPs in Food study, the sample of Mackerel was offered for analysis of PFAS (as well as for POPs), for the determination of the following PFASs:

PFOS, PFHxS, PFOA, PFNA, PFDA and PFUnDA. As for the other matrices, the Mackerel 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.  $S/N \geq 3$ ) in the Mackerel 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](http://www.fhi.no/ILC) on November 5<sup>th</sup>, 2024.

## Collection, preparation and distribution of samples

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

- Mackerel (~90 g)
- Cream (~50 g)
- Egg yolk (~70 g)

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

The Mackerel, Cream and Egg yolk samples were bought from local stores.

The Mackerel arrived as frozen fileted fish. It was defrosted, pooled and grinded, and finally homogenized thoroughly.

Two brands of Cream were combined and kept on low heat while mixed with a magnet stirrer. After having reached 20°C after two hours, it was considered homogenous.

The Egg yolk of two batches, one frozen since 2020 and one newly bought, were mixed thoroughly.

Sub-samples of at least 90 g of Mackerel (Mackerel-2024), 50 g of Cream (Cream-2024) and 70 g of Egg yolk (Egg yolk-2024) 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

As for previous rounds, this is the 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 which exceeded twice the median of all values and thus removed from the data set.

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

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

TEQs were calculated from the consensus medians for PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs, using the toxic equivalency factors derived by WHO in 2005 and 2022, and published in 2006 and 2024. 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<sub>2024</sub>TEFs), the sum of six indicator PCBs, the sum of eight PBDEs, total HBCD and for each HBCD congener were calculated for each laboratory according to the following equation:

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

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

## The final report and certificate

The draft of the final report was prepared by the coordinators and published electronically in December 2024.

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

A certificate of participation, stating the participant's laboratory code, will be sent to each participating laboratory that has contributed to the results in February 2025.

## Coordination

The study was initiated and carried out by the Department of Food Safety, Norwegian Institute of Public Health, Oslo, Norway. Members of the coordination committee were:

Mahin Karimi, Senior Engineer  
[mahin.karimi@fhi.no](mailto:mahin.karimi@fhi.no)

Inger-Lise Steffensen, Senior Scientist  
[inger-lise.karin.steffensen@fhi.no](mailto:inger-lise.karin.steffensen@fhi.no)

Cathrine Thomsen, Department Director  
[cathrine.thomsen@fhi.no](mailto:cathrine.thomsen@fhi.no)

## Results

### Presentations in the report

Fifty-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 performance are based on several factors, it is recommended that each laboratory carefully evaluate the factors that, favourably or unfavourably, 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, HBCD and PFAS 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  $\pm 20\%$  from the consensus TEQ<sub>2024</sub>-values.

Individual results reported by the laboratories for each congener are given for Mackerel, Cream and Egg yolk in Appendices 2, 3 and 4, respectively. The results for PFAS in the sample of Mackerel are presented in Appendix 5 and results of the lipid determinations are presented in Appendix 6.

### Summary of the results

#### *PCDDs/PCDFs*

##### **Analyte solution-2024**

Concentrations of PCDDs/PCDFs were reported by 42 laboratories. The mean RSD for the 17 congeners was 7.1% ranging from 6.1% for 2,3,4,7,8-PeCDF to 11% for 1,2,3,4,6,7,8,9-OCDD. The calculation of Z-scores for the TEQs (target 10.1 pg TEQ/ $\mu$ L based on TEF<sub>2024</sub>-values) of the PCDD/PCDF standard solution showed that 100% of the laboratories had z-scores within the range of  $\pm 2$  of the consensus value. This clearly demonstrates that the calibration solutions for PCDDs/PCDFs used by the laboratories generally are of high quality.

##### **Mackerel-2024**

For the sample of Mackerel, PCDD/PCDF results from 49-50 laboratories were received. From these results, the calculated consensus TEQ (PCDD/PCDF TEQ based on WHO<sub>2024</sub>-TEFs) was 0.13 pg TE/g fresh weight and 0.81 pg TE/g lipid weight.

The mean RSD was 47%, ranging from 24% for 2,3,7,8-TCDF to 70% for 1,2,3,4,6,7,8-HpCDF. Z-scores for the TEQs within  $\pm 1$  were obtained by 48% of the laboratories and 70% of the laboratories had Z-scores within  $\pm 2$  (fresh weight basis).

##### **Cream-2024**

PCDD/PCDF concentrations in the Cream sample were reported by 38-39 laboratories. The consensus TEQ was 0.027 pg TEQ/g fresh weight and 0.074 pg TEQ/g lipid weight (PCDD/PCDF TEQ based on WHO<sub>2024</sub>-TEFs). The mean RSD was 55% ranging from 36-77%

(for 1,2,3,4,6,7,8-HpCDD and 1,2,3,4,6,7,8-HpCDF, respectively). Z-scores were within  $\pm 1$  for 23% of the laboratories and within  $\pm 2$  for 49% of the laboratories (fresh weight basis).

### **Egg yolk-2024**

PCDD/PCDF concentrations in the sample of Egg yolk were determined by 38-40 laboratories. The consensus TEQ for PCDD/PCDF based on WHO<sub>2024</sub>TEFs was 0.023 pg TEQ/g fresh weight and 0.10 pg TEQ/g lipid weight (PCDD/PCDF TEQ based on WHO<sub>2024</sub>TEFs). The mean RSD was 49% ranging from 35% for 1,2,3,4,7,8,9-HpCDF and 1,2,3,4,6,7,8,9-OCDF to 62% (1,2,3,4,6,7,8,9-OCDD). Z-scores for PCDD/PCDF TEQ within  $\pm 1$  were obtained by 33% of the laboratories and 50% had Z-scores within  $\pm 2$  (fresh weight basis).

### *Dioxin-like PCBs*

#### **Analyte solution-2024**

The 12 dioxin-like PCBs in the analyte solution were analysed and reported by 41-42 laboratories. The RSDs for the different congeners were ranging from 5.7% for PCB-77 to 8.7% for PCB-156, with a mean of 7.6%.

#### **Mackerel-2024**

Dioxin-like PCB concentrations in the sample of Mackerel were reported from 49-50 laboratories. The concentrations of the 12 congeners varied between 0.62 pg/g fresh weight (PCB-169) and 581 pg/g fresh weight (PCB-118). The mean RSD for concentrations of individual dioxin-like PCB congeners was 24%, ranging from 14% for PCB-189 to 31% for PCB-81.

The dioxin-like PCBs contributed 67% to the total TEQ (WHO TEF<sub>2024</sub>) in the sample with PCB-126 as the main contributor (83%).

#### **Cream-2024**

Of the participating laboratories, 39-40 measured and reported dioxin-like PCB concentrations in the Cream sample. The concentrations ranged from 0.041 pg/g fresh weight for PCB-81 to 31 pg/g fresh weight for PCB-118. The mean RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 35%, ranging from 23% for PCB-156 to 53% for PCB-77.

The dioxin-like PCBs contribute to about 33% of the total TEQ in the sample with PCB-126 as the main contributor (85%).

### **Egg yolk-2024**

Dioxin-like PCBs in Egg yolk were reported by 39-40 laboratories. Levels were ranging from 0.040 pg/g fresh weight for PCB-169 to 68 pg/g fresh weight for PCB-118. The mean RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 28%, ranging from 16% for PCB-118 to 47% for PCB-81.

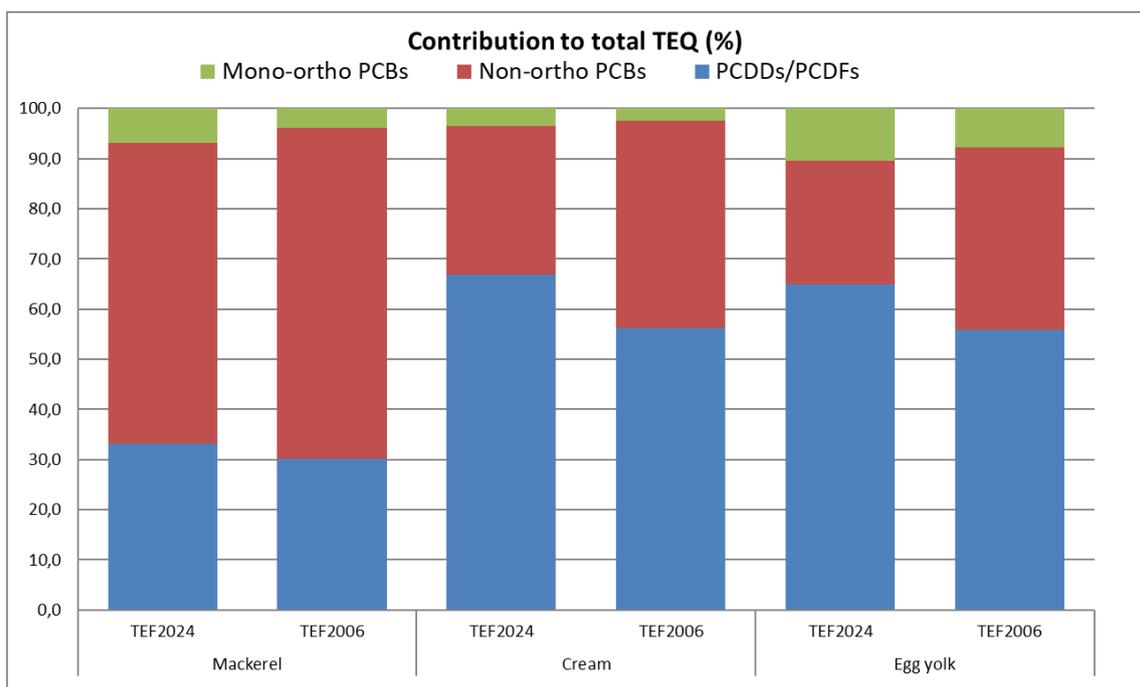
The contribution of the dioxin-like PCBs to the total TEQ was about 36% with PCB-126 as the main contributor (62% of total TEQ).

### *Total TEQ*

The total TEQ for the sample of Mackerel was 0.39 pg TEQ/g fresh weight and 2.4 pg TEQ/g lipid weight (WHO TEF<sub>2024</sub>). The total TEQ of the Cream sample was 0.040 pg TEQ/g fresh weight and 0.11 pg TEQ/g lipid weight, and the Egg yolk contained 0.036 pg TEQ/g fresh weight and 0.15 pg TEQ/g lipid weight.

In Figure 1, the percentage contribution to the TEQ values for the three groups of compounds is depicted based on WHO TEF<sub>2024</sub> and WHO TEF<sub>2006</sub>, respectively. For the selection of food items included in this study, the dioxin-like PCBs contributed from 33% to 67% to the total TEQ (using WHO TEF<sub>2024</sub>), 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<sub>2024</sub> TEFs and WHO<sub>2006</sub> TEFs, in the three food samples**



## *Indicator PCBs*

### **Analyte solution-2024**

In all, 39 laboratories reported indicator PCBs in the analyte solution. The mean RSD was 7.9%, ranging from 6.5% for PCB101 to 9.6% for PCB28 and PCB180.

### **Mackerel-2024**

For the sample of Mackerel, results for indicator PCBs were received from 47 laboratories. The consensus concentrations varied between 131 pg/g fresh weight (PCB-28) and 1655 pg/g fresh weight (PCB-153). The consensus median for the sum of indicator PCBs was 4259 pg/g fresh weight. The RSDs ranged from 22% to 30% for PCB-52 and PCB-138, respectively, with a mean of 26% for all indicator PCBs.

### **Cream-2024**

For the sample of Cream, 37 laboratories reported results for indicator PCBs. The consensus concentrations ranged from 11 pg/g fresh weight (PCB-28) to 67 pg/g fresh weight (PCB-153) with a consensus median for the sum of indicator PCBs of 182 pg/g fresh weight. The mean RSD was 42%, ranging from 26% for PCB-180 to 70% for PCB-28.

### **Egg yolk-2024**

For the sample of Egg yolk, results were obtained from 39 laboratories for indicator PCBs. The consensus concentrations of indicator PCBs in Egg yolk ranged from 17 pg/g fresh weight (PCB-52) to 294 pg/g (PCB-153) and the consensus median for the sum was 764 pg/g fresh weight. The mean RSD was 29%, ranging from 20% to 42% for PCB-180 and PCB-52, respectively.

## *PBDEs*

### **Analyte solution-2024**

The tri- to hepta-PBDE standard solution was analysed by 19 laboratories and 16 laboratories reported values for PBDE-209. The RSDs were between 10% for PBDE-209 and 14% for PBDE-183, with a mean of 12% including PBDE-209.

### **Mackerel-2024**

The PBDE concentrations in Mackerel were reported by 20 laboratories, except for PBDE-209, for which 16 results were received. The consensus concentrations were in the range of 1.4 pg/g fresh weight for PBDE-183 to 191 pg/g fresh weight for PBDE-47. The consensus concentration for PBDE-209 was 11 pg/g fresh weight. The sum of tri- to hepta-PBDEs was 395 pg/g fresh weight. The range of RSDs on fresh weight basis varied from 23% for PBDE-47 to 66% for PBDE-209, with a mean of 33 including PBDE-209.

### **Cream-2024**

Of the laboratories, 14 reported results for tri- to hepta-PBDEs in Cream and 10 reported results for PBDE-209. The consensus concentrations varied between 0.2 pg/g fresh weight (PBDE-28) and 5.2 pg/g fresh weight (PBDE-47). The concentration for PBDE-209 was 9.6 pg/g fresh weight. The sum of tri- to hepta-PBDEs was 11 pg/g fresh weight. The RSD calculated from the concentrations on fresh weight ranged from 16% for PBDE-153 to 68% for PBDE-128, with a mean of 42% for PBDEs including PBDE-209.

### **Egg yolk-2024**

Among the laboratories, 17 reported results for tri- to hepta-PBDEs in Egg yolk and 14 reported results for PBDE-209. The concentrations varied between 0.13 pg/g fresh weight (PBDE-28) and 8.8 pg/g (PBDE-99). The concentration for PBDE-209 was 69 pg/g. The sum of tri- to hepta-PBDEs was 22 pg/g fresh weight. The RSDs for the individual congeners were ranging from 30% for PBDE-47 to 44% for PBDE-209, with a mean of 36% including PBDE-209.

### *HBCD*

Also, in this round of the study, the isomers  $\alpha$ -,  $\beta$ - and  $\gamma$ -HBCD as well as total HBCD could be determined and reported. The consensus concentrations calculated for HBCDs are only indicative, since very few laboratories reported results across the three food samples (n=2-4).

### *PFASs*

A sample of Mackerel was offered to the participants for the determination of PFASs. For the reported PFAS analyses, we requested additional information from laboratories regarding whether the reported concentrations were for linear PFASs, branched PFASs or the combined total of both. Thanks to the assistance of the participants, this year we were able to calculate results specifically for three sets of PFOS data (All reported, Sum or Linear PFOS). No laboratory reported only branched PFOS. For the other PFAS compounds, the results are presented as provided by the participating laboratories, without distinguishing between the branched and linear PFAS.

Results on various PFASs were reported by 6-15 laboratories. The consensus concentration of the sum of individual PFASs groups was 448 pg/g fresh weight, with PFOS as the main contributor (272 pg/g fresh weight for PFOS – sum of branched and linear, n=9). The concentrations of PFUnDA, PFDA and PFNA in the sample were 98, 30 and 20 pg/g fresh weight, respectively. The consensus values for PFHxS and PFOA were 17 and 11 pg/g fresh weight, respectively. All values, except for PFOS – All reported and PFUnDA, are only indicative due to many reported non-detects.

The RSD values for the individual PFASs ranged from 12% for PFOS – Sum (branched and linear PFOS) to 107% for PFOA, with a mean RSD of 51% for all PFASs (all except PFOS without distinguishing between the branched and linear PFAS).

### *Lipid content*

The mean lipid % and % RSDs (in parentheses) for the lipid contents of the food samples were calculated to be 16% (8.7%) for the sample of Mackerel, 37% (11%) for the Cream sample and 24% (10%) for the sample of Egg yolk.

## 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 Cambridge Isotope Laboratories, Inc. for providing the standard solutions for this interlaboratory study.

## **Appendix A:**

Participant's affiliations  
and addresses



## Affiliations and addresses of participants

<p style="text-align: center;"><b>Additives, Contaminants and Composition Section</b></p> <p style="text-align: center;">Dr. C. C. Cheng Hong Kong P.R. China cccheng@govtlab.gov.hk</p>	<p style="text-align: center;"><b>ALS Czech Republic, s.r.o.</b></p> <p style="text-align: center;">Miloslav Sebránek Pardubice, CZ-530 02 Czech Republic miloslav.sebranek@alsglobal.com</p>
<p style="text-align: center;"><b>Arkansas Human and Animal Food Laboratory</b></p> <p style="text-align: center;">J. Marc Gentry Jefferson, AR 72079 USA james.gentry@fda.hhs.gov</p>	<p style="text-align: center;"><b>AsureQuality Ltd-Wellington Laboratory</b></p> <p style="text-align: center;">Mekaela Khan Wellington 5040 New Zealand Wgtn-Quality@asurequality.com</p>
<p style="text-align: center;"><b>Australian Ultra Trace Laboratory</b></p> <p style="text-align: center;">Dr. Alan Yates Sydney, NSW 2113 Australia dioxins@measurement.gov.au</p>	<p style="text-align: center;"><b>BC Food Laboratory, Regulatory Operations and Enforcement Branch, Health Canada</b></p> <p style="text-align: center;">Arman Alimkulov, Phillip Wong, Daniel Sit Burnaby, V5G 4P2 Canada arman.alimkulov@hc-sc.gc.ca</p>
<p style="text-align: center;"><b>Biodetection Systems</b></p> <p style="text-align: center;">Kees Swart 1098 XH Amsterdam The Netherlands kees.swart@bds.nl</p>	<p style="text-align: center;"><b>BUREAU VERITAS CANADA (2019) INC.</b></p> <p style="text-align: center;">Salima Haniff Mississauga, ON L5N 2L8 Canada salima.haniff@bureauveritas.com</p>
<p style="text-align: center;"><b>Canadian Food Inspection Agency (CFIA)</b></p> <p style="text-align: center;">Nishma Karim Calgary, Alberta T2L 2L1 Canada nishma.karim@inspection.gc.ca</p>	<p style="text-align: center;"><b>CARSO-LSEHL</b></p> <p style="text-align: center;">Stéphanie Defour 69200 Vénissieux France sdefour@groupecarso.com</p>
<p style="text-align: center;"><b>Central Laboratory of Residue Analysis of Pesticides and Heavy Metals in Foods</b></p> <p style="text-align: center;">Dr. Emad Ramadan Atala Giza, 12311 Arabic Republic of Egypt (ARE) emadata@yahoo.com</p>	<p style="text-align: center;"><b>Chemisches und Veterinäruntersuchungsamt (CVUA) Freiburg</b></p> <p style="text-align: center;">Dr. Marco Mueller D-79114 Freiburg Germany marco.mueller@cvafr.bwl.de</p>

<p><b>China National Center for Food Safety Risk Assessment</b></p> <p>Lei Zhang Beijing 100080 P.R. China Zhanglei1@cfsa.net.cn (Lei Zhang)</p>	<p><b>CSIR-National Institute for Interdisciplinary Science &amp; Technology (CSIR-NIIST)</b></p> <p>Dr. K. P. Prathish Thiruvananthapuram, 695 019 India prathishkp@niist.res.in</p>
<p><b>CVUA MEL</b></p> <p>Dr. Thorsten Bernsmann Münster, 48147 Germany thorsten.bernsmann@cvua-mel.de</p>	<p><b>Danish Veterinary and Food Administration</b></p> <p>Søren Sørensen 4100 Ringsted Denmark ssn@fvst.dk</p>
<p><b>Eurofins Lab Zeeuws Vlaanderen (CNL027)</b></p> <p>S. van Goethem 4569 TC Graauw The Netherlands saskia.vangoethem@ftbnl.eurofins.com</p>	<p><b>Eurofins GfA Lab Service GmbH</b></p> <p>Steffi Rolle 21079 Hamburg Germany Steffi.Rolle@ftdach.eurofins.com</p>
<p><b>Havforskningsinstituttet (Institute of Marine Research)</b></p> <p>Britt Elin Øye and Bergitte Reiersen 5005 Bergen Norway bro@hi.no and bre@hi.no</p>	<p><b>Hubei Provincial Center for Disease Control and Prevention</b></p> <p>Xiaofang Liu Wuhan 430079 P.R. China 13971689391@163.com</p>
<p><b>Japan Food Research Laboratories</b></p> <p>Shuichi Inohana and Nakamura Ayumu Tokyo 206-0025 Japan inohanas@jfri.or.jp and nakamura@jfri.or.jp</p>	<p><b>Laboratoire de l'Environnement et de l'Alimentation de la Vendée</b></p> <p>Alexia Pajot 85000 La Roche sur Yon France alexia.pajot@vendee.fr</p>
<p><b>Laboratory of SGS Bulgaria</b></p> <p>Veselka Pashova Varna 9003 Bulgaria veselka.pashova@sgs.com</p>	<p><b>Landesamt für Umweltschutz Sachsen-Anhalt</b></p> <p>Dr. Melanie Kampe 06114 Halle/Saale Germany Melanie.Kampe@lau.mwu.sachsen-anhalt.de</p>

<p align="center"><b>Landesuntersuchungsamt</b></p> <p>Hildegard Gerstner and Stefanie Schmitt 67346 Speyer Germany poststelle.ilcsp@lua.rlp.de</p>	<p align="center"><b>Marchwood Scientific Services</b></p> <p>Giuseppe Reitano Southampton, SO15 0HW United Kingdom Giuseppe.Reitano@Marchwood-Scientific.co.uk</p>
<p align="center"><b>MicroPolluants Technologie SAS</b></p> <p>Karim Guerras and Cedric Dechoux F 57070 Saint Julien les Metz France qualite@mp-tech.net</p>	<p align="center"><b>National Cheng Kung University</b></p> <p>Dr. Ching-Chang Lee, Wei-Hsiang Chang and I-Chia Chen 704 Taiwan (R.O.C) cclee@ncku.edu.tw</p>
<p align="center"><b>Ningbo Customs District Technology Center</b></p> <p>Yingying Zhong Shanghai 201901 P.R. China wangyuan8912854@126.com</p>	<p align="center"><b>NofaLab B.V.</b></p> <p>Sonja Renaud 3115 JG Schiedam The Netherlands qesh@nofagroup.nl</p>
<p align="center"><b>Oekometric</b></p> <p>Horst Rottler 95448 Bayreuth Germany rottler@oekometric.de</p>	<p align="center"><b>Pacific Rim Laboratories Inc.</b></p> <p>David Hope Surrey, BC V3S 8P8 Canada dave@pacificrimlabs.com</p>
<p align="center"><b>POP Lab, Shenzhen Center for Disease Control &amp; Prevention, Guangdong, PRC</b></p> <p>Jianqing Zhang and Yousheng Jiang Shanghai 201901 P.R. China 969676617@qq.com</p>	<p align="center"><b>Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences</b></p> <p>Yingming Li Beijing 100085 P.R. China ymli@rcees.ac.cn</p>
<p align="center"><b>SGS Analytics Germany GmbH Jena</b></p> <p>Bianca Braha D 07743 Jena Germany de.hn.jen.qm@sgs.com</p>	<p align="center"><b>SGS Institut Fresenius GmbH, Hamburg</b></p> <p>Robin Heimes D 95448 Bayreuth Germany robin.heimes@sgs.com</p>

<p><b>SGS Institut Fresenius GmbH, Berlin</b></p> <p>Dr. Niels Münster D 10589 Berlin Germany niels.muenster@sgs.com</p>	<p><b>SGS Taiwan Ltd.</b></p> <p>Hunting Chen New Taipei City 24803 Taiwan (R.O.C.) hunting.chen@sgs.com</p>
<p><b>Shanghai Academy of Agricultural Sciences (Shanghai Co-Elite Agro-food Testing Technical Service Co., Ltd.)</b></p> <p>Qinxiongrao Rao Shanghai 201901 P.R. China Qinxiongrao@163.com</p>	<p><b>Shanghai Municipal Center for Disease Control and Prevention</b></p> <p>Yuanjie Lin Shanghai 201901 P.R. China jasonlin3000@sina.com</p>
<p><b>Shimadzu Techno-Research, Inc.</b></p> <p>Motoi Shibayama Kyoto 604-8436 Japan m_shibayama00@shimadzu-techno.co.jp</p>	<p><b>SINTEF Industri</b></p> <p>Trude Sophie Guldberg 7034 Trondheim Norway trude.guldberg@sintef.no</p>
<p><b>Stiftelsen NILU</b></p> <p>Stine Marie Bjørneby 2007 Kjeller Norway smbj@nilu.no</p>	<p><b>Super Micro Mass Research &amp; Technology Center, Cheng Shiu University</b></p> <p>Huang Ming Feng Niaosong District, Kaohsiung City 833 Taiwan (R.O.C.) k6208@gcloud.csu.edu.tw</p>
<p><b>Swedish Food Agency</b></p> <p>Matilda Näslund SE-752 37 Uppsala Sweden matilda.naslund@slv.se</p>	<p><b>T.L.R. International Laboratories</b></p> <p>Gerard Clavan Ridderkerk 2988 DB The Netherlands QC@tlr.nl</p>
<p><b>Umeå University, Department of Chemistry</b></p> <p>Peter Haglund Umeå S-901 87 Sweden peter.haglund@umu.se</p>	<p><b>Wellington Laboratories Inc.</b></p> <p>Dave Potter Guelph, Ontario N1G 3M5 Canada dpotter@well-labs.com</p>

<p><b>Zhejiang Provincial Center for Disease Control and Prevention</b></p> <p>Zheng YiBin Shanghai 201901 P.R. China ybzheng@cdc.zj.cn</p>	<p><b>Wessling GmbH</b></p> <p>Lars Richter Altenberge 48341 Germany lars.richter@wessling.de</p>
<p><b>LMS Agrarberatung GmbH LUFA Rostock</b></p> <p>Susanne Koth 18059 Rostock Meckelnburg-Vorpommern Germany skoth@lms-lufa.de</p>	<p><b>TERANA</b></p> <p>Benoit Planel and Anne-Gaelle Valade 26000 Valence France benoit.planel@labo-terana.fr</p>



## **Appendix B:**

Study announcement and  
instructions for participants



## Announcement for Interlaboratory Comparison on POPs in Food 2024

---

### Introduction

We hereby announce the 25<sup>th</sup> 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 Food Safety at the Norwegian Institute of Public Health, Oslo, Norway. The study is scheduled to take place from March to June 2024.

A draft report will be available by October 2024, and the final report will be available to the participants by December 2024. 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, HBCDs and PFAS in regular food items known to contribute to the intake in the general population. Further, the world-wide readiness and capacity in analysing halogenated persistent organic pollutants in food will be demonstrated. The study also serves as a tool of quality assurance for the participating laboratories.

### Participants

We encourage all laboratories 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, PCB-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: PCB-28, 52, 101, 138, 153 and 180 and PBDE-28, 47, 99, 100, 153, 154, 183 and 209.

The concentration of  $\alpha$ -HBCD,  $\beta$ -HBCD and  $\gamma$ -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 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, except if only reporting PFAS.

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

### **Test material**

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

- Mackerel (labelled “MACKEREL 2024”) ~90 g (to be used for PFAS analysis also).
- Cream (labelled “CREAM 2024”) ~50 g
- Egg yolk (labelled “EGG YOLK 2024”) ~70 g

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

### **Please note:**

**In order to avoid delay or retention of the samples at customs, please inform us if there are import restrictions in your country for any of the samples. If the samples are retained in customs and a second shipment is required, please note that the associated costs for the second shipment will be the responsibility of the participating laboratory.**

### **Instructions for analysis and reporting**

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

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

### **Time schedule**

Announcement	<b>February 2024</b>
Return of registration form	<b>February 20<sup>th</sup>, 2024</b>
Shipment of test material	<b>From February to March, 2024</b>
Confirmation of receipt of test material by participant	<b>Within 7 days after receipt</b>
Reporting of test results	<b>June 30<sup>th</sup>, 2024</b>
Publication of draft report on website	<b>October 2024</b>

Final report available to all participants

**December 2024****Participation fee**

All laboratories that have received the test materials will receive a corresponding invoice in Norwegian kroner (NOK). The participation fee for any combination of the analytes in one food item is 13 700 NOK, in two food items 14 700 NOK and 15 700 NOK for three food items. Please note that if you choose to participate in the PFAS analysis you are required to pay for one additional matrix (16 700 NOK). Mackerel-2024 contains enough sample material for both POPs and PFAS.

**Co-ordinating group**

Mahin Karimi  
[mahin.karimi@fhi.no](mailto:mahin.karimi@fhi.no)  
Phone: +47 40071694

Cathrine Thomsen  
[cathrine.thomsen@fhi.no](mailto:cathrine.thomsen@fhi.no)  
Phone: +47 99644715

Inger-Lise Steffensen  
[inger-lise.karin.steffensen@fhi.no](mailto:inger-lise.karin.steffensen@fhi.no)

***E-mail Address***

For all enquiries by e-mail, please use [dioxin@fhi.no](mailto:dioxin@fhi.no).

***Postal Address:***

Norwegian Institute of Public Health  
P.O. Box 222 Skøyen  
N-0213 Oslo, Norway



## Interlaboratory Comparison on Dioxins in Food 2024

---

### Instructions for participants

March 2024

#### 1. Introduction

This is the 25<sup>th</sup> Round of the Interlaboratory Comparison Study on the Determination of POPs in Food organised by the Department of Food Safety, 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 indicator 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, indicator PCBs, PBDEs and HBCD in food. Instructions for the analysis and submission of results are given below.

Additionally, we also offer a fish sample for the determination of poly- and perfluoroalkyl substances (PFAS). This year it is a shared sample of Mackerel-2024 for PFAS and POPs analysis, ensuring there's enough for both tests in a single container for participants to divide as desired.

**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:  $\alpha$ -HBCD,  $\beta$ -HBCD,  $\gamma$ -HBCD and total HBCD

in the following samples:

Mackerel (Mackerel-2024), Cream (Cream-2024), and Egg Yolk (Egg Yolk-2024)

The mentioned analytes can also be determined in respective six standard solutions.

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:

- Mackerel (Mackerel-2024)

## 2. Design of the study

### 2.1 Test materials

#### Samples

One standard solution of each:

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

One sample of each

- approx. 90 g of Mackerel (enough for both POPs and PFAS analyses)
- approx. 50 g of Cream
- approx. 70 g of Egg Yolk

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

#### Fortification

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.

## 2.2 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 returned to the coordinators by e-mail. The code of the laboratory will then be given by the coordinators. The laboratory codes will not be revealed to the other participants or to any third parties.

### Coding of samples

Mackerel	Mackerel-2024
Cream	Cream-2024
Egg yolk	Egg Yolk 2024

*The above sample coding is marked on the sample bottles.*

## 2.3 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 HBCDs 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 of the analytes as non-detected. The sample amount dispatched is not meant for replicate analyses.

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

An estimate of the lipid content in the samples follows below:

- Mackerel: 15-30%

- Cream: 35-38 %
- Egg yolk: 26-28 %

### 3. Reporting

#### 3.1 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 fish sample designated for the analysis of PFAS.

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 Report Form “PFAS-2024” for PFASs.

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

For the reporting of PFAS: The results should be reported as the **anion**, not the salt! Also, be aware that PFAS should be reported as **pg/g**, not ng/g!

**Please inform us which form of PFAS you are reporting for each PFAS substance, i.e. whether it is the linear, branched or the sum of both isomers.**

#### 3.2 Checklist

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

#### 3.3 Submitting results

Four Microsoft Excel files are provided to each participant comprising:

##### **Participants confirmation**

- Confirmation of receiving test materials

##### **Report form dioxins and dioxin-like PCBs**

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

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

- 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 since this may cause problems in the automatic program calculations, causing risk of errors and additional work!**

**Please write your Lab code only in Report Form A of Dioxin report form and Report Form I of Marker PCB, PBDE report form. It will be automatically copied to the other forms in the same file.**

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

## Deadline

**The reports must be in our hands no later than June 30<sup>th</sup>, 2024** to enable us to prepare the draft report to be published by the end of October 2024. 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.

## 4. Statistical evaluations

Prior to the final report, a draft version will be prepared based on the data reported by the end of October 2024. 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.

## 5. Final report

The final report will be prepared by the coordinators and published in December 2024 and will then be made available for all interested parties in an electronic version on <http://www.fhi.no>.

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

## 6. Fee

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

- NOK 13 700 for one food item
- NOK 14 700 for two food items
- NOK 15 700 for three food items.
- NOK 16 700 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.

## 7. Time schedule

Announcement	<b>February 2024</b>
Return of registration form	<b>February 20<sup>th</sup>, 2024</b>
Shipment of test material	<b>From February to March, 2024</b>
Confirmation of receipt of test material by participant	<b>Within 7 days after reception</b>
<a href="#">Reporting of test results</a>	<b>June 30<sup>th</sup>, 2024</b>
Publication of draft report on web-site	<b>October 2024</b>
Final report available to all participants	<b>December 2024</b>

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

## 8. Co-ordinators of the study

Mahin Karimi  
[mahin.karimi@fhi.no](mailto:mahin.karimi@fhi.no)  
Phone: +47 40071694

Cathrine Thomsen  
[cathrine.thomsen@fhi.no](mailto:cathrine.thomsen@fhi.no)  
Phone: +47 99644715

Inger-Lise Steffensen  
[inger-lise.karin.steffensen@fhi.no](mailto:inger-lise.karin.steffensen@fhi.no)

**Postal Address:**

Norwegian Institute of Public Health  
att. Cathrine Thomsen  
Postboks 222 Skøyen  
N-0213 Oslo, Norway

---

## 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 non-detected congeners marked with ND in the Comments column?



## **Appendix C:**

WHO TEFs for human risk assessment



## WHO TEFs for human risk assessment

The WHO TEF values used for human risk assessment are based on the conclusions of the European Centre of Environmental Health of the World Health Organization (ECEH-WHO) and the International programme on Chemical Safety (IPCS) (ECEH-WHO/IPCS) meeting in Stockholm, Sweden, June 15-18, 1997 (M. van den Berg et al., Environ. Health Perspect., 106(12), 775-792, 1998, <https://doi.org/10.1289/ehp.98106775>), WHO - International Programme on Chemical Safety (IPCS) expert meeting in Geneva, Switzerland, June, 2005 (2005 WHO-TEFs) (M. van den Berg et al., Toxicol. Sci., 93(2), 223-241, 2006, <https://doi.org/10.1093/toxsci/kfl055>) and WHO expert meeting, Lisbon, Portugal, October 17-21, 2022 (2022 WHO-TEFs) ((M. DeVito et al., Regul. Toxicol. Pharmacol., 146, 105525, 2024, <https://doi.org/10.1016/j.yrtph.2023.105525>).

Congener	2005 WHO-TEF (2006)	2022 WHO-TEF (2024)
<i>Chlorinated dibenzo-p-dioxins</i>		
2,3,7,8-TCDD	1	1
1,2,3,7,8-PeCDD	1	0.4
1,2,3,4,7,8-HxCDD	0.1	0.09
1,2,3,6,7,8-HxCDD	0.1	0.07
1,2,3,7,8,9-HxCDD	0.1	0.05
1,2,3,4,6,7,8-HpCDD	0.01	0.05
OCDD	0.0003	0.001
<i>Chlorinated dibenzofurans</i>		
2,3,7,8-TCDF	0.1	0.07
1,2,3,7,8-PeCDF	0.03	0.01
2,3,4,7,8-PeCDF	0.3	0.1
1,2,3,4,7,8-HxCDF	0.1	0.3
1,2,3,6,7,8-HxCDF	0.1	0.09
1,2,3,7,8,9-HxCDF	0.1	0.2
2,3,4,6,7,8-HxCDF	0.1	0.1
1,2,3,4,6,7,8-HpCDF	0.01	0.02
1,2,3,4,7,8,9-HpCDF	0.01	0.1
OCDF	0.0003	0.002
<i>Non-ortho substituted PCBs</i>		
PCB 77	0.0001	0.0003
PCB 81	0.0003	0.006
PCB 126	0.1	0.05
PCB 169	0.03	0.005
<i>Mono-ortho substituted PCBs</i>		
PCB 105	0.00003	0.00003
PCB 114	0.00003	0.00003
PCB 118	0.00003	0.00003
PCB 123	0.00003	0.00003
PCB 156	0.00003	0.00003
PCB 157	0.00003	0.00003
PCB 167	0.00003	0.00003
PCB 189	0.00003	0.00003

Abbreviations used: T: tetra; Pe: penta; Hx: hexa; Hp: hepta; O: octa;  
CDD: chlorodibenzo-*p*-dioxin; CDF: chlorodibenzofuran; PCB: polychlorinated biphenyl.



## **Appendix D:**

---

Homogeneity testing



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

## Introduction

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

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

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

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

## Consequences for the Interlaboratory Comparison on Dioxins in Food

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

### 1.

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

**2.**

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

**3.**

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

### **Conclusion**

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

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

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

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

When testing homogeneity of the food samples, sodium chloride was added to about 10% of the test material in such an amount that the conductivity was about doubled compared to the natural conductivity. This sub-sample was added to the total sample. For example, to 1 kg of homogenised chicken meat, 150 g NaCl were added resulting in an addition of 1 % NaCl to the final test material of 15 kg. Conductivity measurements are performed as follows: boiling water is added to 10.0 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  $RSD_{\text{inhomogeneity}}^2 = RSD_{\text{between}}^2 - RSD_{\text{within}}^2$ <sup>1</sup> was 2.2 % and hence small and acceptable. The total uncertainty for the determination of PCDD/Fs is usually considerably larger, so the measured contribution of inhomogeneity to the total uncertainty can be neglected

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



## **Appendix E:**

---

### Summary results

Consensus of congener concentrations

Consensus of TEQ values

Consensus statistics

Laboratories' reported TEQs

Laboratories' Z-scores

Z-score plots



## Consensus of congener concentrations

	Mackerel		Cream		Egg yolk	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
<b>2,3,7,8-TCDD</b>	0,027	0,17	0,0075	0,021	0,0048	0,021
<b>1,2,3,7,8-PeCDD</b>	0,036	0,22	0,0090	0,025	0,0069	0,029
<b>1,2,3,4,7,8-HxCDD</b>	0,0051	0,031	0,0075	0,021	0,0059	0,025
<b>1,2,3,6,7,8-HxCDD</b>	0,0083	0,052	0,011	0,030	0,0075	0,032
<b>1,2,3,7,8,9-HxCDD</b>	0,0049	0,030	0,0077	0,021	0,0050	0,021
<b>1,2,3,4,6,7,8-HpCDD</b>	0,020	0,13	0,040	0,11	0,039	0,17
<b>1,2,3,4,6,7,8,9-OCDD</b>	0,035	0,22	0,054	0,15	0,12	0,51
<b>2,3,7,8-TCDF</b>	0,94	5,8	0,010	0,027	0,029	0,12
<b>1,2,3,7,8-PeCDF</b>	0,036	0,22	0,0071	0,019	0,011	0,049
<b>2,3,4,7,8-PeCDF</b>	0,15	0,95	0,026	0,071	0,019	0,081
<b>1,2,3,4,7,8-HxCDF</b>	0,0065	0,040	0,013	0,036	0,015	0,064
<b>1,2,3,6,7,8-HxCDF</b>	0,0060	0,037	0,012	0,032	0,0083	0,035
<b>2,3,4,6,7,8-HxCDF</b>	0,0090	0,056	0,012	0,032	0,010	0,044
<b>1,2,3,7,8,9-HxCDF</b>	0,0049	0,030	0,0076	0,021	0,0058	0,025
<b>1,2,3,4,6,7,8-HpCDF</b>	0,010	0,061	0,011	0,030	0,015	0,064
<b>1,2,3,4,7,8,9-HpCDF</b>	0,0050	0,031	0,0074	0,020	0,0073	0,031
<b>1,2,3,4,6,7,8,9-OCDF</b>	0,012	0,074	0,030	0,082	0,020	0,087
<b>PCB-77</b>	21	127	0,43	1,2	1,0	4,3
<b>PCB-126</b>	4,4	27	0,23	0,62	0,16	0,69
<b>PCB-169</b>	0,62	3,8	0,055	0,15	0,040	0,17
<b>PCB-81</b>	1,2	7,7	0,041	0,11	0,058	0,25
<b>PCB-105</b>	182	1127	7,1	20	18	77
<b>PCB-114</b>	8,9	55	0,68	1,9	1,2	5,1
<b>PCB-118</b>	581	3593	31	85	68	292
<b>PCB-123</b>	9,2	57	0,43	1,2	0,79	3,4
<b>PCB-156</b>	54	334	4,5	12	21	92
<b>PCB-157</b>	17	106	0,84	2,3	2,3	10
<b>PCB-167</b>	43	264	2,2	6,0	8,9	38
<b>PCB-189</b>	5,3	33	0,44	1,2	3,7	16

fw. - fresh weight

lw. - lipid weight

## Consensus of congener concentrations

	Mackerel		Cream		Egg yolk	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
<b>PCB- 28</b>	131	812	11	29	24	104
<b>PCB- 52</b>	368	2274	14	39	17	71
<b>PCB- 101</b>	783	4840	11	29	19	83
<b>PCB- 138</b>	1004	6205	53	145	223	951
<b>PCB- 153</b>	1655	10228	67	185	294	1257
<b>PCB- 180</b>	317	1962	26	72	187	798
<b>PBDE- 28</b>	12	75	0,19	0,52	0,13	0,55
<b>PBDE- 47</b>	191	1180	5,2	14	5,0	21
<b>PBDE- 99</b>	63	389	3,8	10	8,8	38
<b>PBDE- 100</b>	57	355	0,82	2,2	2,6	11
<b>PBDE- 153</b>	14	87	0,60	1,6	3,0	13
<b>PBDE- 154</b>	57	350	0,29	0,79	1,6	6,8
<b>PBDE- 183</b>	1,4	8,8	0,28	0,77	1,1	4,9
<b>PBDE- 209</b>	11	69	9,6	26	69	293
<b>α-HBCD*</b>	81	501	7,0	19	9,0	38
<b>β-HBCD*</b>	**	**	**	**	**	**
<b>γ-HBCD*</b>	10	64	2,0	5,5	2,0	8,5
<b>Tot HBCD*</b>	81	501	8,0	22	10	43
<b>Sum PCB</b>	4259	26322	182	500	764	3264
<b>Sum PBDE without 209</b>	395	2444	11	31	22	95
<b>Sum PBDE</b>	407	2513	21	57	91	389

fw. - fresh weight

lw. - lipid weight

\*: Indicative value due to few reported values

\*\* : Unable to calculate consensus value due to few submitted results

**Fish 2024: PFAS, consensus values**

	<b>Mackerel pg/g fw.</b>
<b>PFOS - All reported</b>	261
<b>PFOS - Sum*</b>	272
<b>PFOS - Linear*</b>	252
<b>PFHxS*</b>	17
<b>PFOA*</b>	11
<b>PFNA*</b>	20
<b>PFDA*</b>	30
<b>PFUnDA</b>	98
<b>Sum PFAS</b>	448

fw. - fresh weight

\*: Indicative value due to few reported values



**Consensus of TEQs**

TEF2024

	<b>Mackerel</b>		<b>Cream</b>		<b>Egg yolk</b>	
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
<b>2,3,7,8-TCDD</b>	0,027	0,17	0,0075	0,021	0,0048	0,021
<b>1,2,3,7,8-PeCDD</b>	0,014	0,089	0,0036	0,010	0,0028	0,012
<b>1,2,3,4,7,8-HxCDD</b>	0,00046	0,0028	0,00068	0,0019	0,00053	0,0023
<b>1,2,3,6,7,8-HxCDD</b>	0,00058	0,0036	0,00077	0,0021	0,00052	0,0022
<b>1,2,3,7,8,9-HxCDD</b>	0,00025	0,0015	0,00038	0,0011	0,00025	0,0011
<b>1,2,3,4,6,7,8-HpCDD</b>	0,0010	0,0063	0,0020	0,0055	0,0020	0,0084
<b>1,2,3,4,6,7,8,9-OCDD</b>	0,000035	0,00022	0,000054	0,00015	0,00012	0,00051
<b>2,3,7,8-TCDF</b>	0,066	0,41	0,00070	0,0019	0,0020	0,0085
<b>1,2,3,7,8-PeCDF</b>	0,00036	0,0022	0,000071	0,00019	0,00011	0,00049
<b>2,3,4,7,8-PeCDF</b>	0,015	0,095	0,0026	0,0071	0,0019	0,0081
<b>1,2,3,4,7,8-HxCDF</b>	0,0019	0,012	0,0040	0,011	0,0045	0,019
<b>1,2,3,6,7,8-HxCDF</b>	0,00054	0,0033	0,0011	0,0029	0,00075	0,0032
<b>2,3,4,6,7,8-HxCDF</b>	0,00090	0,0056	0,0012	0,0032	0,0010	0,0044
<b>1,2,3,7,8,9-HxCDF</b>	0,00098	0,0061	0,0015	0,0042	0,0012	0,0050
<b>1,2,3,4,6,7,8-HpCDF</b>	0,00020	0,0012	0,00022	0,00061	0,00030	0,0013
<b>1,2,3,4,7,8,9-HpCDF</b>	0,00050	0,0031	0,00074	0,0020	0,00073	0,0031
<b>1,2,3,4,6,7,8,9-OCDF</b>	0,000024	0,00015	0,000060	0,00016	0,000041	0,00017
<b>PCB-77</b>	0,0062	0,038	0,00013	0,00036	0,00031	0,0013
<b>PCB-126</b>	0,22	1,3	0,011	0,031	0,0081	0,035
<b>PCB-169</b>	0,0031	0,019	0,00027	0,00075	0,00020	0,00085
<b>PCB-81</b>	0,0075	0,046	0,00025	0,00068	0,00035	0,0015
<b>PCB-105</b>	0,0055	0,034	0,00021	0,00059	0,00054	0,0023
<b>PCB-114</b>	0,00027	0,0017	0,000020	0,000056	0,000036	0,00015
<b>PCB-118</b>	0,017	0,11	0,00093	0,0026	0,0020	0,0088
<b>PCB-123</b>	0,00028	0,0017	0,000013	0,000035	0,000024	0,00010
<b>PCB-156</b>	0,0016	0,010	0,00014	0,00037	0,00064	0,0027
<b>PCB-157</b>	0,00051	0,0032	0,000025	0,000069	0,000070	0,00030
<b>PCB-167</b>	0,0013	0,0079	0,000066	0,00018	0,00027	0,0011
<b>PCB-189</b>	0,00016	0,00098	0,000013	0,000036	0,00011	0,00048
<b>PCDDs/PCDFs</b>	0,13	0,81	0,027	0,074	0,023	0,10
<b>Non-ortho PCBs</b>	0,23	1,5	0,012	0,033	0,0090	0,038
<b>Mono-ortho PCBs</b>	0,027	0,17	0,0014	0,0039	0,0037	0,016
<b>Total TEQ</b>	0,39	2,4	0,040	0,11	0,036	0,15

fw. - fresh weight

lw. - lipid weight

**Consensus of TEQs**

TEF2006

	<b>Mackerel</b>		<b>Cream</b>		<b>Egg yolk</b>	
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
<b>2,3,7,8-TCDD</b>	0,027	0,17	0,0075	0,021	0,0048	0,021
<b>1,2,3,7,8-PeCDD</b>	0,036	0,22	0,0090	0,025	0,0069	0,029
<b>1,2,3,4,7,8-HxCDD</b>	0,00051	0,0031	0,00075	0,0021	0,00059	0,0025
<b>1,2,3,6,7,8-HxCDD</b>	0,00083	0,0052	0,0011	0,0030	0,00075	0,0032
<b>1,2,3,7,8,9-HxCDD</b>	0,00049	0,0030	0,00077	0,0021	0,00050	0,0021
<b>1,2,3,4,6,7,8-HpCDD</b>	0,00020	0,0013	0,00040	0,0011	0,00039	0,0017
<b>1,2,3,4,6,7,8,9-OCDD</b>	0,000011	0,000065	0,000016	0,000045	0,000035	0,00015
<b>2,3,7,8-TCDF</b>	0,094	0,58	0,0010	0,0027	0,0029	0,012
<b>1,2,3,7,8-PeCDF</b>	0,0011	0,0067	0,00021	0,00058	0,00034	0,0015
<b>2,3,4,7,8-PeCDF</b>	0,046	0,28	0,0077	0,021	0,0057	0,024
<b>1,2,3,4,7,8-HxCDF</b>	0,00065	0,0040	0,0013	0,0036	0,0015	0,0064
<b>1,2,3,6,7,8-HxCDF</b>	0,00060	0,0037	0,0012	0,0032	0,00083	0,0035
<b>2,3,4,6,7,8-HxCDF</b>	0,00090	0,0056	0,0012	0,0032	0,0010	0,0044
<b>1,2,3,7,8,9-HxCDF</b>	0,00049	0,0030	0,00076	0,0021	0,00058	0,0025
<b>1,2,3,4,6,7,8-HpCDF</b>	0,00010	0,00061	0,00011	0,00030	0,00015	0,00064
<b>1,2,3,4,7,8,9-HpCDF</b>	0,000050	0,00031	0,000074	0,00020	0,000073	0,00031
<b>1,2,3,4,6,7,8,9-OCDF</b>	0,0000036	0,000022	0,0000090	0,000025	0,0000061	0,000026
<b>PCB-77</b>	0,0021	0,013	0,000043	0,00012	0,00010	0,00043
<b>PCB-126</b>	0,44	2,7	0,023	0,062	0,016	0,069
<b>PCB-169</b>	0,019	0,12	0,0016	0,0045	0,0012	0,0051
<b>PCB-81</b>	0,00037	0,0023	0,000012	0,000034	0,000017	0,000074
<b>PCB-105</b>	0,0055	0,034	0,00021	0,00059	0,00054	0,0023
<b>PCB-114</b>	0,00027	0,0017	0,000020	0,000056	0,000036	0,00015
<b>PCB-118</b>	0,017	0,11	0,00093	0,0026	0,0020	0,0088
<b>PCB-123</b>	0,00028	0,0017	0,000013	0,000035	0,000024	0,00010
<b>PCB-156</b>	0,0016	0,010	0,00014	0,00037	0,00064	0,0027
<b>PCB-157</b>	0,00051	0,0032	0,000025	0,000069	0,000070	0,00030
<b>PCB-167</b>	0,0013	0,0079	0,000066	0,00018	0,00027	0,0011
<b>PCB-189</b>	0,00016	0,0010	0,000013	0,000036	0,00011	0,00048
<b>PCDDs/PCDFs</b>	0,21	1,3	0,033	0,091	0,027	0,12
<b>Non-ortho PCBs</b>	0,46	2,8	0,024	0,067	0,018	0,075
<b>Mono-ortho PCBs</b>	0,027	0,17	0,0014	0,0039	0,0037	0,016
<b>Total TEQ</b>	0,69	4,3	0,059	0,16	0,048	0,21

fw. - fresh weight

lw. - lipid weight



2024

## Consensus statistics

## Consensus statistics

### Analyte solution

	Target value pg/μl	Consensus median, pg/μl	Median all values pg/μl	Consensus mean, pg/μl	Standard deviation, pg/μl	Relative standard deviation, %	No. of values reported	No. of values removed
2,3,7,8-TCDD	2,0	2,0	2,0	2,0	0,15	7,6	42	0
1,2,3,7,8-PeCDD	5,0	5,0	5,0	5,1	0,33	6,6	42	1
1,2,3,4,7,8-HxCDD	5,0	5,0	5,0	5,0	0,32	6,3	42	0
1,2,3,6,7,8-HxCDD	5,0	4,9	4,9	4,8	0,36	7,4	42	0
1,2,3,7,8,9-HxCDD	5,0	4,9	4,9	4,9	0,30	6,2	42	0
1,2,3,4,6,7,8-HpCDD	5,0	5,0	5,0	5,0	0,31	6,2	42	0
1,2,3,4,6,7,8,9-OCDD	10	9,6	9,6	9,6	1,1	11	42	0
2,3,7,8-TCDF	2,0	2,0	2,0	2,0	0,14	7,0	42	1
1,2,3,7,8-PeCDF	5,0	5,0	5,0	5,0	0,35	7,0	42	0
2,3,4,7,8-PeCDF	5,0	4,9	4,9	4,9	0,30	6,1	42	0
1,2,3,4,7,8-HxCDF	5,0	4,9	4,9	5,0	0,31	6,3	42	0
1,2,3,6,7,8-HxCDF	5,0	5,0	5,0	5,0	0,33	6,6	42	0
2,3,4,6,7,8-HxCDF	5,0	5,0	5,0	4,9	0,35	7,2	42	0
1,2,3,7,8,9-HxCDF	5,0	5,0	5,0	5,1	0,34	6,8	42	0
1,2,3,4,6,7,8-HpCDF	5,0	4,9	4,9	4,9	0,37	7,5	42	0
1,2,3,4,7,8,9-HpCDF	5,0	4,9	4,9	4,9	0,32	6,5	42	1
1,2,3,4,6,7,8,9-OCDF	10	10	10	9,9	0,78	7,9	42	0
PCB 77	10	10	10	10	0,58	5,7	42	0
PCB 126	10	10	10	10	0,79	8,0	42	0
PCB 169	10	10	10	10	0,72	7,2	42	0
PCB 81	10	10	10	10	0,59	5,9	42	0
PCB 105	100	100	100	101	8,1	8,0	41	0
PCB 114	100	100	100	102	8,5	8,3	41	0
PCB 118	100	100	100	101	8,6	8,5	41	0
PCB 123	100	101	101	103	7,9	7,7	41	0
PCB 156	100	102	102	102	8,9	8,7	41	0
PCB 157	100	101	101	101	8,1	8,0	41	0
PCB 167	100	100	100	102	7,3	7,1	41	0
PCB 189	100	100	100	103	8,0	7,8	41	0

## Consensus statistics

2024

### Analyte solution

	Target value pg/μl	Median, pg/μl all values	Median, pg/μl outliers removed	Mean, pg/μl all values	Mean, pg/μl outliers removed
<b>PCB-28</b>	100	100	100	101	101
<b>PCB-52</b>	100	101	101	103	103
<b>PCB-101</b>	100	100	100	101	101
<b>PCB-138</b>	100	101	101	101	101
<b>PCB-153</b>	100	101	101	101	101
<b>PCB-180</b>	100	100	100	102	102
<b>PBDE-28</b>	25	25	25	26	26
<b>PBDE-47</b>	25	25	25	25	25
<b>PBDE-99</b>	25	25	25	25	25
<b>PBDE-100</b>	25	24	24	25	25
<b>PBDE-153</b>	25	25	25	25	25
<b>PBDE-154</b>	25	24	24	24	24
<b>PBDE-183</b>	25	24	24	24	23
<b>PBDE-209</b>	100	100	100	98	98
<b>α-HBCD *</b>	500	505	505	500	500

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	No. of values reported values	No. of reported outliers
<b>PCB-28</b>	10	9,6	39	0
<b>PCB-52</b>	6,8	6,8	39	0
<b>PCB-101</b>	6,5	6,5	39	0
<b>PCB-138</b>	7,3	7,3	39	0
<b>PCB-153</b>	7,3	7,3	39	0
<b>PCB-180</b>	10	10	39	0
<b>PBDE-28</b>	12	12	19	0
<b>PBDE-47</b>	11	11	19	0
<b>PBDE-99</b>	11	11	19	0
<b>PBDE-100</b>	13	13	19	0
<b>PBDE-153</b>	12	12	19	0
<b>PBDE-154</b>	12	12	19	0
<b>PBDE-183</b>	18	14	19	1
<b>PBDE-209</b>	10	10	16	0
<b>α-HBCD*</b>	9,2	9,2	4	0

\*: Indicative value due to few reported values

2024

## Consensus statistics

### Mackerel, 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	0,027	0,030	0,028	0,0097	35	49	8	11
1,2,3,7,8-PeCDD	0,036	0,040	0,038	0,015	38	49	8	11
1,2,3,4,7,8-HxCDD	0,0051	0,0085	0,0063	0,0030	48	49	17	27
1,2,3,6,7,8-HxCDD	0,0083	0,011	0,0093	0,0042	45	49	14	22
1,2,3,7,8,9-HxCDD	0,0049	0,0064	0,0049	0,0026	52	49	18	32
1,2,3,4,6,7,8-HpCDD	0,020	0,025	0,023	0,012	53	49	11	18
1,2,3,4,6,7,8,9-OCDD	0,035	0,059	0,043	0,023	54	49	14	14
2,3,7,8-TCDF	0,94	0,94	0,90	0,22	24	50	1	0
1,2,3,7,8-PeCDF	0,036	0,037	0,038	0,011	28	49	11	7
2,3,4,7,8-PeCDF	0,15	0,16	0,15	0,043	28	49	5	1
1,2,3,4,7,8-HxCDF	0,0065	0,010	0,0070	0,0030	43	49	17	26
1,2,3,6,7,8-HxCDF	0,0060	0,0091	0,0066	0,0029	44	49	16	24
2,3,4,6,7,8-HxCDF	0,0090	0,012	0,0087	0,0040	46	49	16	20
1,2,3,7,8,9-HxCDF	0,0049	0,0064	0,0051	0,0033	64	49	16	36
1,2,3,4,6,7,8-HpCDF	0,010	0,016	0,013	0,0087	70	49	12	24
1,2,3,4,7,8,9-HpCDF	0,0050	0,0080	0,0059	0,0038	64	49	18	32
1,2,3,4,6,7,8,9-OCDF	0,012	0,017	0,013	0,0090	68	49	16	25
PCB-77	21	21	20	4,9	24	50	0	2
PCB-126	4,4	4,4	4,1	1,2	29	50	0	1
PCB-169	0,62	0,63	0,61	0,18	29	49	5	6
PCB-81	1,2	1,2	1,1	0,35	31	50	5	4
PCB-105	182	182	184	44	24	50	0	1
PCB-114	8,9	9,0	9,2	2,6	29	50	1	2
PCB-118	581	581	589	124	21	50	0	1
PCB-123	9,2	9,6	9,4	3,0	31	50	7	2
PCB-156	54	54	54	10	19	49	0	1
PCB-157	17	17	17	3,4	20	49	0	2
PCB-167	43	43	42	8,2	20	50	3	1
PCB-189	5,3	5,3	5,1	0,72	14	50	1	2

## Consensus statistics

2024

### Mackerel, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
<b>PCB-28</b>	134	131	131	151	135	136
<b>PCB-52</b>	368	368	368	352	352	351
<b>PCB-101</b>	794	794	783	763	763	749
<b>PCB-138</b>	1008	1008	1004	1071	1071	1051
<b>PCB-153</b>	1660	1660	1655	1564	1564	1544
<b>PCB-180</b>	318	318	317	317	317	311
<b>PBDE-28</b>	13	12	12	15	11	12
<b>PBDE-47</b>	191	191	191	178	178	178
<b>PBDE-99</b>	63	63	63	59	59	59
<b>PBDE-100</b>	57	57	57	55	55	55
<b>PBDE-153</b>	14	14	14	13	13	13
<b>PBDE-154</b>	57	57	57	56	56	56
<b>PBDE-183</b>	1,6	1,5	1,4	2,4	1,4	1,4
<b>PBDE-209</b>	24	13	11	71	13	13
<b>α-HBCD *</b>	80	80	81	70	70	84
<b>β-HBCD *</b>	8,0	8,0	**	7,8	7,8	**
<b>γ-HBCD *</b>	9,1	9,1	10	8,7	8,7	10
<b>Tot HBCD *</b>	81	81	81	87	87	87

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	No. of values reported	No. of reported outliers	No. of reported NDs
<b>PCB-28</b>	52	32	29	47	3	3
<b>PCB-52</b>	29	29	22	47	0	2
<b>PCB-101</b>	29	29	27	47	0	1
<b>PCB-138</b>	32	32	30	47	0	1
<b>PCB-153</b>	28	28	28	47	0	1
<b>PCB-180</b>	26	26	23	47	0	1
<b>PBDE-28</b>	59	33	25	20	3	2
<b>PBDE-47</b>	23	23	23	20	0	0
<b>PBDE-99</b>	25	25	25	20	0	0
<b>PBDE-100</b>	28	28	28	20	0	0
<b>PBDE-153</b>	26	26	26	20	0	0
<b>PBDE-154</b>	30	30	30	20	0	0
<b>PBDE-183</b>	112	37	39	20	3	3
<b>PBDE-209</b>	109	60	66	16	7	5
<b>α-HBCD*</b>	41	41	9,4	4	0	1
<b>β-HBCD*</b>	73	73	**	4	0	4
<b>γ-HBCD*</b>	23	23	**	4	0	3
<b>Tot HBCD*</b>	16	16	16	3	0	0

NDs: Non-detects

\*: Indicative value due to few reported values

\*\*: Not possible to calculate results due to few reported results

2024

## Consensus statistics

### Cream, 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	0,0075	0,010	0,0079	0,0046	59	39	11	20
1,2,3,7,8-PeCDD	0,0090	0,011	0,010	0,0051	50	39	12	22
1,2,3,4,7,8-HxCDD	0,0075	0,010	0,0083	0,0045	54	39	13	22
1,2,3,6,7,8-HxCDD	0,011	0,013	0,012	0,0064	53	39	10	11
1,2,3,7,8,9-HxCDD	0,0077	0,010	0,0086	0,0053	61	38	10	23
1,2,3,4,6,7,8-HpCDD	0,040	0,047	0,045	0,017	36	39	5	8
1,2,3,4,6,7,8,9-OCDD	0,054	0,067	0,053	0,024	45	39	13	8
2,3,7,8-TCDF	0,010	0,012	0,0093	0,0046	50	39	13	15
1,2,3,7,8-PeCDF	0,0071	0,011	0,0075	0,0036	48	39	16	20
2,3,4,7,8-PeCDF	0,026	0,028	0,028	0,012	43	39	5	8
1,2,3,4,7,8-HxCDF	0,013	0,015	0,014	0,0073	51	39	11	13
1,2,3,6,7,8-HxCDF	0,012	0,013	0,012	0,0060	49	39	11	16
2,3,4,6,7,8-HxCDF	0,012	0,015	0,013	0,0074	57	39	11	17
1,2,3,7,8,9-HxCDF	0,0076	0,012	0,0090	0,0062	69	38	12	24
1,2,3,4,6,7,8-HpCDF	0,011	0,026	0,018	0,014	77	39	13	14
1,2,3,4,7,8,9-HpCDF	0,0074	0,012	0,0084	0,0043	52	39	15	21
1,2,3,4,6,7,8,9-OCDF	0,030	0,046	0,032	0,023	73	39	11	20
PCB-77	0,43	0,64	0,56	0,30	53	40	8	6
PCB-126	0,23	0,23	0,23	0,076	33	40	6	8
PCB-169	0,055	0,061	0,053	0,024	45	39	8	12
PCB-81	0,041	0,050	0,047	0,024	51	39	10	12
PCB-105	7,1	7,2	7,8	2,0	26	40	4	2
PCB-114	0,68	0,76	0,74	0,31	42	40	7	9
PCB-118	31	32	33	7,7	24	40	3	0
PCB-123	0,43	0,49	0,47	0,16	35	40	13	10
PCB-156	4,5	4,6	4,8	1,1	23	39	3	1
PCB-157	0,84	1,0	0,90	0,30	33	39	6	6
PCB-167	2,2	2,2	2,4	0,64	27	40	4	4
PCB-189	0,44	0,46	0,45	0,14	31	40	9	11

## Consensus statistics

2024

### Cream, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
<b>PCB-28</b>	21	10	11	35	14	15
<b>PCB-52</b>	18	14	14	29	16	16
<b>PCB-101</b>	12	11	11	24	12	12
<b>PCB-138</b>	57	53	53	66	56	55
<b>PCB-153</b>	71	67	67	81	71	70
<b>PCB-180</b>	27	26	26	38	26	26
<b>PBDE-28</b>	0,23	0,17	0,19	0,56	0,17	0,18
<b>PBDE-47</b>	5,2	5,2	5,2	5,7	5,7	5,8
<b>PBDE-99</b>	3,9	3,8	3,8	4,6	4,0	3,9
<b>PBDE-100</b>	0,88	0,81	0,82	1,4	0,82	0,89
<b>PBDE-153</b>	0,70	0,60	0,60	1,2	0,61	0,63
<b>PBDE-154</b>	0,46	0,29	0,29	1,0	0,34	0,29
<b>PBDE-183</b>	0,36	0,28	0,28	1,2	0,28	0,32
<b>PBDE-209</b>	23	9,6	9,6	83	13	13
<b>α-HBCD *</b>	6,0	6,0	7,0	6,6	6,6	7,0
<b>β-HBCD *</b>	6,0	6,0	**	5,7	5,7	**
<b>γ-HBCD *</b>	6,0	6,0	2,0	6,0	6,0	2,0
<b>Tot HBCD *</b>	8,0	8,0	8,0	8,0	8,0	8,0

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	No. of values reported	No. of reported outliers	No. of reported NDs
<b>PCB-28</b>	111	70	70	37	12	6
<b>PCB-52</b>	120	55	56	37	8	5
<b>PCB-101</b>	150	44	44	37	7	6
<b>PCB-138</b>	56	31	28	37	3	2
<b>PCB-153</b>	51	29	28	37	3	2
<b>PCB-180</b>	92	26	26	37	5	3
<b>PBDE-28</b>	132	70	68	14	4	6
<b>PBDE-47</b>	45	45	32	14	0	2
<b>PBDE-99</b>	57	27	30	14	1	2
<b>PBDE-100</b>	94	44	32	14	3	3
<b>PBDE-153</b>	123	41	16	14	3	4
<b>PBDE-154</b>	150	46	46	14	4	4
<b>PBDE-183</b>	202	59	47	14	5	5
<b>PBDE-209</b>	133	66	66	10	4	3
<b>α-HBCD*</b>	47	47	62	3	0	1
<b>β-HBCD*</b>	80	80	**	3	0	3
<b>γ-HBCD*</b>	67	67	**	3	0	2
<b>Tot HBCD*</b>	36	36	36	2	0	0

NDs: Non-detects

\*: Indicative value due to few reported values

\*\*: Not possible to calculate results due to few reported results

2024

## Consensus statistics

### Egg yolk, 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	0,0048	0,0055	0,0049	0,0026	53	39	13	22
1,2,3,7,8-PeCDD	0,0069	0,0090	0,0075	0,0035	47	39	11	23
1,2,3,4,7,8-HxCDD	0,0059	0,0091	0,0070	0,0039	56	39	11	22
1,2,3,6,7,8-HxCDD	0,0075	0,010	0,0090	0,0049	54	39	11	20
1,2,3,7,8,9-HxCDD	0,0050	0,0086	0,0059	0,0028	47	39	15	22
1,2,3,4,6,7,8-HpCDD	0,039	0,042	0,044	0,016	36	40	4	9
1,2,3,4,6,7,8,9-OCDD	0,12	0,13	0,12	0,042	35	40	8	8
2,3,7,8-TCDF	0,029	0,033	0,031	0,011	37	40	10	5
1,2,3,7,8-PeCDF	0,011	0,014	0,012	0,0058	48	39	9	15
2,3,4,7,8-PeCDF	0,019	0,022	0,023	0,0093	41	40	7	7
1,2,3,4,7,8-HxCDF	0,015	0,016	0,015	0,0060	40	39	8	10
1,2,3,6,7,8-HxCDF	0,0083	0,011	0,010	0,0047	49	39	10	14
2,3,4,6,7,8-HxCDF	0,010	0,012	0,010	0,0054	53	39	12	19
1,2,3,7,8,9-HxCDF	0,0058	0,010	0,0072	0,0044	60,93	38	11	24
1,2,3,4,6,7,8-HpCDF	0,015	0,020	0,017	0,0085	51	39	12	11
1,2,3,4,7,8,9-HpCDF	0,0073	0,010	0,0088	0,0055	62	39	8	22
1,2,3,4,6,7,8,9-OCDF	0,020	0,030	0,025	0,016	62	39	8	18
PCB-77	1,0	1,1	1,1	0,39	35	39	6	2
PCB-126	0,16	0,20	0,18	0,079	44	40	9	6
PCB-169	0,040	0,051	0,043	0,015	36	39	12	14
PCB-81	0,058	0,070	0,061	0,029	47	39	11	10
PCB-105	18	18	18	3,0	17	40	4	0
PCB-114	1,2	1,3	1,3	0,37	28	40	7	7
PCB-118	68	70	68	11	16	40	4	0
PCB-123	0,79	1,0	0,85	0,35	41	40	9	8
PCB-156	21	22	21	5,0	24	39	4	0
PCB-157	2,3	2,4	2,4	0,42	18	39	6	3
PCB-167	8,9	9,0	9,2	1,5	16	40	4	0
PCB-189	3,7	3,8	3,6	0,72	20	40	4	2

## Consensus statistics

2024

### Egg yolk, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
<b>PCB-28</b>	29	24	24	46	27	27
<b>PCB-52</b>	20	17	17	36	20	20
<b>PCB-101</b>	24	19	19	42	23	23
<b>PCB-138</b>	228	223	223	281	231	231
<b>PCB-153</b>	295	294	294	335	291	291
<b>PCB-180</b>	189	187	187	235	192	192
<b>PBDE-28</b>	0,18	0,12	0,13	1,2	0,11	0,14
<b>PBDE-47</b>	5,2	5,0	5,0	15	5,4	5,4
<b>PBDE-99</b>	8,8	8,8	8,8	8,1	8,1	8,5
<b>PBDE-100</b>	2,7	2,6	2,6	3,3	2,5	2,6
<b>PBDE-153</b>	3,0	3,0	3,0	3,7	2,8	2,7
<b>PBDE-154</b>	1,6	1,5	1,6	2,2	1,5	1,5
<b>PBDE-183</b>	1,3	1,1	1,1	2,8	1,0	1,1
<b>PBDE-209</b>	82	69	69	139	75	75
<b>α-HBCD *</b>	8,0	8,0	9,0	8,0	8,0	9,0
<b>β-HBCD *</b>	6,0	6,0	**	5,7	5,7	**
<b>γ-HBCD *</b>	6,0	6,0	2,0	6,0	6,0	2,0
<b>Tot HBCD *</b>	10	10	10	8,8	8,8	8,8

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	No. of values reported	No. of reported outliers	No. of reported NDs
<b>PCB-28</b>	93	34	34	39	8	4
<b>PCB-52</b>	112	42	42	39	10	4
<b>PCB-101</b>	98	34	34	39	11	4
<b>PCB-138</b>	69	24	24	39	3	0
<b>PCB-153</b>	50	21	21	39	3	0
<b>PCB-180</b>	66	20	20	39	3	0
<b>PBDE-28</b>	157	53	32	17	7	7
<b>PBDE-47</b>	194	30	30	17	3	1
<b>PBDE-99</b>	44	44	36	17	0	1
<b>PBDE-100</b>	83	43	37	17	2	3
<b>PBDE-153</b>	82	47	34	17	2	2
<b>PBDE-154</b>	85	46	41	17	3	2
<b>PBDE-183</b>	142	40	37	17	4	3
<b>PBDE-209</b>	134	44	44	14	3	2
<b>α-HBCD*</b>	25	25	16	3	0	1
<b>β-HBCD*</b>	80	80	**	3	0	3
<b>γ-HBCD*</b>	67	67	**	3	0	2
<b>Tot HBCD*</b>	24	24	24	3	0	0

NDs: Non-detects

\*: Indicative value due to few reported values

\*\*: Not possible to calculate results due to few reported results

## Consensus statistics

### Mackerel PFAS, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
<b>PFOS - All reported</b>	266	261	261	327	279	270
<b>PFOS - Sum*</b>	278	272	272	358	278	259
<b>PFOS - Linear*</b>	252	252	252	281	281	281
<b>PFHxS*</b>	46	22	17	98	35	21
<b>PFOA*</b>	50	11	11	91	34	19
<b>PFNA*</b>	48	24	20	85	30	25
<b>PFDA*</b>	40	35	30	93	35	29
<b>PFUnDA</b>	101	98	98	137	87	90

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	No. of reported values	No. of outliers	No. of reported NDs
<b>PFOS - All reported</b>	64	35	28	15	1	3
<b>PFOS - Sum*</b>	72	36	12	9	1	3
<b>PFOS - Linear*</b>	38	38	38	6	0	0
<b>PFHxS*</b>	145	83	81	15	3	7
<b>PFOA*</b>	150	108	107	15	3	10
<b>PFNA*</b>	153	58	54	15	4	7
<b>PFDA*</b>	142	33	27	14	4	6
<b>PFUnDA</b>	87	31	28	14	3	3

NDs: Non-detects

\*: Indicative value due to few reported values



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

TEF2024	Median pg/g	Mean pg/g	Standard deviation, pg/g	Relative standard deviation, %	Min pg/g	Max pg/g	Reporting laboratories
<b>Mackerel, fresh weight</b>							
PCDD/PCDF TEQ	0,14	0,31	0,56	181	0,060	4,0	50
Non-ortho PCB TEQ	0,24	0,23	0,062	28	0,010	0,38	50
Mono-ortho PCB TEQ	0,027	0,028	0,0058	21	0,0043	0,048	50
Total TEQ	0,41	0,50	0,57	113	0,087	4,3	50
Sum indicator PCB	4291	4219	1099	26	4,2	7600	47
Sum PBDE without PBDE-209	401	379	87	23	89	462	20
<b>Cream, fresh weight</b>							
PCDD/PCDF TEQ	0,034	0,091	0,10	113	0,014	0,47	39
Non-ortho PCB TEQ	0,013	0,021	0,024	118	0,00084	0,13	40
Mono-ortho PCB TEQ	0,0015	0,0018	0,00093	52	0,0010	0,0059	40
Total TEQ	0,049	0,10	0,12	119	0,0089	0,55	40
Sum indicator PCB	200	273	198	72	129	1140	37
Sum PBDE without PBDE-209	13	16	8,8	56	3,0	35	14
<b>Egg yolk, fresh weight</b>							
PCDD/PCDF TEQ	0,031	0,11	0,15	139	0,0049	0,73	40
Non-ortho PCB TEQ	0,011	0,029	0,050	174	0,0018	0,24	40
Mono-ortho PCB TEQ	0,0038	0,0054	0,0052	97	0,0023	0,029	40
Total TEQ	0,045	0,13	0,18	147	0,016	0,84	40
Sum indicator PCB	810	975	558	57	330	3010	39
Sum PBDE without PBDE-209	24	37	39	107	7,3	165	17

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

TEF2006	Median pg/g	Mean pg/g	Standard deviation, pg/g	Relative standard deviation, %	Min pg/g	Max pg/g	Reporting laboratories
<b>Mackerel, fresh weight</b>							
PCDD/PCDF TEQ	0,22	0,31	0,43	141	0,086	3,2	50
Non-ortho PCB TEQ	0,46	0,44	0,12	26	0,020	0,67	50
Mono-ortho PCB TEQ	0,027	0,028	0,0058	21	0,0043	0,048	50
Total TEQ	0,72	0,78	0,45	59	0,14	3,7	50
Sum indicator PCB	4291	4219	1099	26	4,2	7600	47
Sum PBDE without PBDE-209	401	379	87	23	89	462	20
<b>Cream, fresh weight</b>							
PCDD/PCDF TEQ	0,040	0,091	0,11	126	0,019	0,48	39
Non-ortho PCB TEQ	0,026	0,042	0,051	120	0,0019	0,27	40
Mono-ortho PCB TEQ	0,0015	0,0018	0,00093	52	0,0010	0,0059	40
Total TEQ	0,069	0,13	0,15	113	0,016	0,75	40
Sum indicator PCB	200	273	198	72	129	1140	37
Sum PBDE without PBDE-209	13	16	8,8	56	3,0	35	14
<b>Egg yolk, fresh weight</b>							
PCDD/PCDF TEQ	0,035	0,11	0,19	167	0,0070	0,84	40
Non-ortho PCB TEQ	0,022	0,058	0,10	174	0,0036	0,47	40
Mono-ortho PCB TEQ	0,0038	0,0054	0,0052	97	0,0023	0,029	40
Total TEQ	0,063	0,17	0,25	145	0,024	1,2	40
Sum indicator PCB	810	975	558	57	330	3010	39
Sum PBDE without PBDE-209	24	37	39	107	7,3	165	17



### Laboratories' Z-scores: Analyte solution

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15	-0,30	-0,30	-0,35	-0,14	-0,38	-0,29	-0,16
16	-0,023	-0,011	-0,21	0,038	0,44		
17							
18	0,31	0,33	0,0041	-0,20	-0,011	-0,071	-0,018
19							
20	-0,056	-0,045	-0,22	-0,11	-0,34		
21	-0,093	-0,10	-0,025	0,054	0,52		
22	-0,16	-0,17	0,028	0,0048	0,016		
23							
24							
25							
26							
27							
28							
29	0,012	0,012	0,0021	0,0056	-0,031		
30							
31							
32							
33	0,37	0,38	0,23	0,85	0,44	-0,15	-0,23
34							
35	-0,27	-0,27	-0,41	-0,050	0,028	0,087	0,0028
36							
37	-0,034	-0,029	-0,13	0,30	-0,29	-1,2	-1,2
38							
39	0,23	0,24	0,024	0,039	-0,0069	0,17	0,25
40							
41							
42							
43	0,015	0,018	-0,046	0,16	0,00045		
44	0,28	0,31	-0,37	0,63		0,65	1,0
45							
46	-0,0074	-0,037	0,47	0,072	-0,12	-0,059	-0,18
47							
48	0,43	0,44	0,26	0,97	1,1		
49							
50	-0,17	-0,18	-0,016	0,014	-0,56		
51							
52							
53	0,22	0,26	-0,48	-0,37	0,038		
54							
55							
56	-0,13	-0,13	-0,16	0,11	0,071	-0,12	0,078
57							
58							
59							
60	0,33	0,35	0,021	0,19	0,41		
61							
62							
63	-0,030	-0,058	0,43	-0,10	0,28	0,056	0,14
64	-0,40	-0,39	-0,59	-0,18	-0,037		
65							
66	-0,13	-0,14	-0,054	0,21	-0,58	-2,1	-0,37
67							
68	-0,042	-0,078	0,54	0,15	0,0057		
69							
70	-0,23	-0,26	0,33	-0,059	0,11	-0,091	-0,19

**Laboratories' Z-scores: Analyte solution (continued)**

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72							
73							
74							
75	-0,19	-0,18	-0,33	-0,19	-0,27	1,4	1,5
76							
77	-0,46	-0,46	-0,25		-0,026		
78							
79							
80	-0,26	-0,27	-0,21	0,23	-0,063		
81							
82							
83	-0,019	-0,047	0,45	-0,015	0,080	-0,0015	-0,021
84	-0,30	-0,28	-0,63	-0,41	-0,13		
85							
86							
87							
88							
89							
90	-0,25	-0,30	0,52	0,76	0,60	-0,043	-0,15
91							
92							
93							
94	-0,019	-0,024	0,056	0,30	0,24		
95							
96							
97							
98							
99	-0,20	-0,22	0,030	0,19	-0,038	-0,032	0,13
100					0,097	-0,27	-0,27
101							
102							
103							
104	-0,10	-0,059	-0,70	-0,34	-0,46		
105							
106	0,034	0,051	-0,24	-0,20	-0,32		
107							
108	-0,086	-0,087	-0,060	-0,16	-0,17		
109							
110	0,64	0,64	0,67	0,90	0,58	-2,0	-0,25
111	-0,60	-0,57	-1,0	-0,78			
112	0,028	0,023	0,10	0,58	0,14		
113							
114	0,00000	0,00000	0,00000	0,00000			
115							
116	-0,28	-0,29	-0,12	-0,25			
117							
118	0,59	0,61	0,26	0,49	0,063	-1,3	0,91
119	-0,066	-0,072	0,025	0,15	0,30		
120							

### Laboratories' Z-scores: Mackerel, fresh weight

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15	-0,68	5,3	-4,1	0,63	0,94	1,8	0,84
16	-0,91	-0,19	-1,4	-0,022	0,28	-0,0067	0,13
17							
18	1,1	2,2	0,66	-0,16	0,062	0,44	0,43
19							
20	-0,12	-1,2	0,45	0,051	0,70		
21	0,24	0,33	0,16	0,45	0,25		
22	6,2	20	-1,2	1,4	-1,0		
23							
24							
25	1,4	3,5	0,27	1,7	0,072		
26							
27							
28							
29	0,72	1,1	0,60	-0,17	-0,71		
30	-0,028	0,031	-0,13	0,55	-0,25		
31							
32	-1,9	0,23	-3,3	-0,46	-0,20	-0,41	-0,49
33	-0,69	-2,7	0,19	1,3	0,96	2,4	0,051
34							
35	4,6	7,2	3,2	3,9	3,9	1,8	0,74
36							
37	0,038	0,084	0,035	-0,15	-0,38	0,24	-1,1
38							
39	1,8	5,0	0,29	-0,052	-0,18	-3,9	-3,9
40	0,31	-0,087	0,59	-0,18	1,8		
41							
42							
43	1,9	6,1	-0,22	-0,021	-0,14		
44	-0,31	-0,52	-0,24	0,11		0,64	0,80
45							
46	0,28	-0,47	0,77	-0,37	-0,26	0,018	-0,15
47							
48	-0,42	0,18	-0,89	0,79	0,98		
49							
50	0,40	0,89	0,078	0,79	-0,49		
51							
52							
53	0,12	1,1	-0,34	-0,72	0,12		
54							
55							
56	0,33	1,4	-0,23	-0,062	0,19	0,46	0,32
57							
58	0,46	0,23	0,59	0,43			
59							
60	0,23	0,94	-0,18	0,24	0,30		
61							
62							
63	0,96	0,59	1,2	0,56	1,1	0,62	0,66
64	0,088	0,10	0,062	0,24	0,28		
65							
66	-0,41	-1,5	0,15	-0,26	0,069	-0,53	-0,40
67							
68	-0,58	-1,3	-0,17	-0,57	-0,64		
69							
70	50	150	0,83	0,72	1,3	-0,17	-0,24

**Laboratories' Z-scores: Mackerel, fresh weight (continued)**

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72	2,7	6,4	0,97	0,0037	-5,0		
73							
74							
75	0,16	0,78	-0,14	-0,24	-0,29	2,7	0,44
76							
77	-0,66	-0,72	-0,60	-0,79	-0,13		
78							
79							
80	0,94	0,93	0,86	1,6	-0,38		
81							
82							
83	0,20	-0,33	0,55	-0,29	-0,56	0,00035	0,097
84	-1,4	-1,3	-1,5	-1,1	-0,42		
85							
86							
87							
88	4,5	14	-0,39	-0,48	0,81		
89							
90	1,8	3,4	1,1	1,0	0,35	2,2	-0,42
91							
92							
93							
94	0,74	0,43	0,94	0,39	0,31		
95							
96							
97							
98							
99	-0,042	-0,18	0,0078	0,17	0,037	1,2	0,25
100	-3,9	-2,2	-4,8	-4,2	-4,1		
101							
102							
103							
104	-1,1	-1,6	-0,72	-1,8	-1,5	-2,0	-2,0
105							
106	-1,3	1,0	-2,8	-0,11	-0,22		
107							
108	0,24	0,76	-0,022	-0,0037	0,27		
109							
110	-0,50	-0,39	-0,64	0,18	-0,085	-0,29	-0,16
111	0,15	2,7	-1,1	-1,2	-0,88		
112	0,45	0,026	0,65	0,74	1,2		
113							
114	-0,56	-1,6	-0,065	-0,078	-0,77		
115	2,1	6,2	0,023	0,61	-0,36		
116	-0,69	-1,6	-0,22	-0,48			
117							
118							
119	0,80	0,41	1,1	0,45	0,43		
120							

**Laboratories' Z-scores: Mackerel, lipid weight**

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15	-0,68	5,3	-4,1	0,62	0,93	1,8	0,83
16	-1,2	-0,58	-1,7	-0,42	-0,14	-0,41	-0,28
17							
18	0,77	1,8	0,34	-0,43	-0,23	0,13	0,12
19							
20	-1,1	-1,9	-0,64	-0,95	-0,43		
21	0,013	0,10	-0,059	0,21	0,024		
22	9,5	28	-0,050	3,3	0,17		
23							
24							
25	1,5	3,6	0,33	1,8	0,14		
26							
27							
28							
29	0,89	1,3	0,77	-0,025	-0,58		
30	-0,046	0,012	-0,14	0,53	-0,27		
31							
32							
33	-0,75	-2,7	0,12	1,2	0,88	2,3	-0,017
34							
35	5,0	7,7	3,6	4,3	4,3	2,1	1,0
36							
37	0,36	0,41	0,36	0,16	-0,086	0,58	-0,88
38							
39	1,6	4,6	0,11	-0,22	-0,34	-3,9	-3,9
40	0,27	-0,12	0,54	-0,22	1,7		
41							
42							
43							
44	-0,43	-0,64	-0,36	-0,018		0,50	0,66
45							
46	0,76	-0,052	1,3	0,059	0,18	0,48	0,30
47							
48	-0,55	0,029	-1,0	0,63	0,81		
49							
50	0,39	0,88	0,072	0,78	-0,50		
51							
52							
53	1,1	2,2	0,52	0,075	1,1		
54							
55							
56	0,50	1,6	-0,083	0,089	0,35	0,63	0,49
57							
58							
59							
60	1,2	2,1	0,74	1,2	1,3		
61							
62							
63	1,0	0,64	1,3	0,61	1,2	0,67	0,71
64	-0,11	-0,094	-0,13	0,034	0,076		
65							
66	-0,47	-1,5	0,091	-0,32	0,0075	-0,58	-0,46
67							
68	1,6	0,48	2,2	1,6	1,5		
69							
70	51	152	0,92	0,81	1,4	-0,097	-0,17

**Laboratories' Z-scores: Mackerel, lipid weight (continued)**

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72	3,0	6,9	1,2	0,23	-5,0		
73							
74							
75	0,17	0,79	-0,13	-0,23	-0,29	2,7	0,44
76							
77	-0,12	-0,19	-0,061	-0,27	0,47		
78							
79							
80	2,3	2,3	2,2	3,2	0,71		
81							
82							
83	0,44	-0,11	0,81	-0,069	-0,35	0,23	0,33
84	0,44	0,65	0,26	0,94	1,9		
85							
86							
87							
88	5,0	15	-0,16	-0,25	1,1		
89							
90	1,4	2,9	0,69	0,62	0,019	1,8	-0,70
91							
92							
93							
94	1,4	1,0	1,6	0,99	0,91		
95							
96							
97							
98							
99	0,13	-0,0074	0,18	0,35	0,21	1,4	0,43
100	-3,5	-1,3	-4,7	-4,0	-3,8		
101							
102							
103							
104	1,0	0,30	1,6	-0,14	0,42	-0,33	-0,39
105							
106	-1,4	0,89	-2,8	-0,20	-0,31		
107							
108	0,19	0,70	-0,072	-0,054	0,22		
109							
110	-1,1	-1,0	-1,2	-0,52	-0,75	-0,93	-0,81
111	0,051	2,6	-1,2	-1,2	-0,95		
112	0,37	-0,047	0,57	0,66	1,1		
113							
114	-0,74	-1,7	-0,26	-0,27	-0,94		
115	0,24	3,3	-1,3	-0,87	-1,6		
116	-1,2	-2,0	-0,79	-1,0			
117							
118							
119	1,1	0,72	1,4	0,76	0,74		
120							

**Laboratories' Z-scores: Cream, fresh weight**

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15							
16	-2,9	-2,3	-4,6	-0,12	-0,69	-2,1	0,44
17							
18							
19							
20							
21							
22	57	81	7,3	-0,69	0,50		
23							
24							
25	18	20	15	16	13		
26							
27							
28							
29							
30	-0,50	-0,16	-1,2	-0,72	-1,4		
31							
32							
33	-3,9		-1,8	-0,47	0,064	49	11
34							
35							
36							
37	0,79	0,082	2,2	2,0	5,4	75	0,72
38							
39	22	30	3,7	3,3	2,5	6,2	2,7
40	3,4	0,65	9,6	2,2			
41							
42							
43	6,0	8,7	0,32	1,6	0,62		
44	0,11	0,52	-0,82	0,14		1,4	6,8
45							
46	-1,5	-2,1	-0,17	-0,16	1,2	0,039	-0,26
47							
48	0,71	1,7	-1,4	0,61	-0,29		
49							
50	5,8	8,2	1,3	-0,12	1,8		
51							
52							
53	23	34	0,38	1,1	26		
54							
55							
56	-1,0	-1,0	-1,1	-0,43	-0,53	-0,19	-0,020
57							
58							
59							
60	0,63	0,49	0,92	0,85	0,41		
61							
62							
63	-1,6	-2,1	-0,84	-0,0043	-0,021	-1,3	-0,49
64	-1,2	-1,8	0,089	0,081	3,8		
65							
66	6,0	9,2	-0,67	0,12	1,6	-1,8	0,92
67							
68	2,4	3,4	-0,42	8,0	4,8		
69							
70							

**Laboratories' Z-scores: Cream, fresh weight (continued)**

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72	28	27	33	0,49	0,23		
73							
74							
75	3,7	6,1	-1,8	5,7	0,016		
76							
77	3,7	3,7	3,7	4,5	4,6		
78							
79							
80	-1,2	-1,2	-1,3	-1,1	1,0		
81							
82							
83	-1,2	-1,7	-0,19	-0,64	-0,34	0,25	0,84
84	3,6	5,8	-0,91	-0,25	1,1		
85							
86							
87							
88	63	72	51	-1,3	-1,0		
89							
90	0,38	-0,13	1,5	0,96	-0,047	9,6	-1,6
91							
92							
93							
94	-0,65	-1,6	1,3	1,3	1,7		
95							
96							
97							
98							
99	0,65	0,79	0,35	0,38	-0,44	48	7,8
100	-0,12	-0,17	-0,0057	-0,24	-0,74		
101							
102							
103							
104	1,6	1,9	1,0	-0,033	0,22	3,3	2,9
105							
106	0,97	1,4	0,21	0,0035	0,05		
107							
108	0,70	1,1	-0,12	0,051	0,17		
109							
110							
111	18	18	21	-1,0	12		
112	7,7	11	1,9	0,74	0,79		
113							
114							
115	29	40	6,5	9,7	14		
116	6,0	9,0	-0,35	1,0			
117							
118	1,1	0,75	1,9	0,52	-0,32	-4,3	-3,7
119	-0,66	-1,5	1,1	1,3	1,6		
120							

### Laboratories' Z-scores: Cream, lipid weight

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15							
16	-2,8	-2,2	-4,6	0,19	-0,42	-1,9	0,79
17							
18							
19							
20							
21							
22	74	106	11	0,53	2,0		
23							
24							
25	17	19	14	15	12		
26							
27							
28							
29							
30	0,42	0,82	-0,46	0,15	-0,72		
31							
32							
33	-3,9		-1,9	-0,53	-0,012	48	10
34							
35							
36							
37	0,30	-0,34	1,6	1,4	4,6	68	0,24
38							
39	13	19	0,91	0,62	0,073	2,6	0,25
40	3,3	0,63	9,6	2,2			
41							
42							
43	3,8	6,0	-0,73	0,27	-0,49		
44	-0,031	0,37	-0,93	-0,00053		1,2	6,5
45							
46	-1,5	-2,1	-0,19	-0,18	1,1	0,018	-0,28
47							
48	0,63	1,6	-1,5	0,54	-0,35		
49							
50	6,7	9,2	1,8	0,26	2,3		
51							
52							
53	22	32	0,13	0,80	25		
54							
55							
56	-0,86	-0,84	-0,96	-0,25	-0,36	-0,0015	0,18
57							
58							
59							
60	0,28	0,15	0,55	0,49	0,070		
61							
62							
63	-1,7	-2,1	-0,90	-0,073	-0,090	-1,3	-0,55
64	-1,3	-1,9	-0,10	-0,11	3,5		
65							
66	6,3	9,6	-0,55	0,26	1,8	-1,7	1,1
67							
68	0,15	0,82	-1,8	4,1	1,8		
69							
70							

**Laboratories' Z-scores: Cream, lipid weight (continued)**

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72	28	27	33	0,45	0,19		
73							
74							
75	11	15	0,66	14	4,0		
76							
77	-0,43	-0,45	-0,44	-0,025	0,0078		
78							
79							
80	-1,0	-1,0	-1,1	-0,96	1,3		
81							
82							
83	-0,38	-0,98	0,91	0,35	0,73	1,5	2,2
84	4,1	6,4	-0,67	0,021	1,4		
85							
86							
87							
88	66	76	54	-1,1	-0,77		
89							
90	0,56	0,038	1,7	1,2	0,12	10	-1,5
91							
92							
93							
94	-0,65	-1,6	1,3	1,3	1,7		
95							
96							
97							
98							
99	0,75	0,90	0,46	0,48	-0,35	49	8,1
100	0,19	0,14	0,31	0,061	-0,46		
101							
102							
103							
104	0,96	1,3	0,44	-0,52	-0,29	2,5	2,1
105							
106	0,68	1,1	-0,037	-0,23	-0,19		
107							
108	0,61	1,0	-0,21	-0,034	0,086		
109							
110							
111	19	19	21	-0,86	12		
112	8,1	11	2,2	0,91	0,96		
113							
114							
115	30	41	6,8	10	14		
116	6,3	9,5	-0,19	1,2			
117							
118	0,32	0,028	1,0	-0,17	-0,91	-4,4	-3,8
119	-0,55	-1,4	1,2	1,4	1,8		
120							

### Laboratories' Z-scores: Egg yolk, fresh weight

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15							
16	-2,3	-2,0	-4,0	0,24	0,31	-3,8	-0,073
17							
18	19	28	3,6	0,17	0,46	6,1	18
19							
20	1,1	0,17	3,8	0,47	1,3		
21							
22	44	64	11	-2,0	-2,8		
23							
24							
25	24	24	24	20	15		
26							
27							
28							
29							
30	-0,37	-0,31	-0,73	0,15	-0,46		
31							
32							
33	-2,8	-3,9	-1,3	0,36	0,91	7,5	3,9
34							
35							
36							
37	0,023	-0,35	1,1	-0,24	-0,83	5,4	-0,41
38							
39	31	14	87	0,33	-0,18	-2,9	-3,4
40	1,3	-1,0	8,2	-0,30	4,8		
41							
42							
43							
44							
45							
46	-0,60	-1,3	1,0	-0,26	-0,34	-0,011	-0,045
47							
48	1,3	1,8	0,51	0,037	0,11		
49							
50	14	20	4,7	0,12	0,013		
51							
52							
53	24	35	3,7	2,2	4,8		
54							
55							
56	0,84	1,6	-0,70	-0,18	-0,28	1,0	0,39
57							
58							
59							
60	0,86	0,55	1,9	0,36	0,88		
61							
62							
63	2,3	3,7	-0,32	-0,11	-0,062	-1,1	-0,37
64	-0,53	-0,78	-0,12	0,016	0,74		
65							
66	2,7	4,7	-1,0	-1,1	-0,57	-3,5	1,1
67							
68	17	17	16	16	14		
69							
70	20	27	13	0,0079	2,2	1,0	0,83

**Laboratories' Z-scores: Egg yolk, fresh weight (continued)**

LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72	3,8	3,6	6,0	0,15	0,20		
73							
74							
75	6,1	9,3	-0,0053	-0,043	-0,85	39	2,9
76							
77	0,25	0,054	0,37	1,1	0,85		
78							
79							
80							
81							
82							
83	-1,7	-1,7	-2,5	-0,14	-0,44	-0,77	0,79
84	-1,9	-2,5	-0,53	-1,1	-0,15		
85							
86							
87							
88	110	136	90	-1,1	0,57		
89							
90	0,17	-0,29	1,1	0,82	0,30	0,68	-0,094
91							
92							
93							
94	0,17	-0,37	1,3	0,79	0,90		
95							
96							
97							
98							
99	0,046	0,027	0,046	0,16	-0,25	13	32
100	55	29	131	33	0,14	-1,1	-1,3
101							
102							
103							
104	-0,38	0,96	-3,9	-0,32	0,19	0,011	1,0
105							
106	0,44	0,75	-0,22	0,065	-0,43		
107							
108	0,35	0,41	0,50	-0,39	-0,22		
109							
110							
111	20	20	29	-1,4	0,97		
112	0,78	1,6	-1,3	0,88	1,3		
113							
114							
115	102	150	14	17	9,6		
116	1,7	2,9	-0,33	-1,2			
117							
118	1,7	1,6	2,7	0,38	0,51	-4,0	-0,77
119	0,12	-0,32	0,97	0,84	0,90		
120							

### Laboratories' Z-scores: Egg yolk, lipid weight

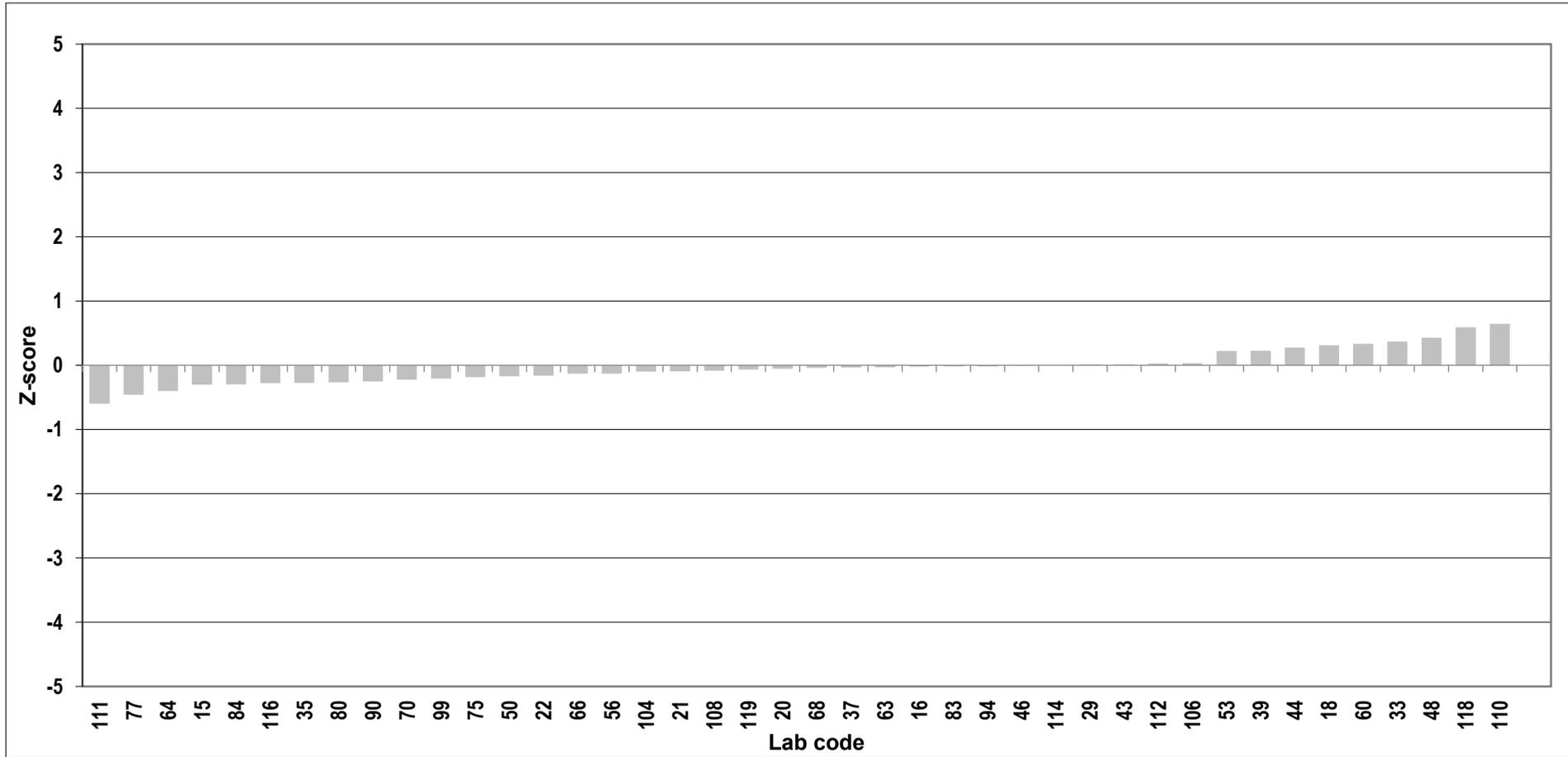
LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15							
16	-2,1	-1,8	-3,9	0,54	0,62	-3,7	0,21
17							
18	19	28	3,7	0,19	0,47	6,1	19
19							
20	0,29	-0,51	2,6	-0,25	0,43		
21							
22	42	60	11	-2,1	-2,9		
23							
24							
25							
26							
27							
28							
29							
30	-0,59	-0,54	-0,94	-0,10	-0,69		
31							
32							
33	-3,2	-4,1	-1,8	-0,42	0,047	5,6	2,6
34							
35							
36							
37	0,49	0,085	1,7	0,21	-0,44	6,3	0,019
38							
39	29	13	81	0,010	-0,47	-3,0	-3,5
40	1,4	-0,97	8,3	-0,26	4,8		
41							
42							
43							
44							
45							
46	-0,071	-0,83	1,8	0,30	0,22	0,58	0,54
47							
48	1,4	2,0	0,66	0,18	0,26		
49							
50	15	21	5,3	0,44	0,33		
51							
52							
53	14	22	0,96	-0,086	1,7		
54							
55							
56	0,62	1,3	-0,86	-0,36	-0,45	0,81	0,19
57							
58							
59							
60	2,3	1,9	3,5	1,6	2,3		
61							
62							
63	2,5	3,9	-0,22	-0,014	0,040	-0,99	-0,27
64	-0,24	-0,50	0,20	0,35	1,1		
65							
66	1,5	3,2	-1,6	-1,7	-1,2	-3,7	0,18
67							
68	19	19	18	18	16		
69							
70	24	32	15	0,78	3,3	1,9	1,7

**Laboratories' Z-scores: Egg yolk, lipid weight (continued)**

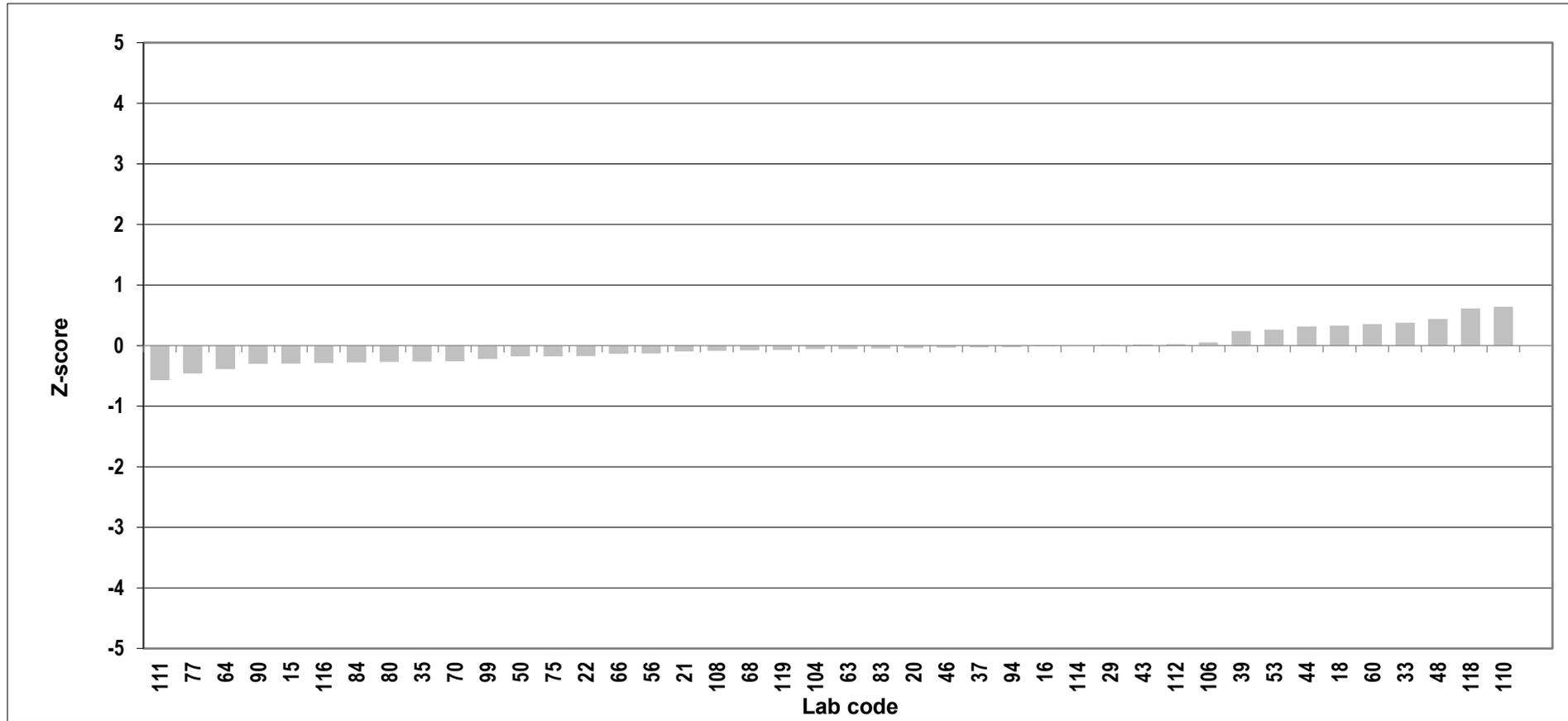
LAB CODE	Sum TE Total TEQ	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum PBDE Sum with 209	Sum PBDE Sum without 209
71							
72	3,5	3,3	5,6	-0,034	0,014		
73							
74							
75	6,0	9,2	-0,048	-0,085	-0,88	39	2,8
76							
77	0,25	0,054	0,37	1,1	0,85		
78							
79							
80							
81							
82							
83	-1,8	-1,8	-2,6	-0,27	-0,56	-0,88	0,64
84	-0,57	-1,5	1,3	0,57	1,9		
85							
86							
87							
88	114	141	93	-0,94	0,77		
89							
90	0,71	0,20	1,8	1,4	0,86	1,3	0,42
91							
92							
93							
94	-0,74	-1,2	0,20	-0,23	-0,14		
95							
96							
97							
98							
99	0,42	0,40	0,42	0,55	0,11	14	35
100	53	28	126	32	-0,030	-1,2	-1,4
101							
102							
103							
104	-0,38	0,96	-3,9	-0,32	0,19	0,011	1,0
105							
106	0,33	0,64	-0,31	-0,031	-0,52		
107							
108	1,2	1,2	1,3	0,32	0,51		
109							
110							
111	21	21	30	-1,3	1,2		
112	0,63	1,4	-1,4	0,73	1,1		
113							
114							
115	90	131	12	14	7,8		
116	0,81	1,9	-0,93	-1,7			
117							
118							
119	-0,80	-1,2	-0,10	-0,20	-0,15		
120							



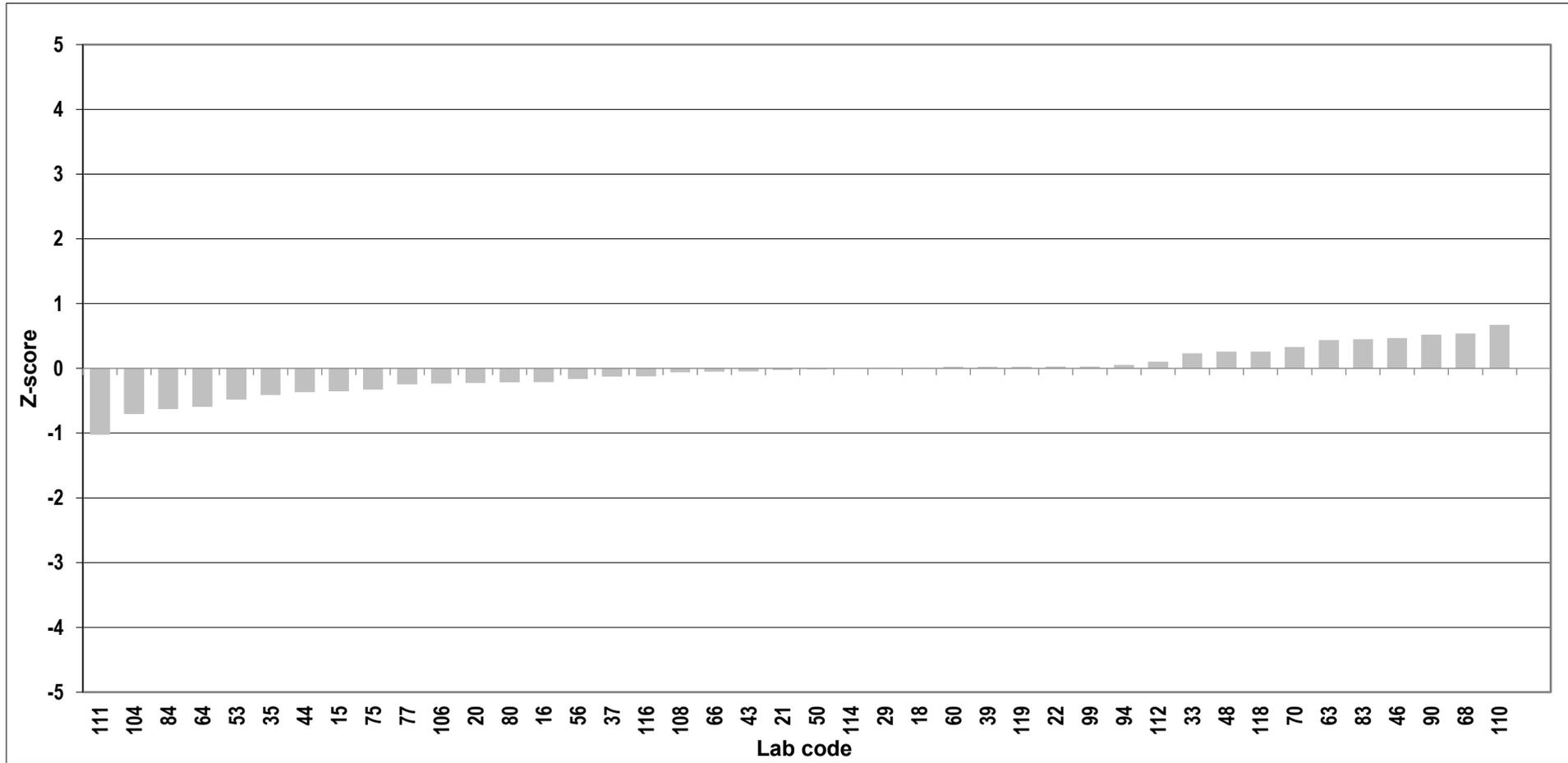
### Z-score Analyte solution; total TEQ



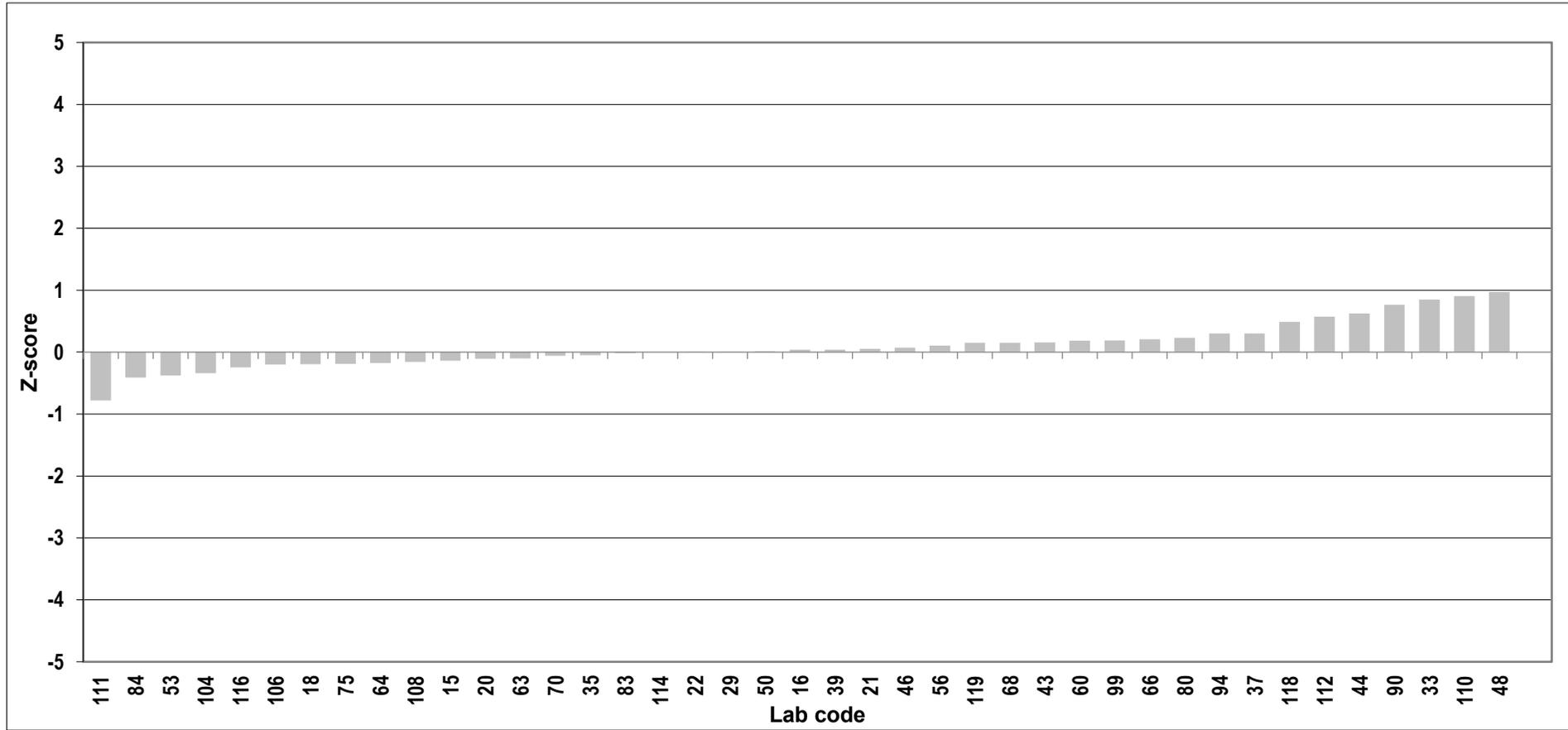
### Z-score Analyte solution; PCDD/PCDF TEQ



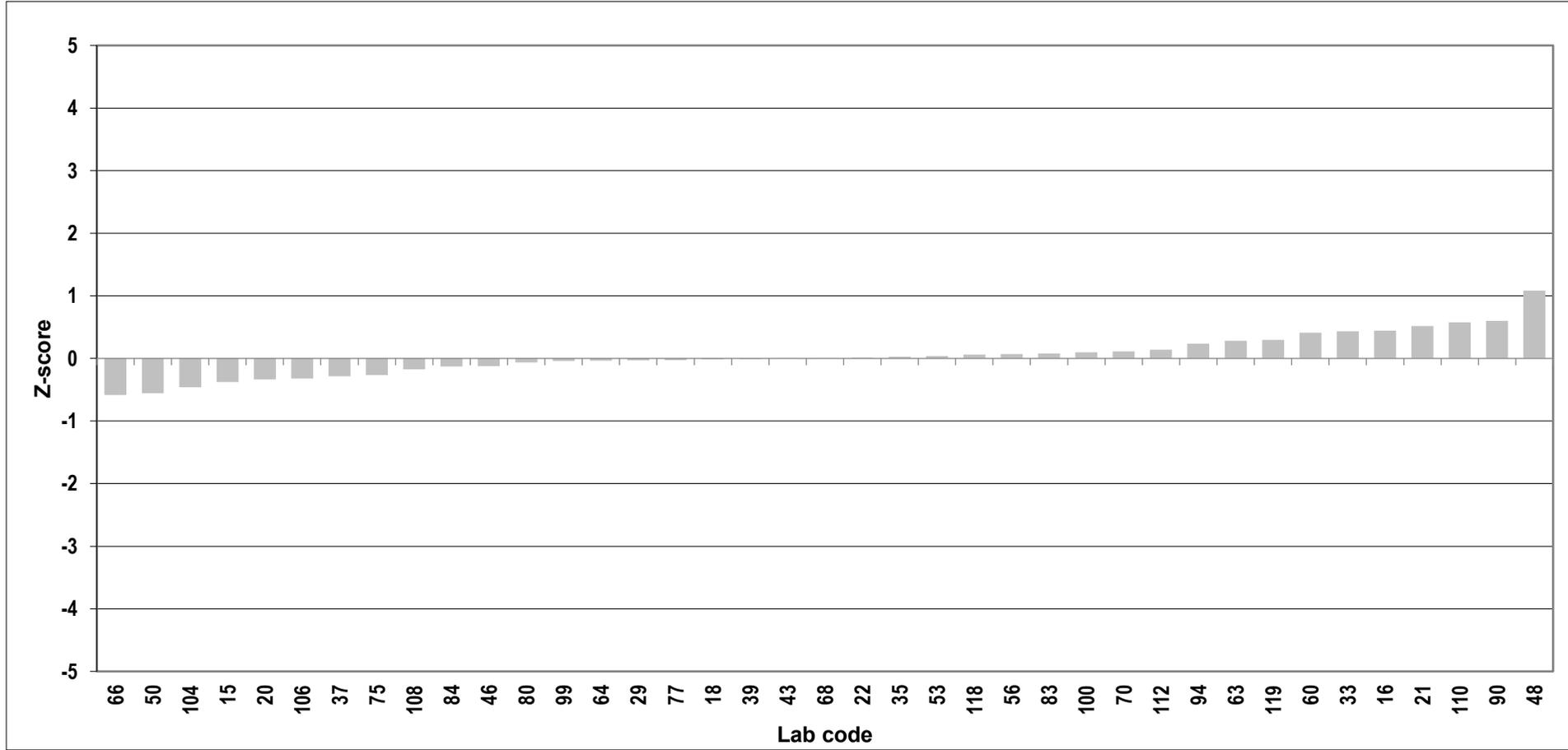
**Z-score Analyte solution; non-ortho PCB TEQ**



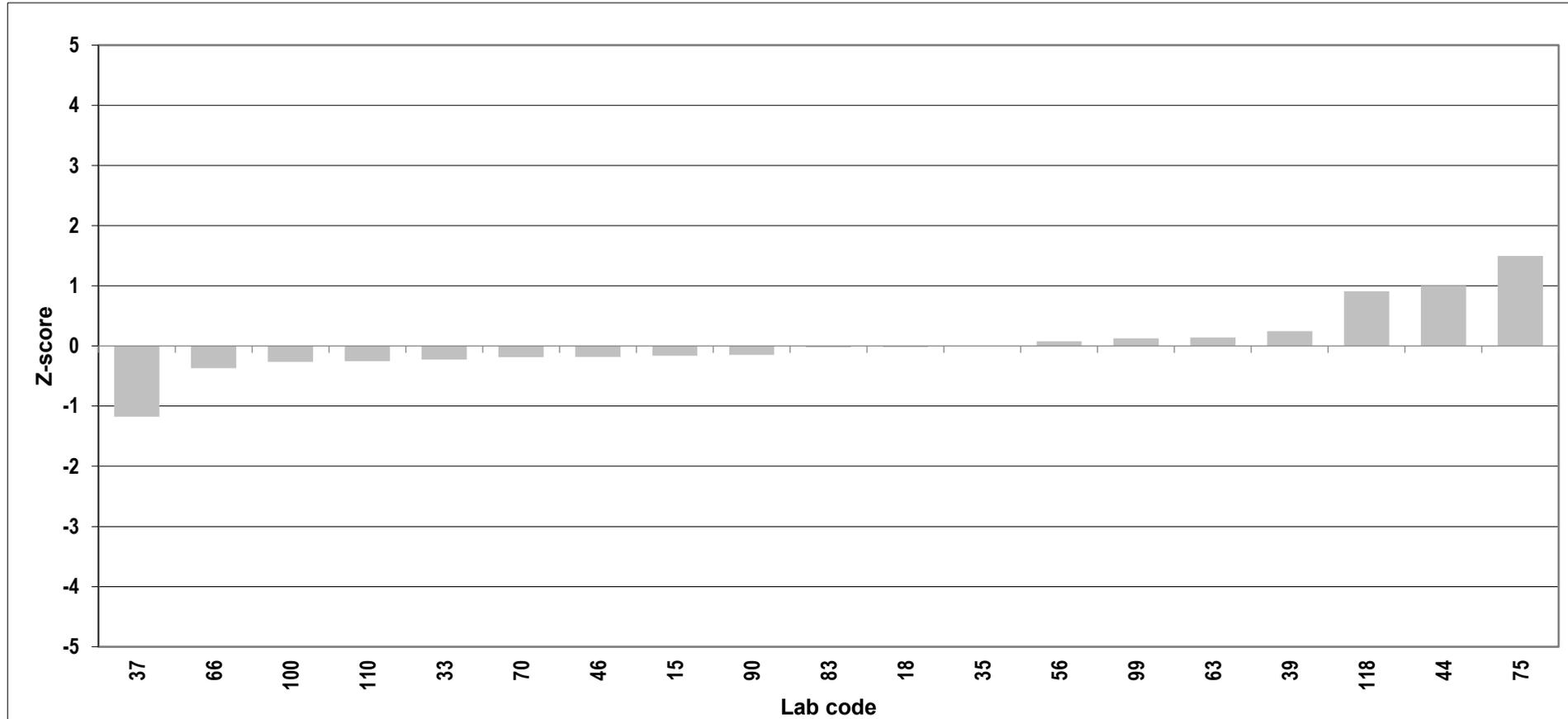
### Z-score Analyte solution; mono-ortho PCB TEQ



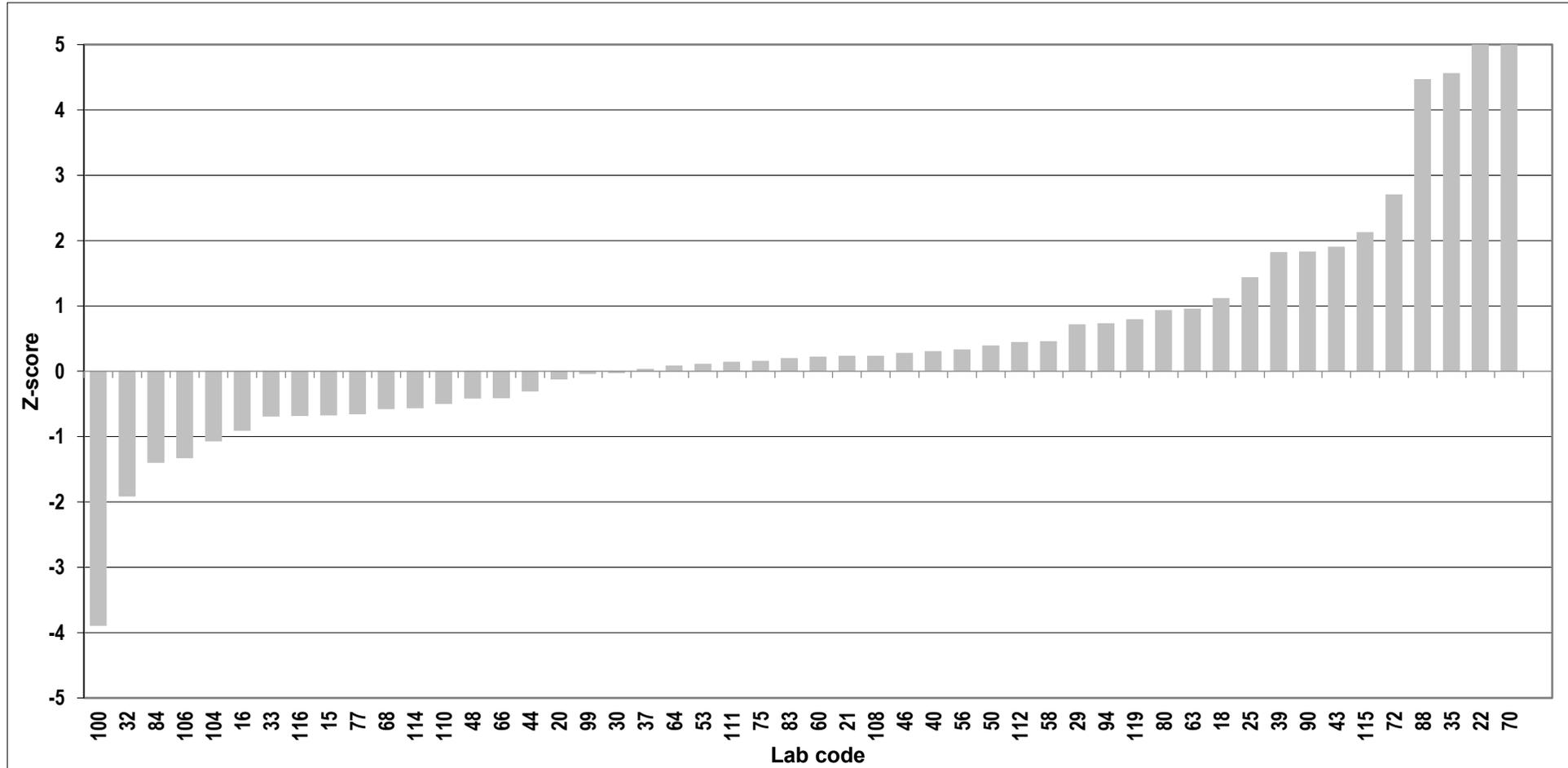
### Z-score Analyte solution; sum indicator PCB



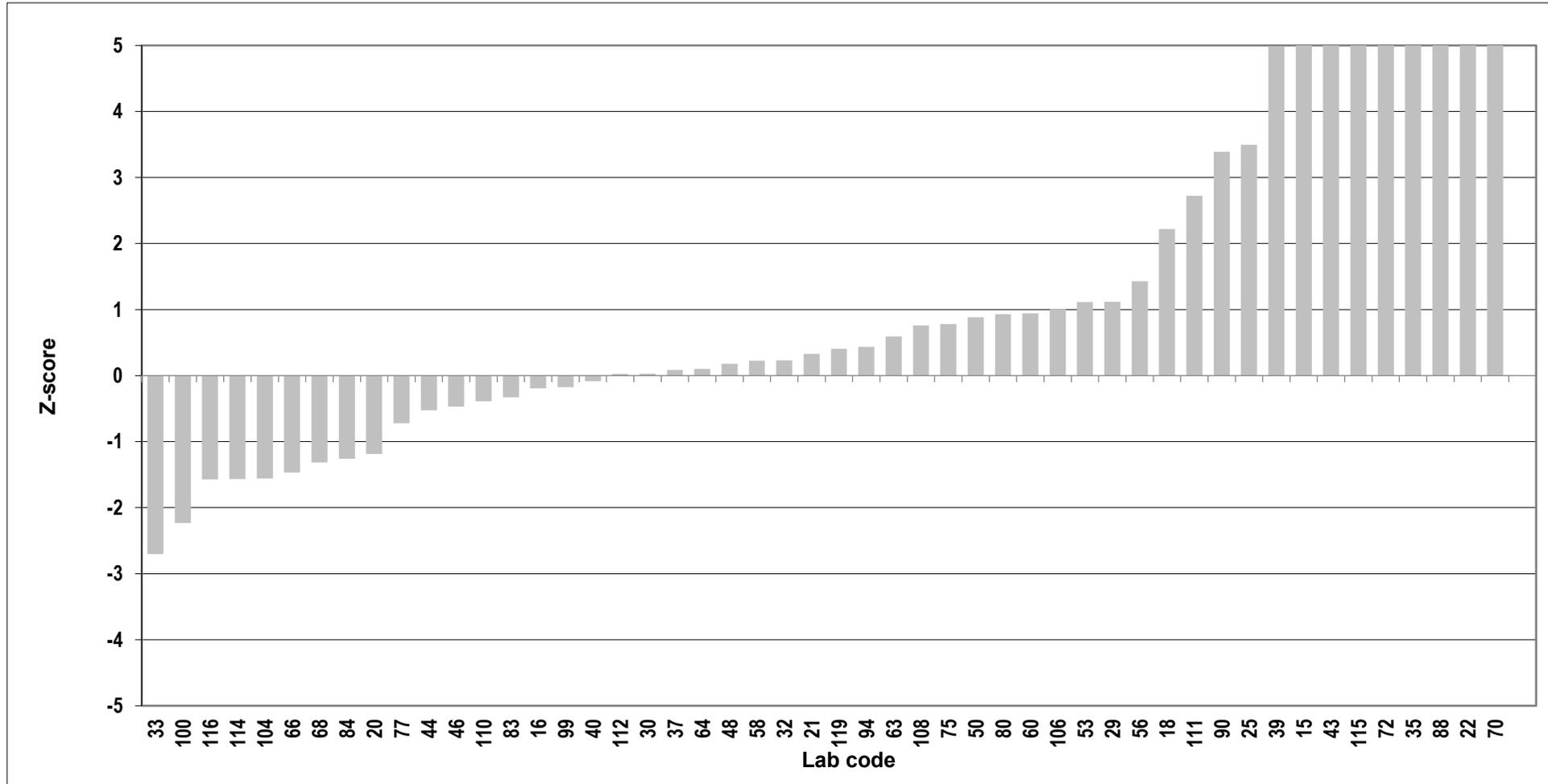
**Z-score Analyte solution; sum PBDE without BDE-209**



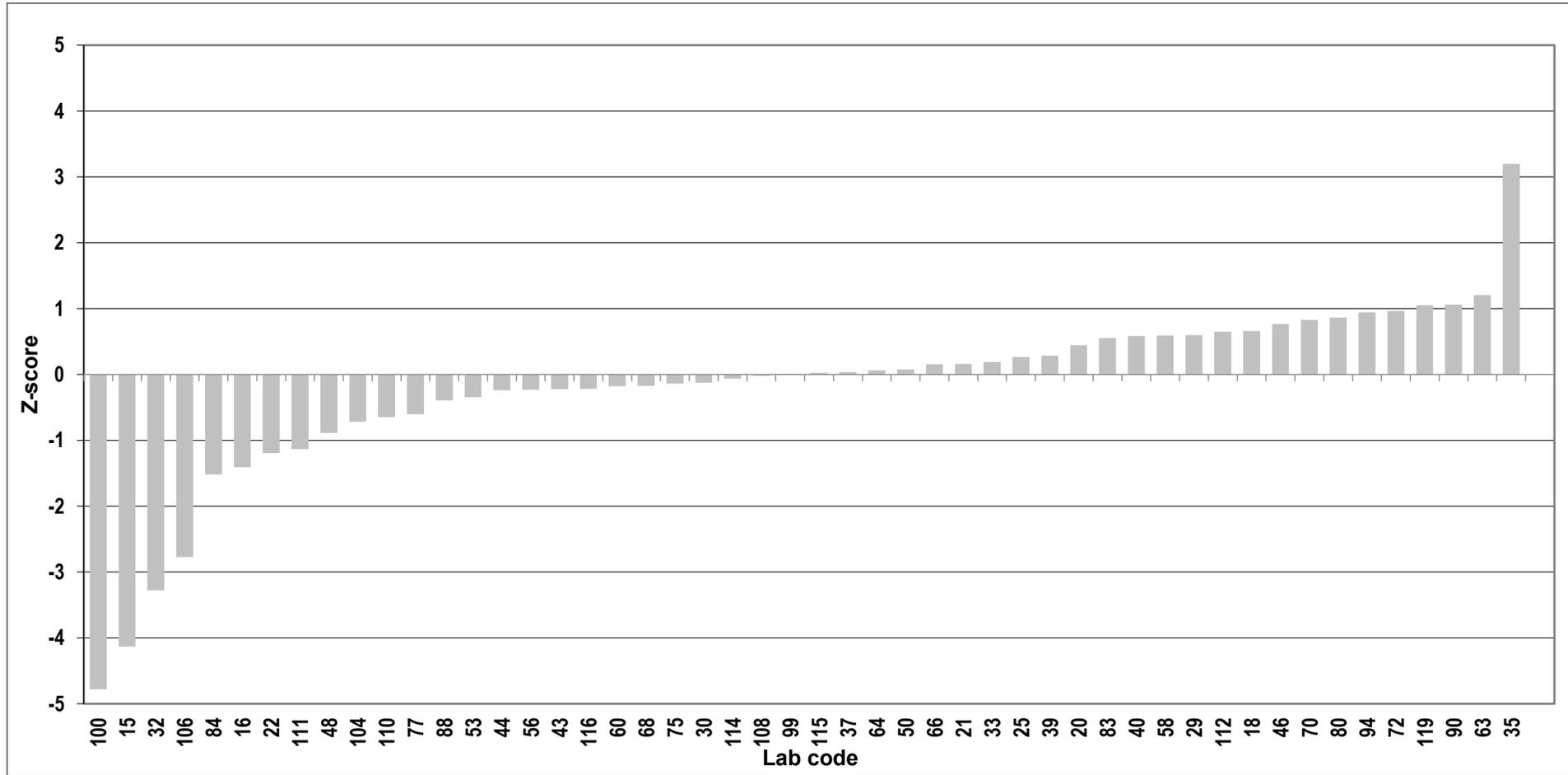
### Z-score Mackerel, fresh weight; total TEQ



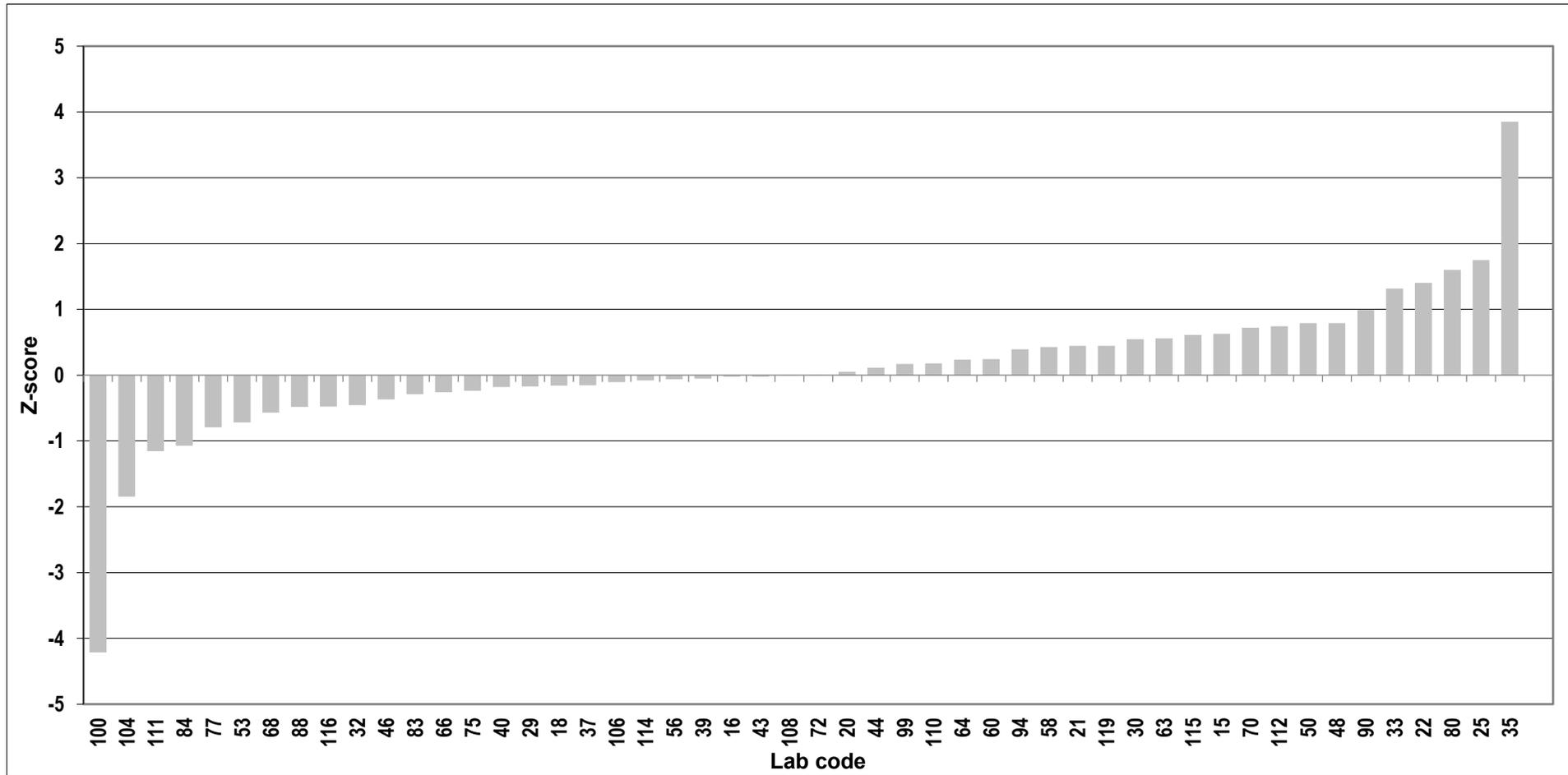
### Z-score Mackerel, fresh weight; PCDD/PCDF TEQ



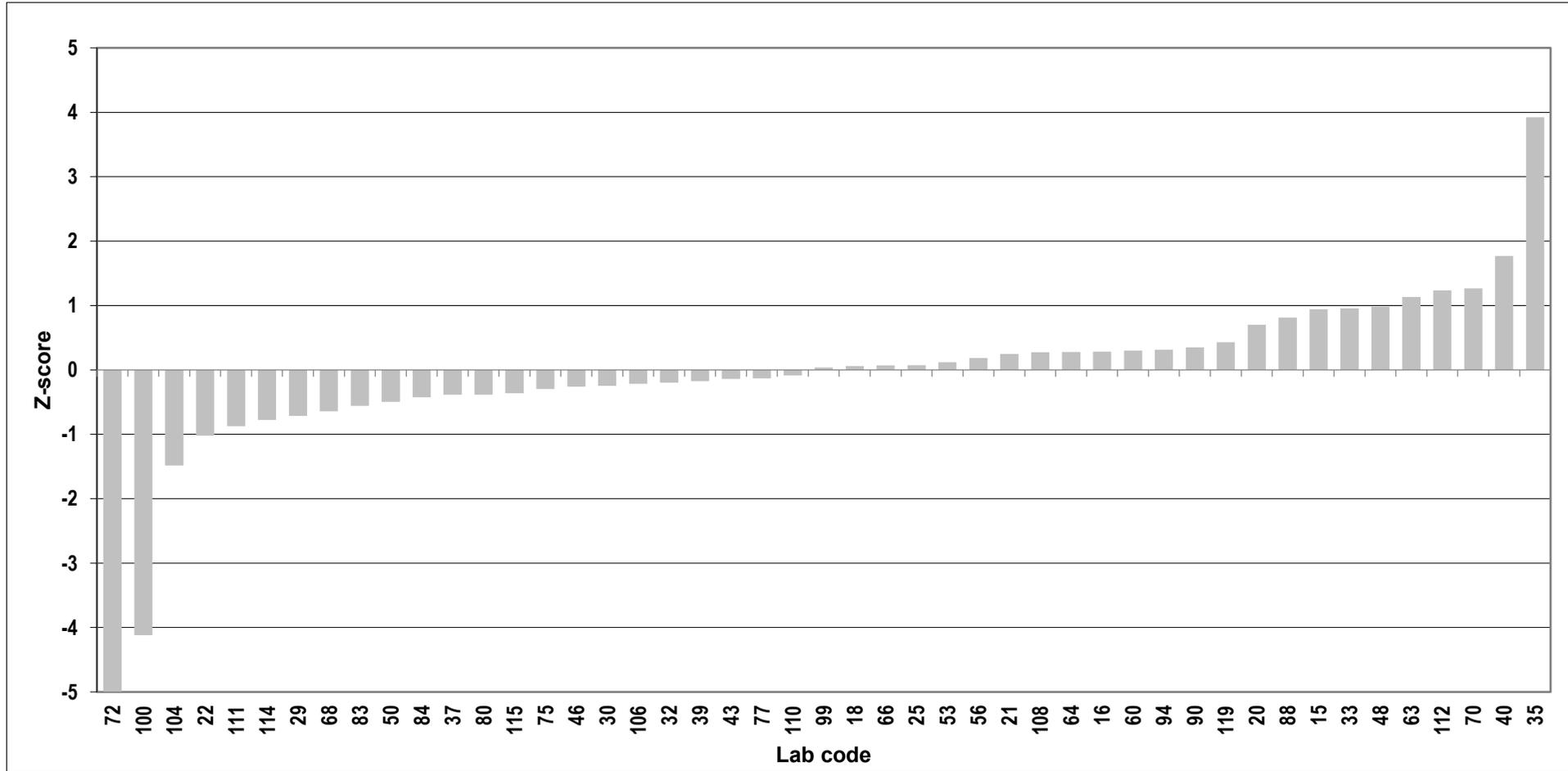
### Z-score Mackerel, fresh weight; non-ortho PCB TEQ



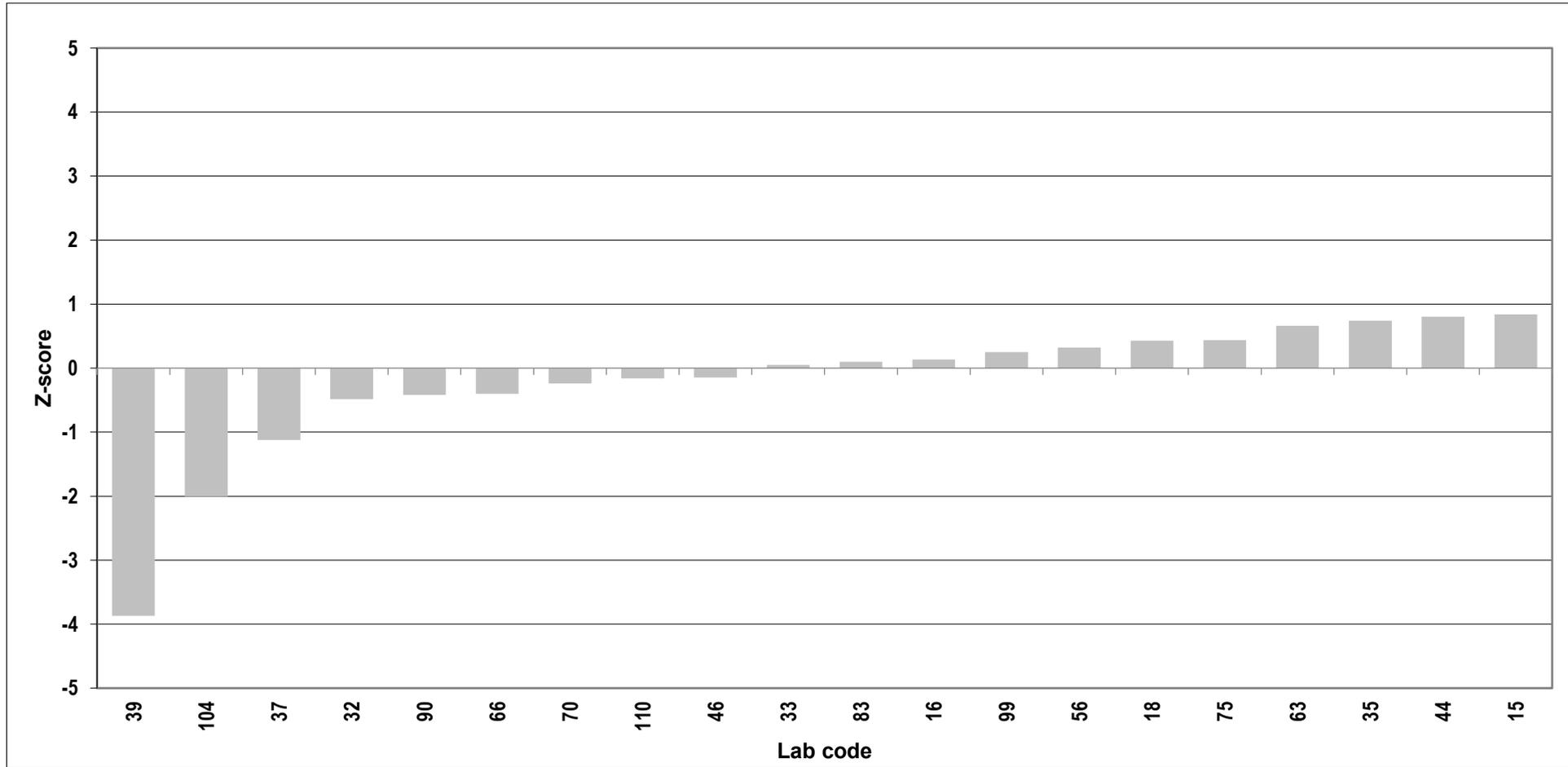
### Z-score Mackerel, fresh weight; mono-ortho PCB TEQ



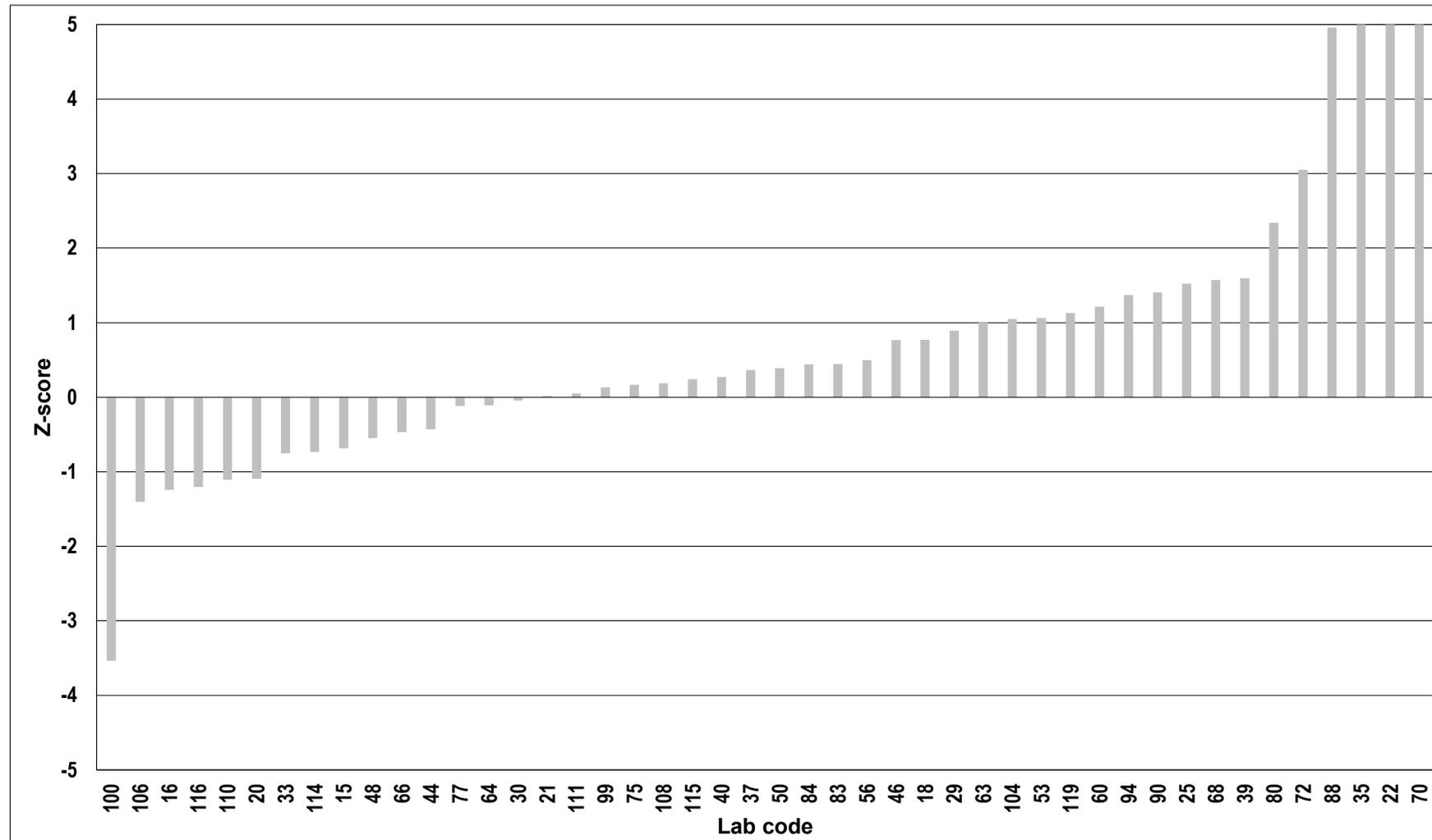
**Z-score Mackerel, fresh weight; sum indicator PCB**



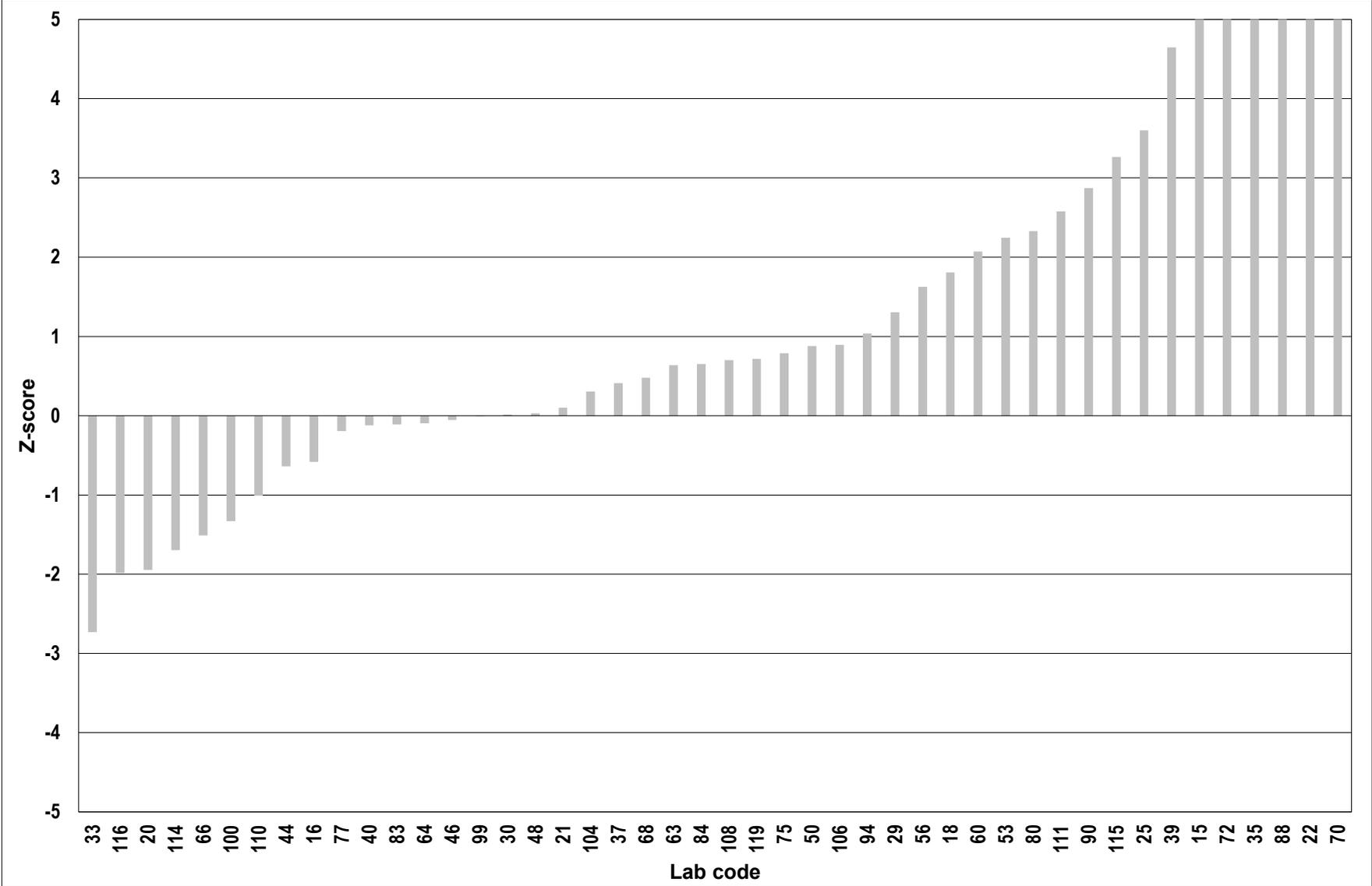
**Z-score Mackerel, fresh weight; sum PBDE without BDE-209**



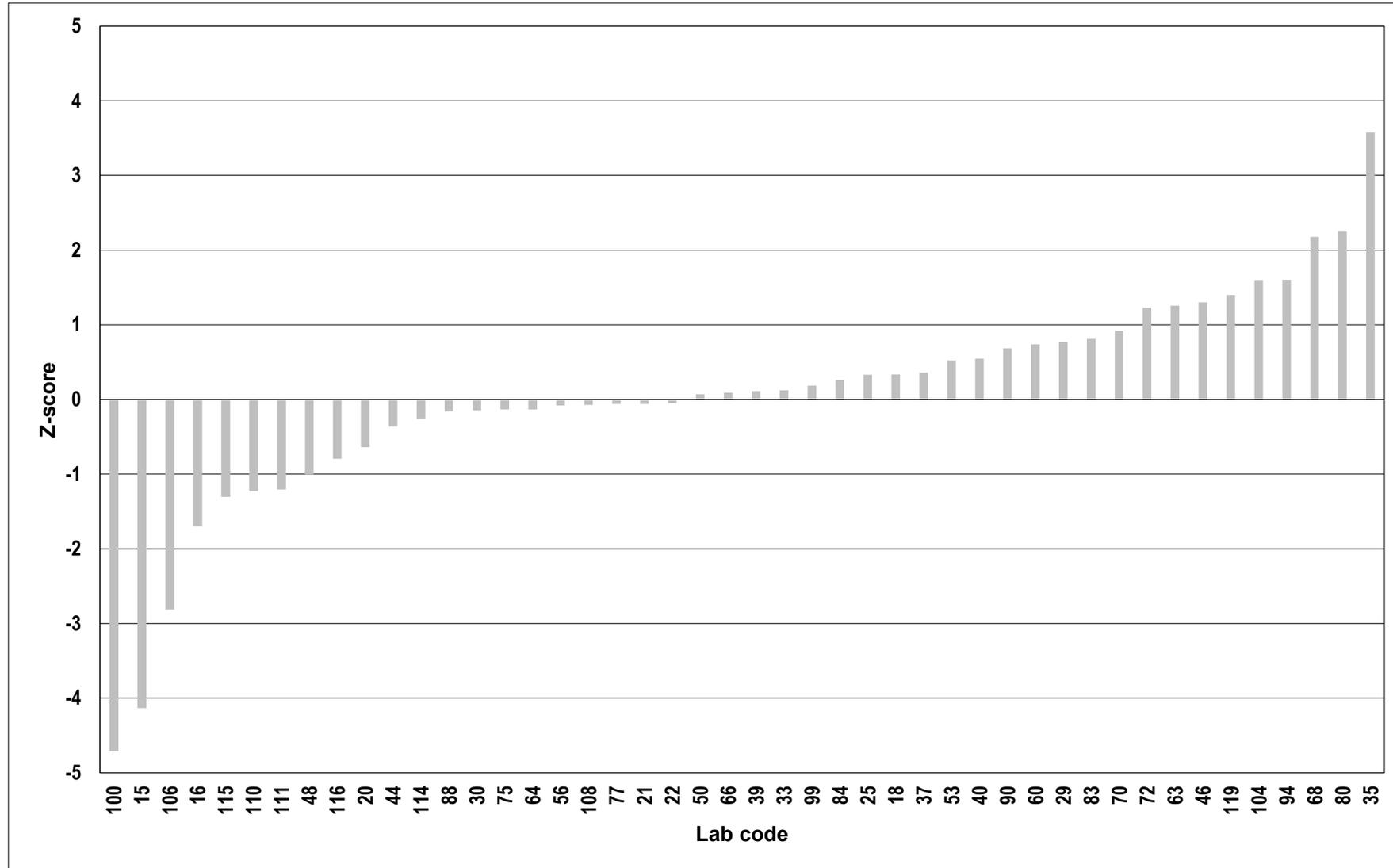
### Z-score Mackerel, lipid weight; total TEQ



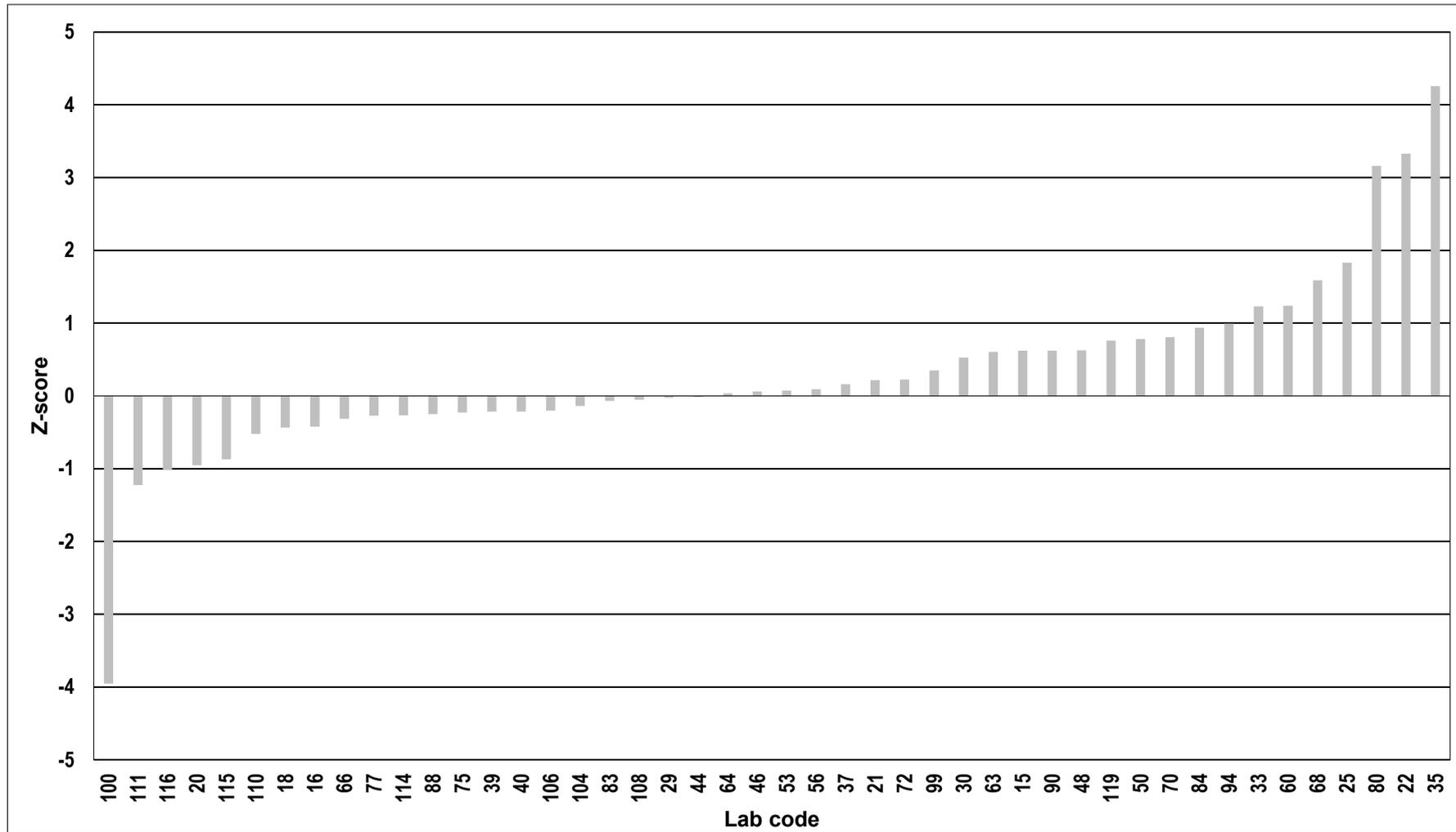
**Z-score Mackerel, lipid weight; PCDD/PCDF TEQ**



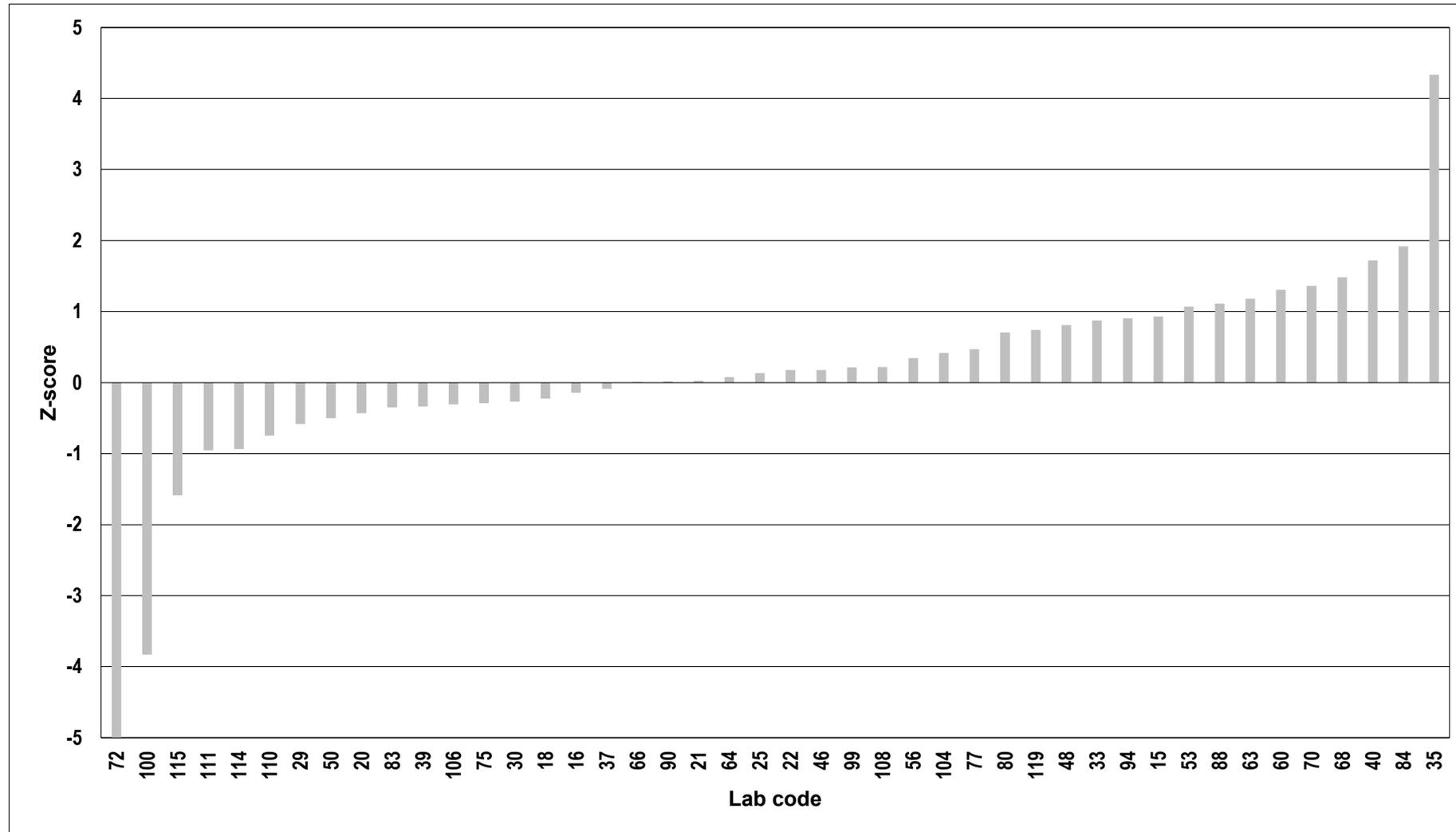
### Z-score Mackerel, lipid weight; non-ortho PCB TEQ



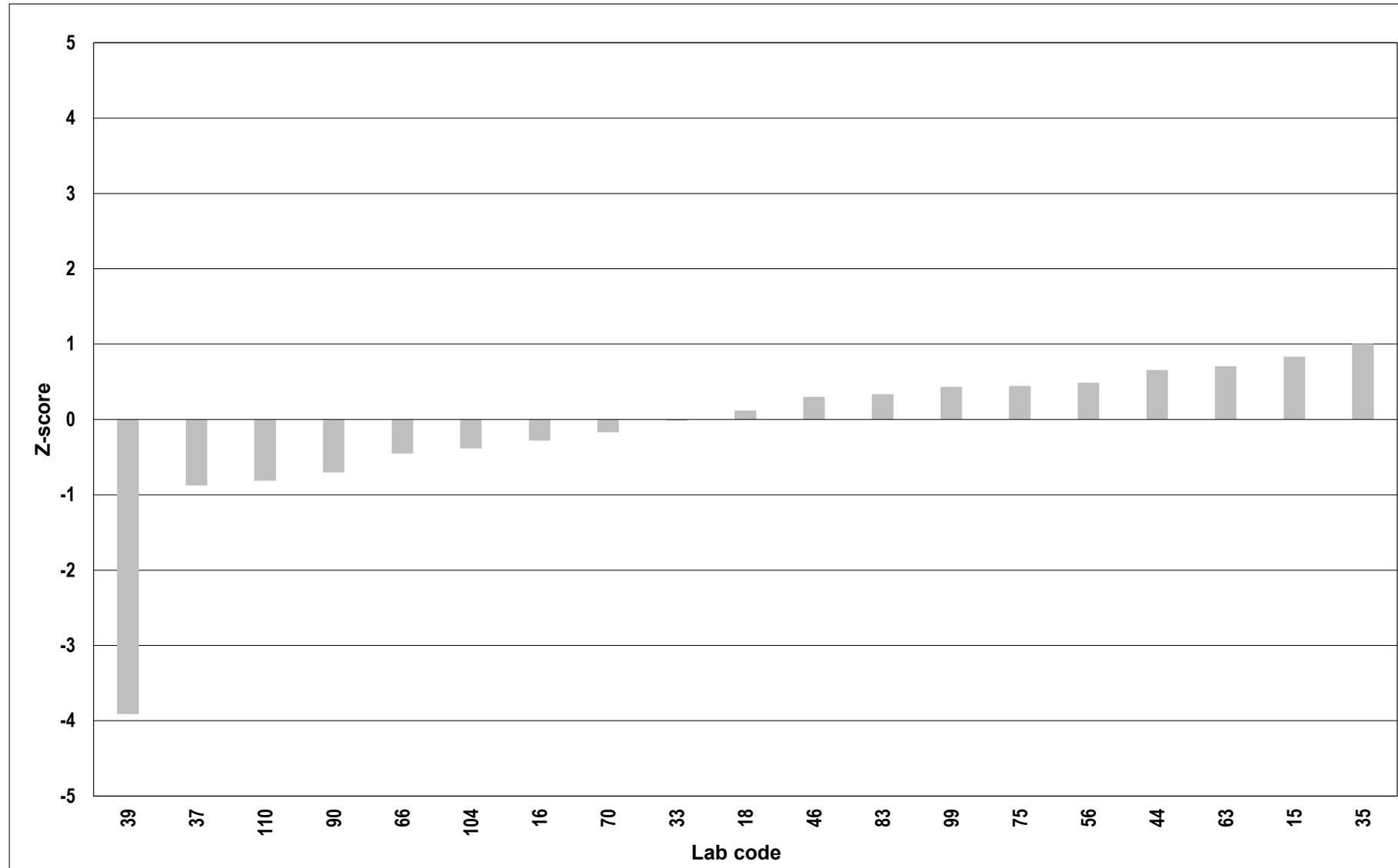
### Z-score Mackerel, lipid weight; mono-ortho PCB TEQ



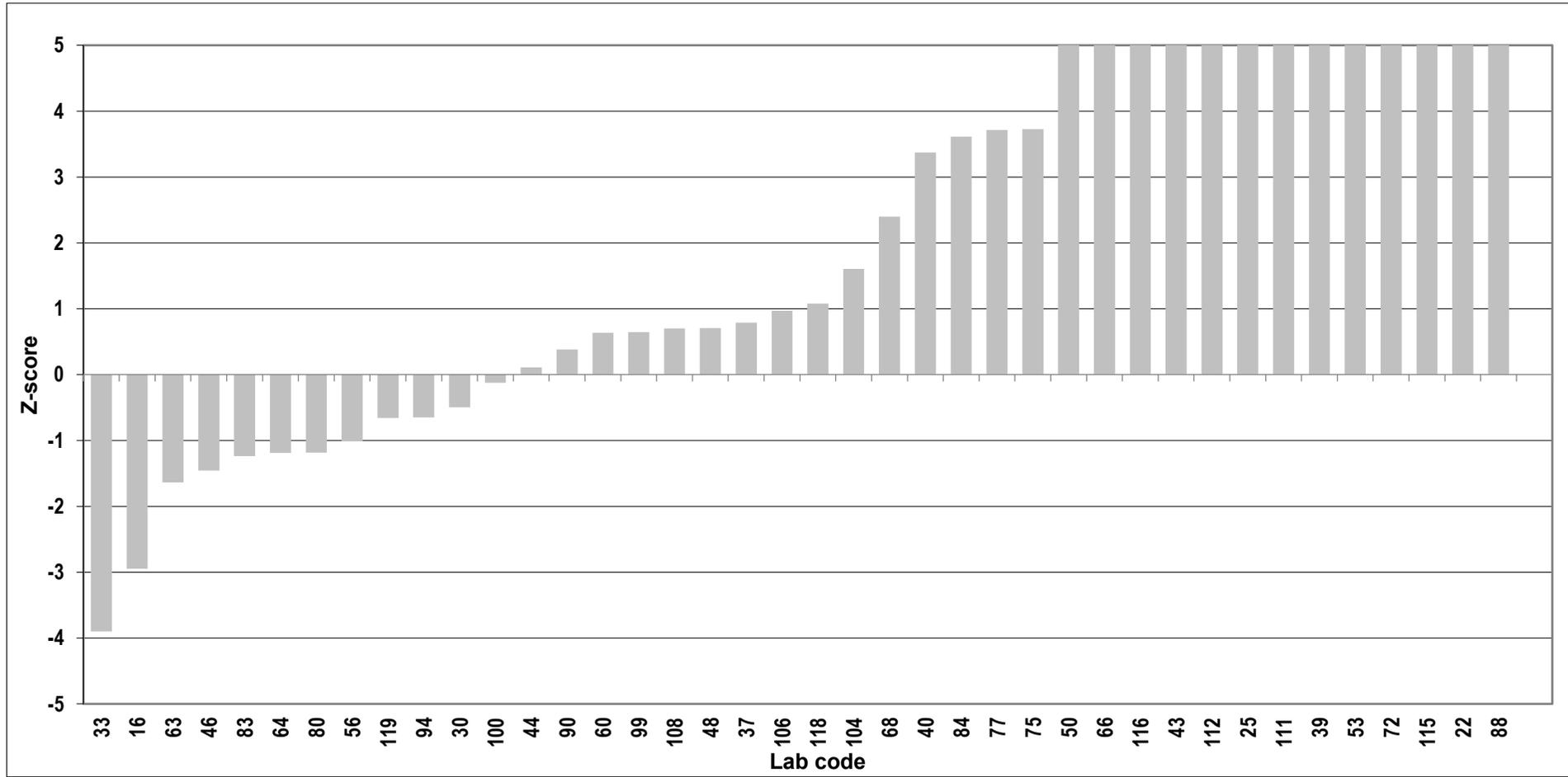
### Z-score Mackerel, lipid weight; sum indicator PCB



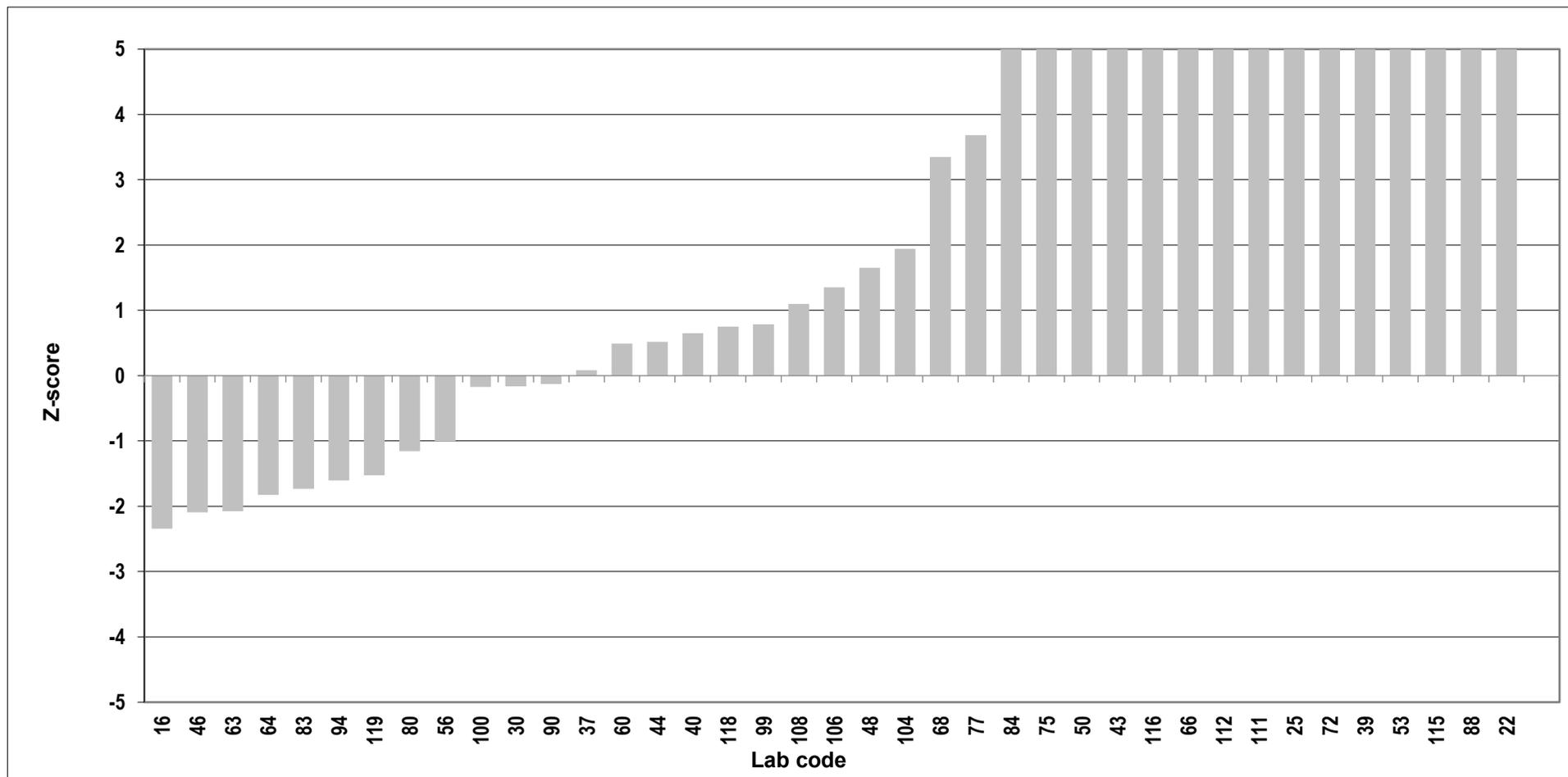
**Z-score Mackerel, lipid weight; sum PBDE without PBDE-209**



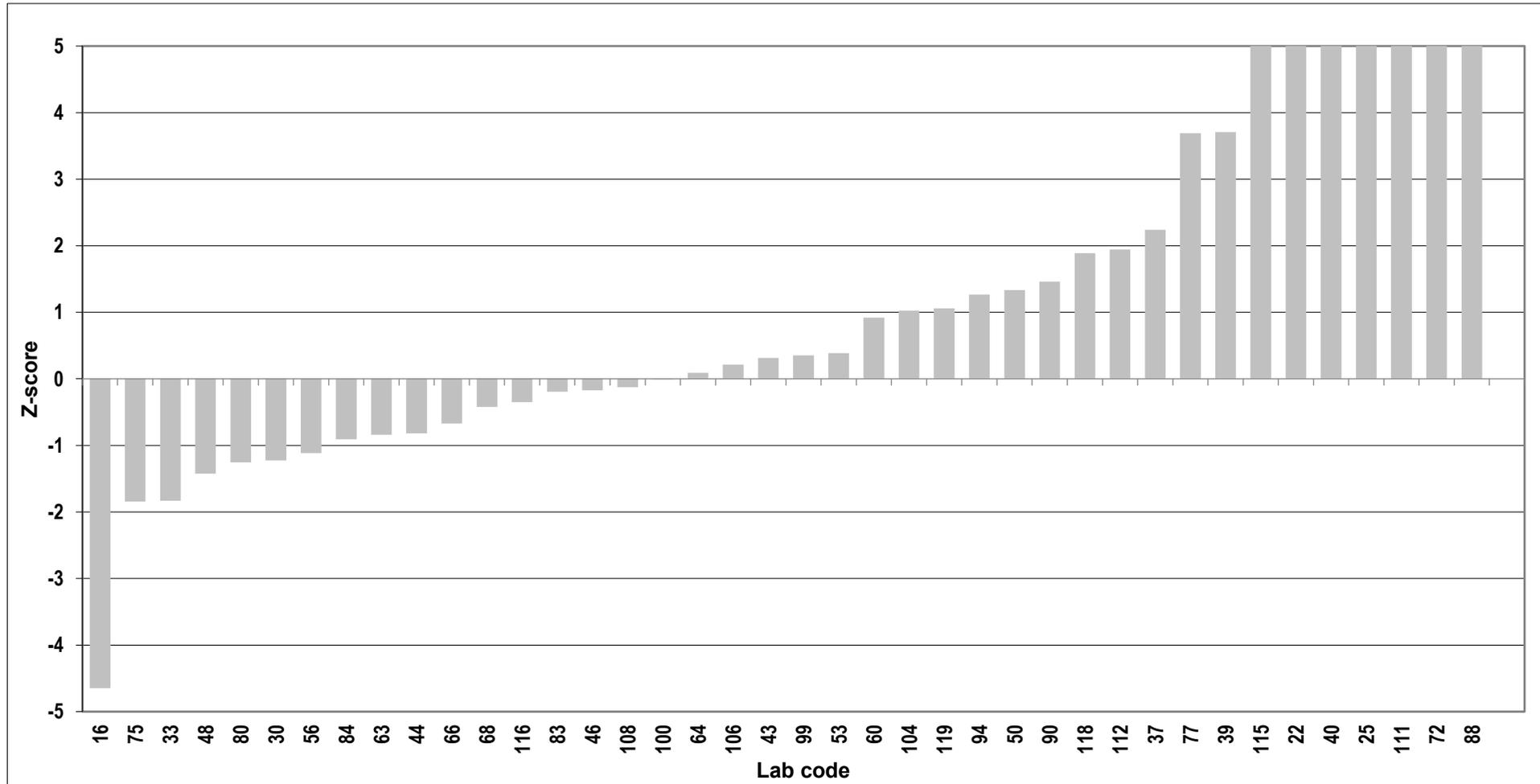
### Z-score Cream, fresh weight; total TEQ



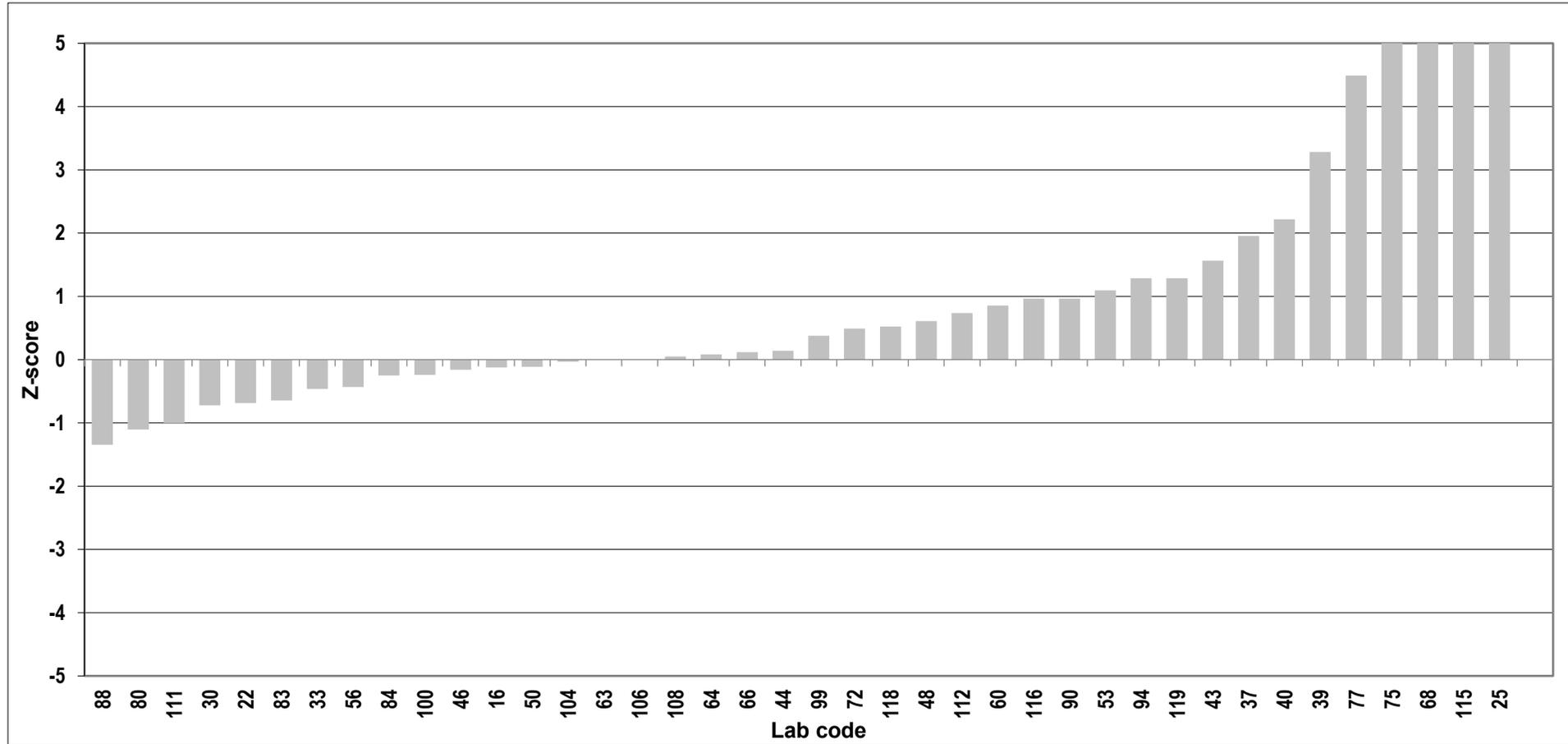
### Z-score Cream, fresh weight; PCDD/PCDF TEQ



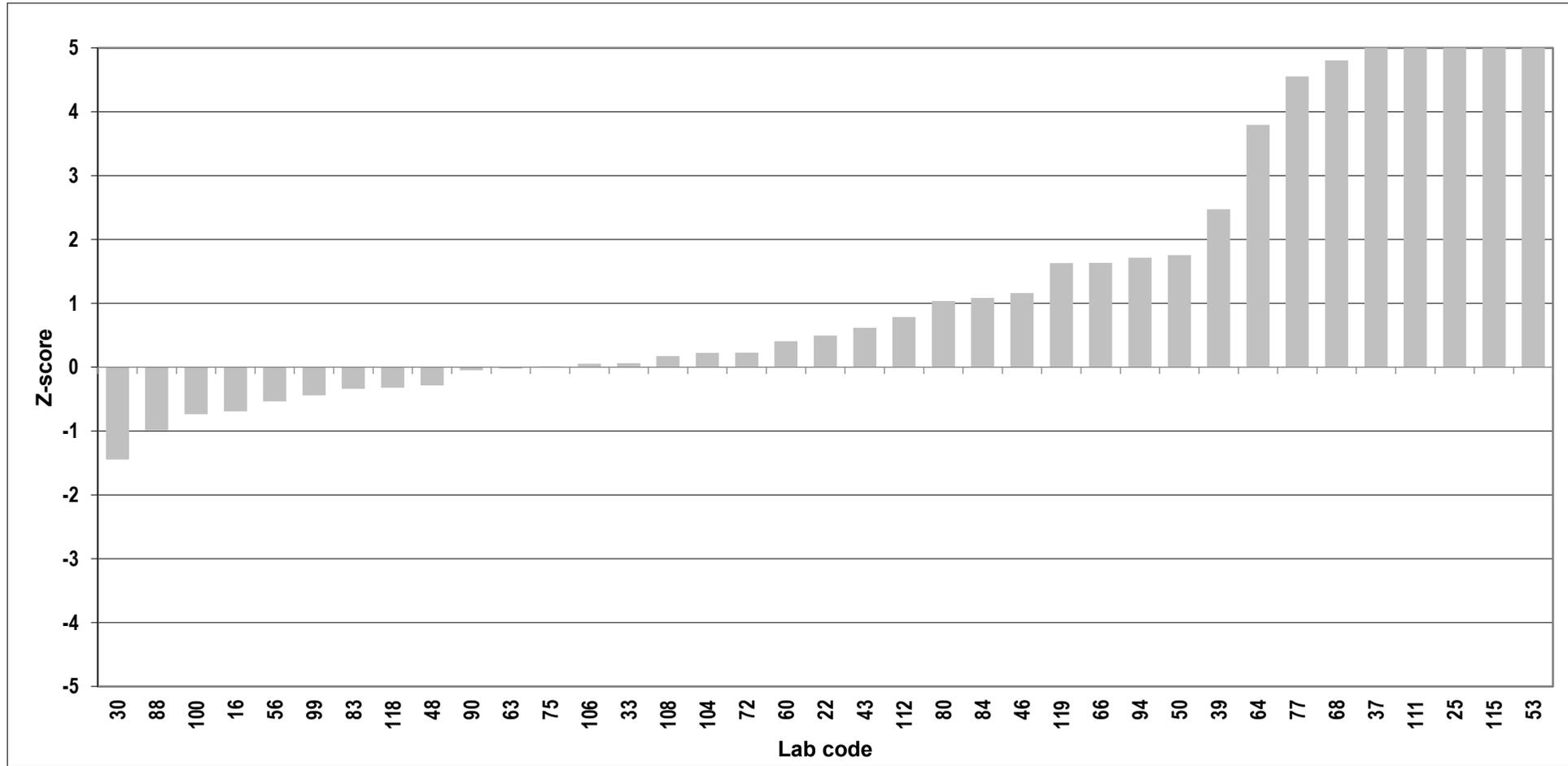
### Z-score Cream, fresh weight; non-ortho PCB TEQ



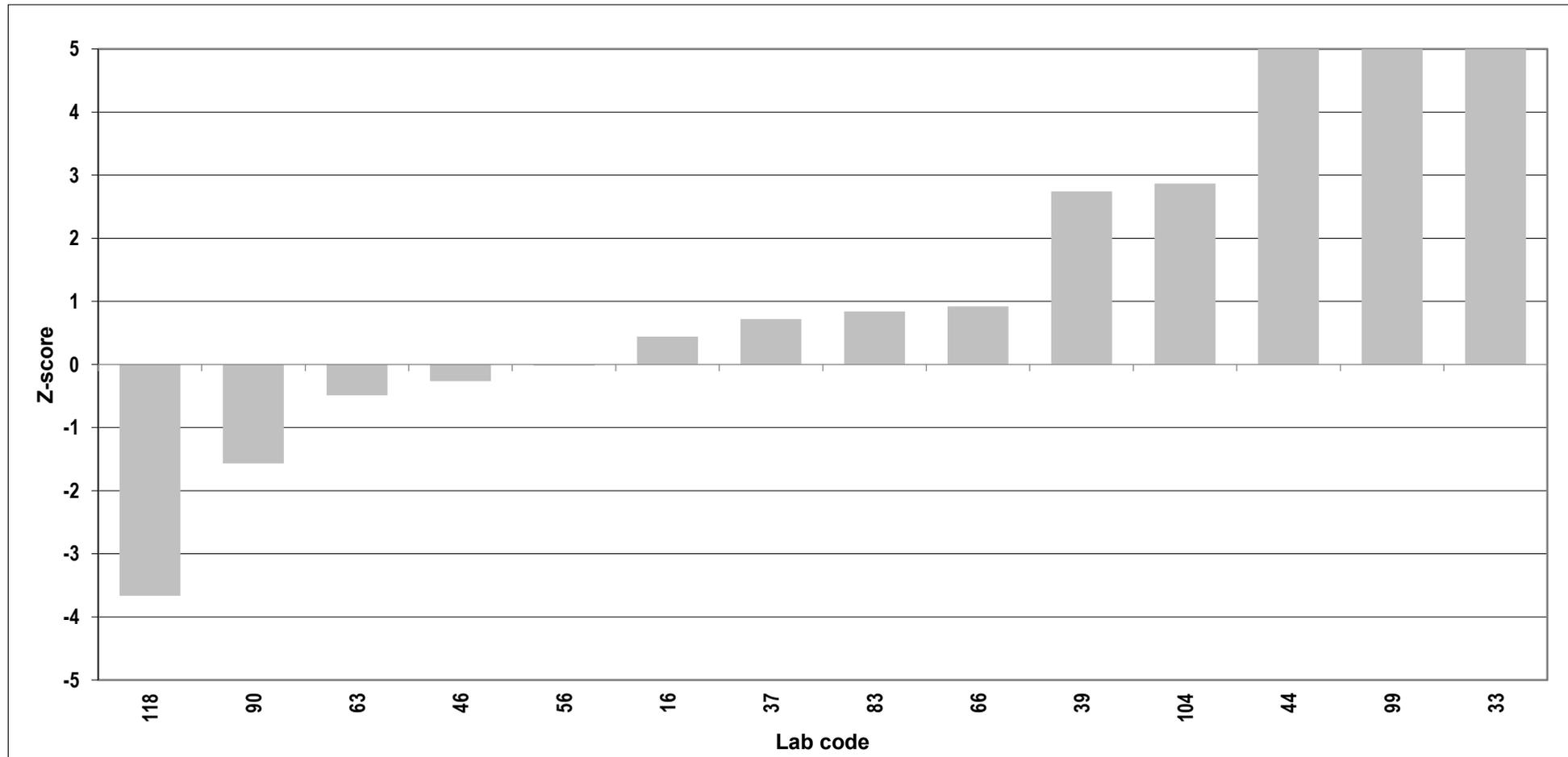
### Z-score Cream, fresh weight; mono-ortho PCB TEQ



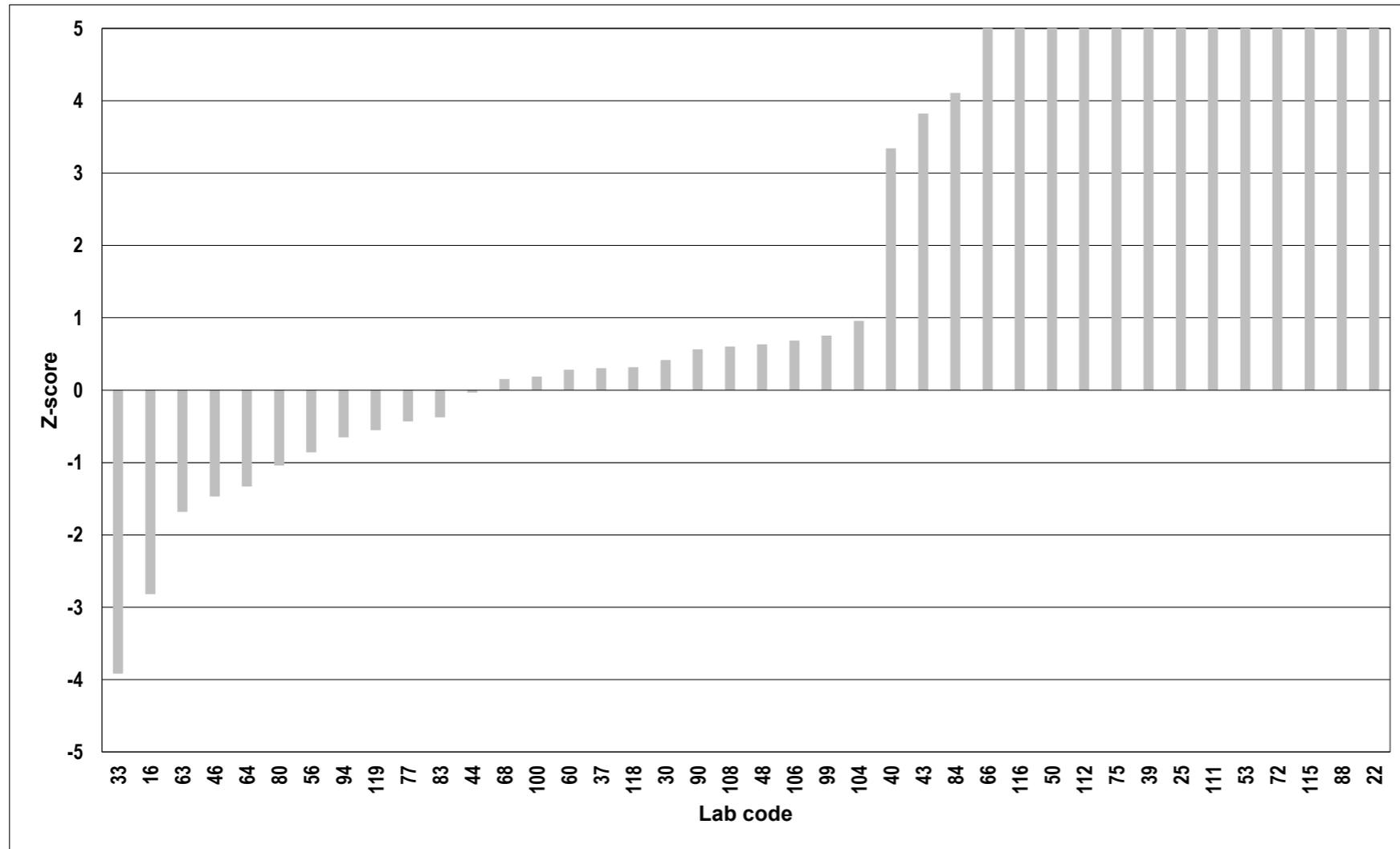
### Z-score Cream, fresh weight; sum indicator PCB



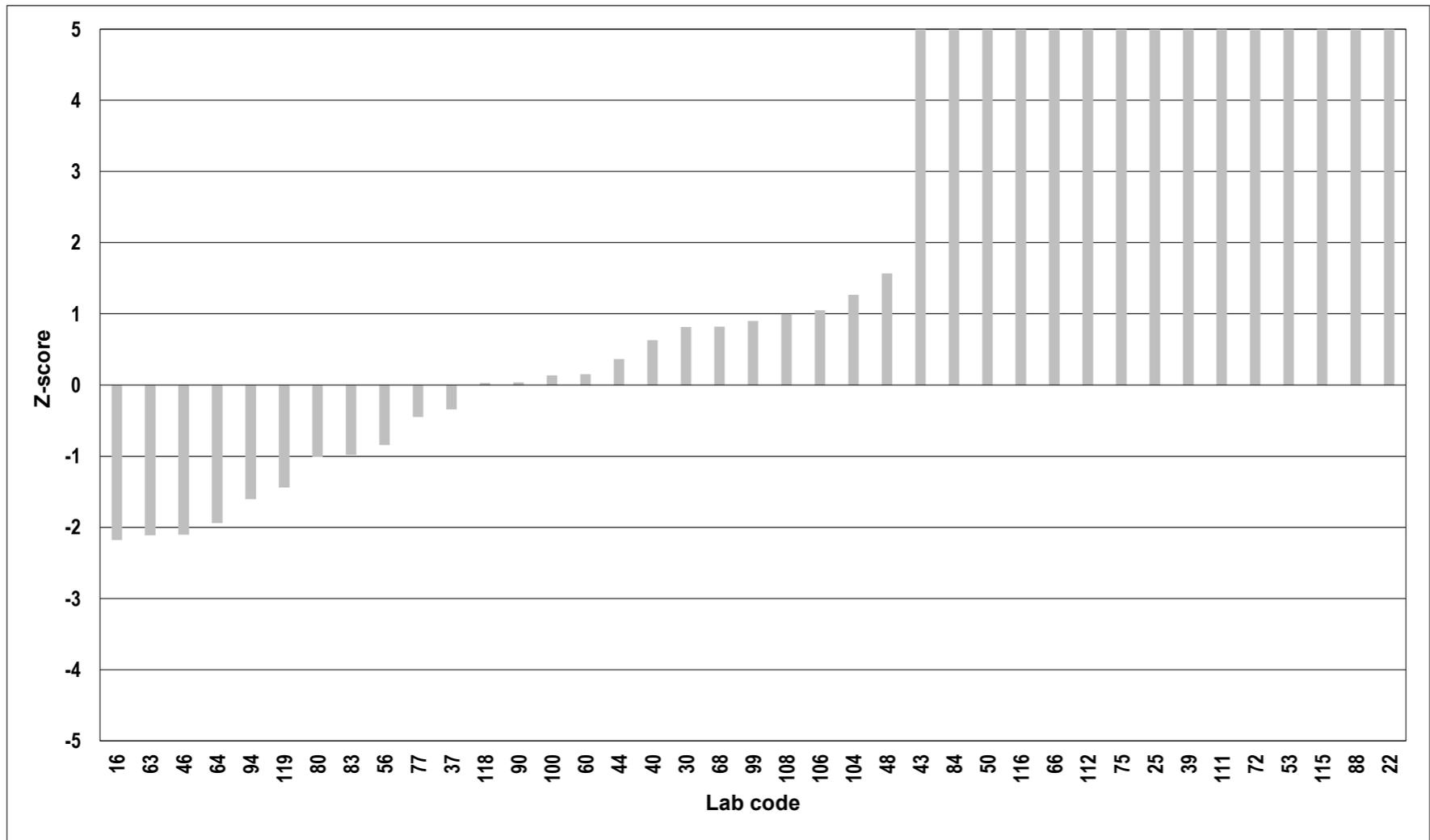
**Z-score Cream, fresh weight; sum PBDE without BDE-209**



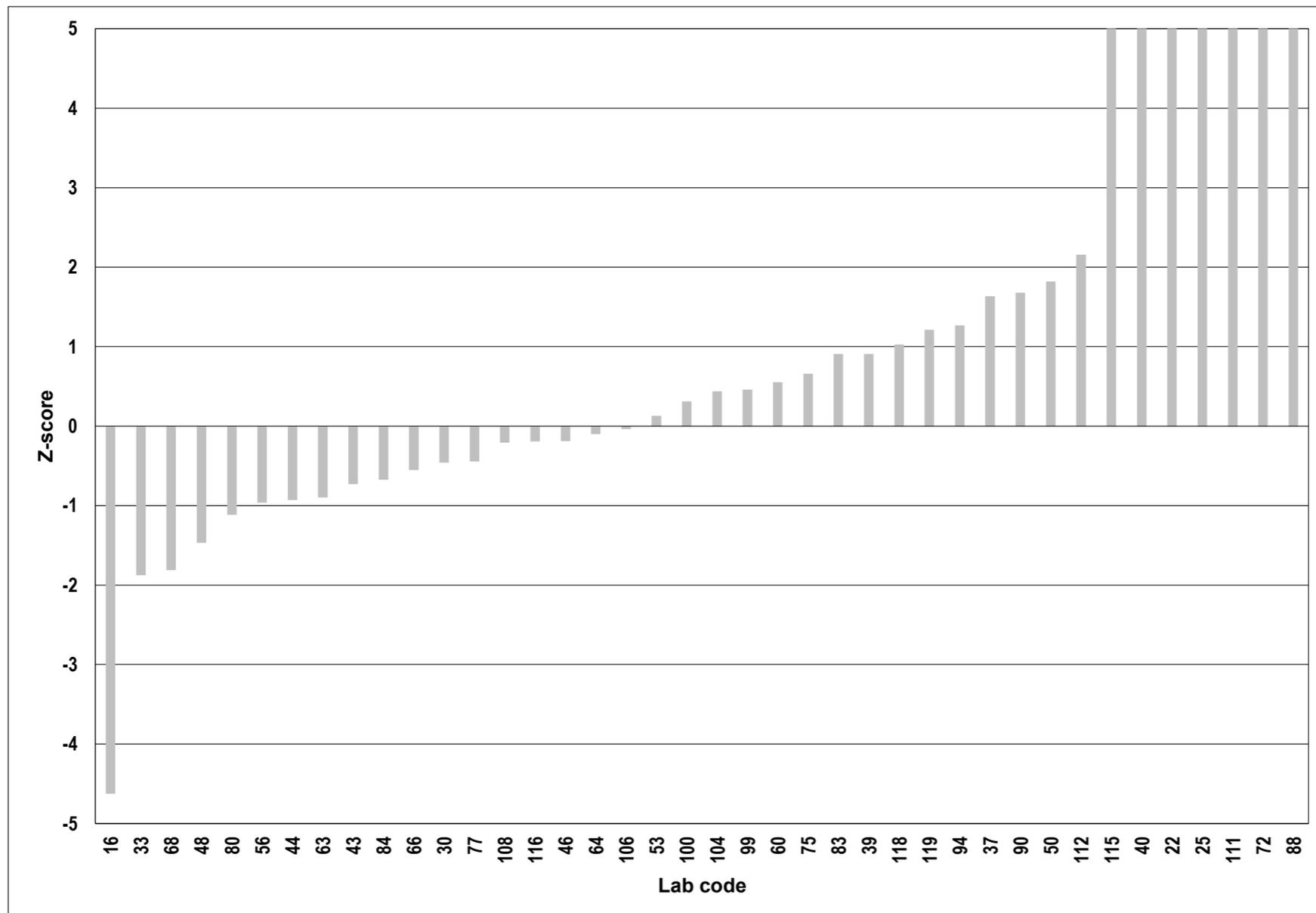
### Z-score Cream, lipid weight; total TEQ



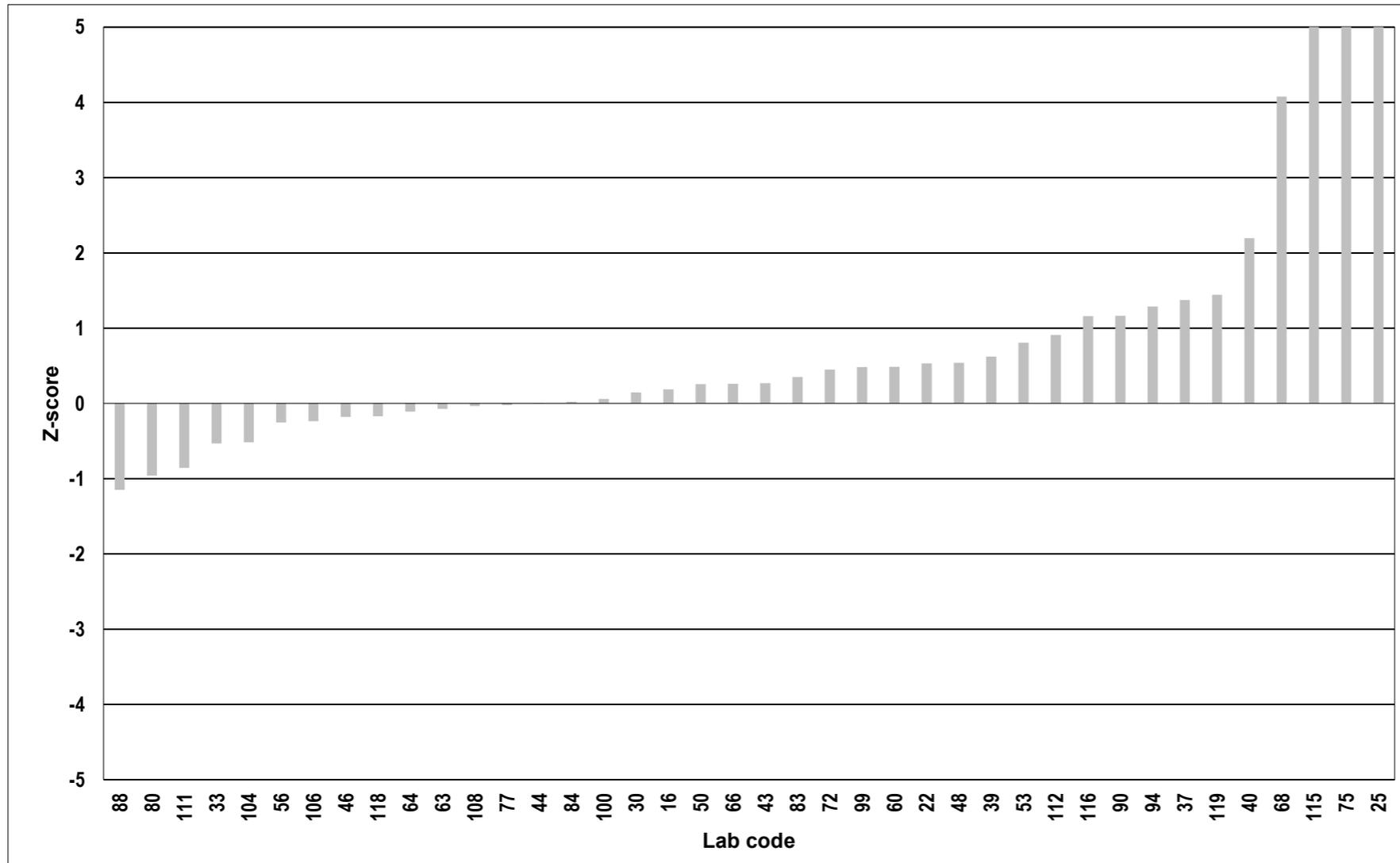
### Z-score Cream, lipid weight; PCDD/PCDF TEQ



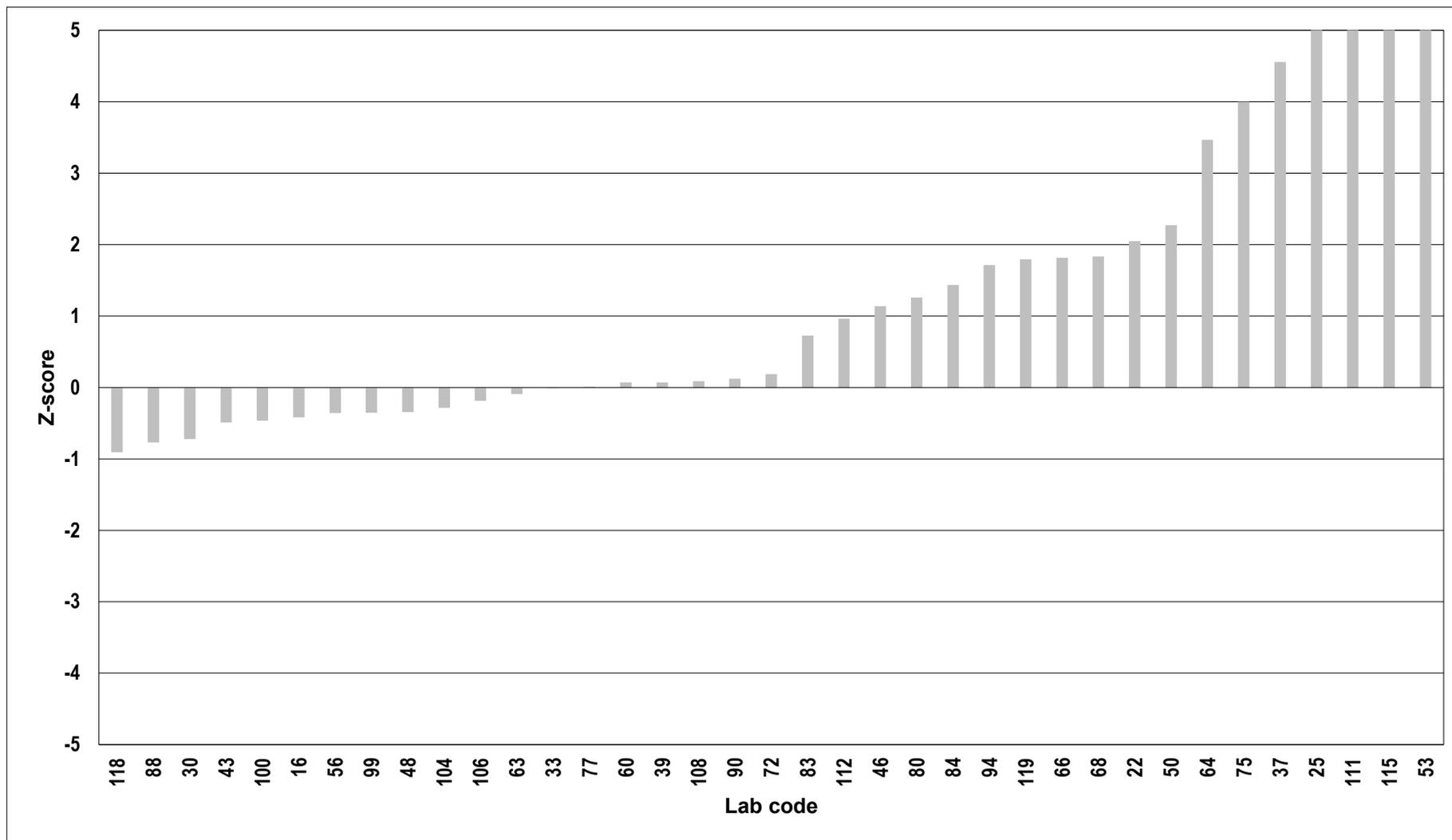
### Z-score Cream, lipid weight; non-ortho PCB TEQ



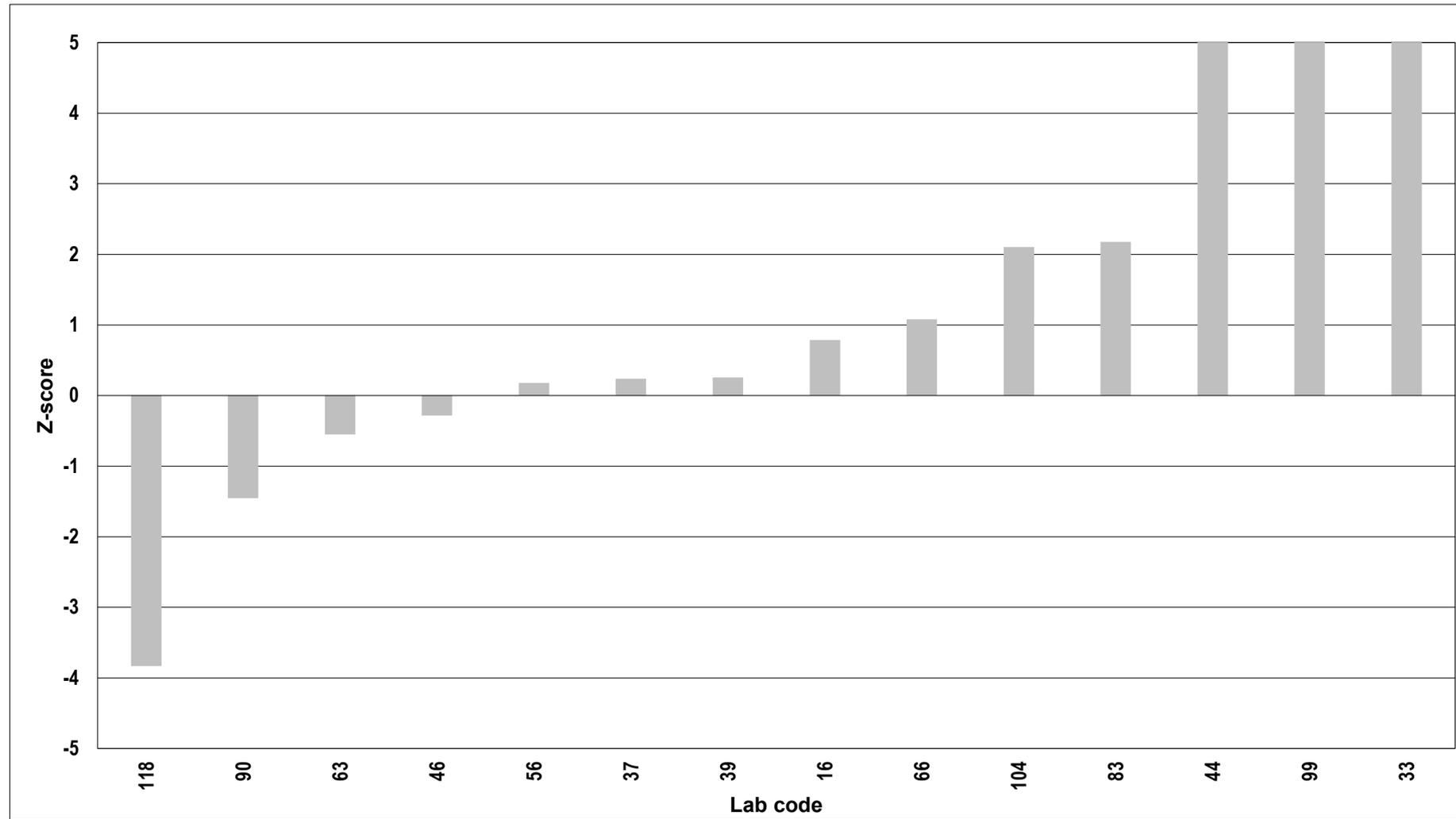
### Z-score Cream, lipid weight; mono-ortho PCB TEQ



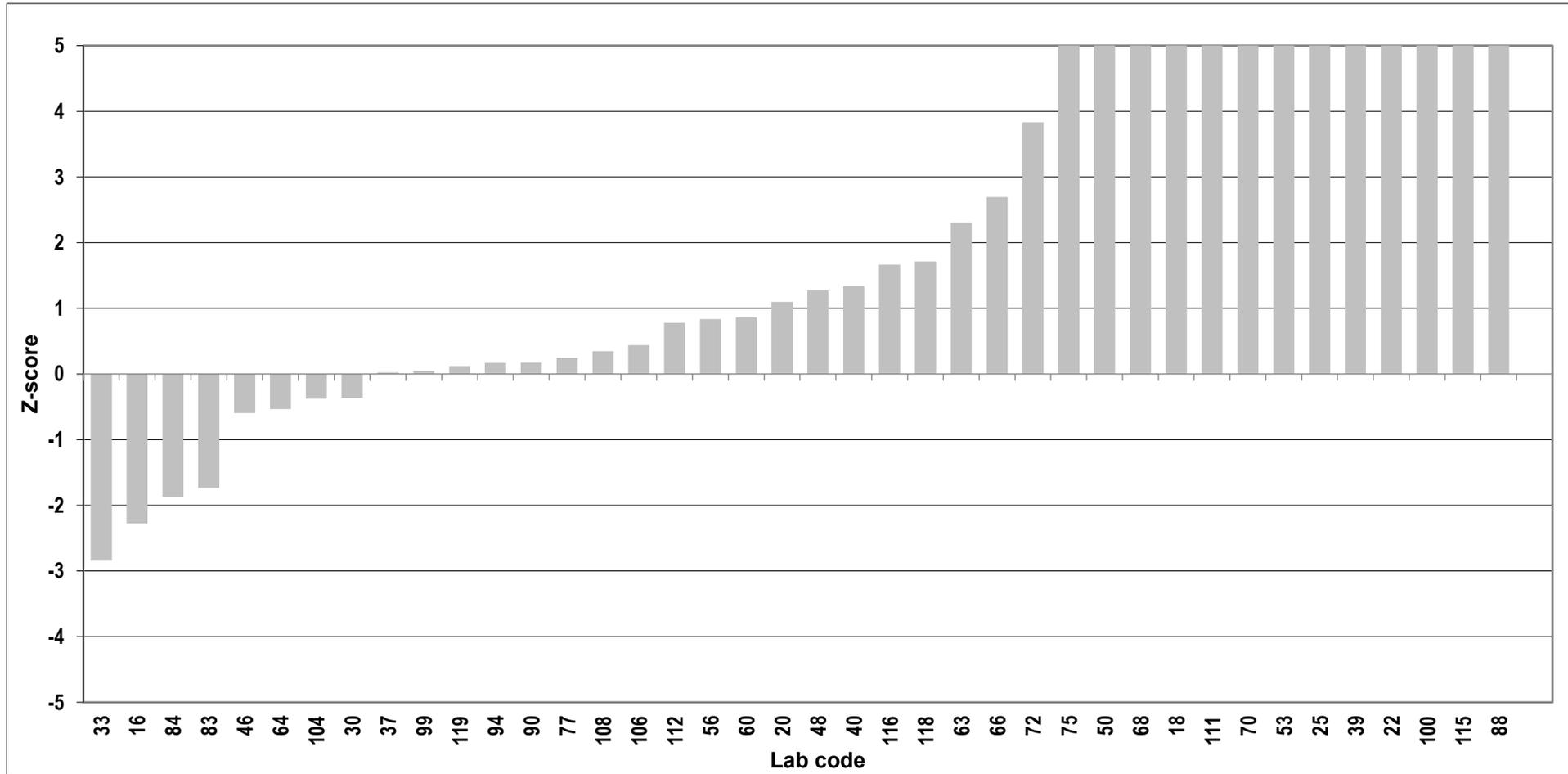
### Z-score Cream, lipid weight; sum indicator PCB



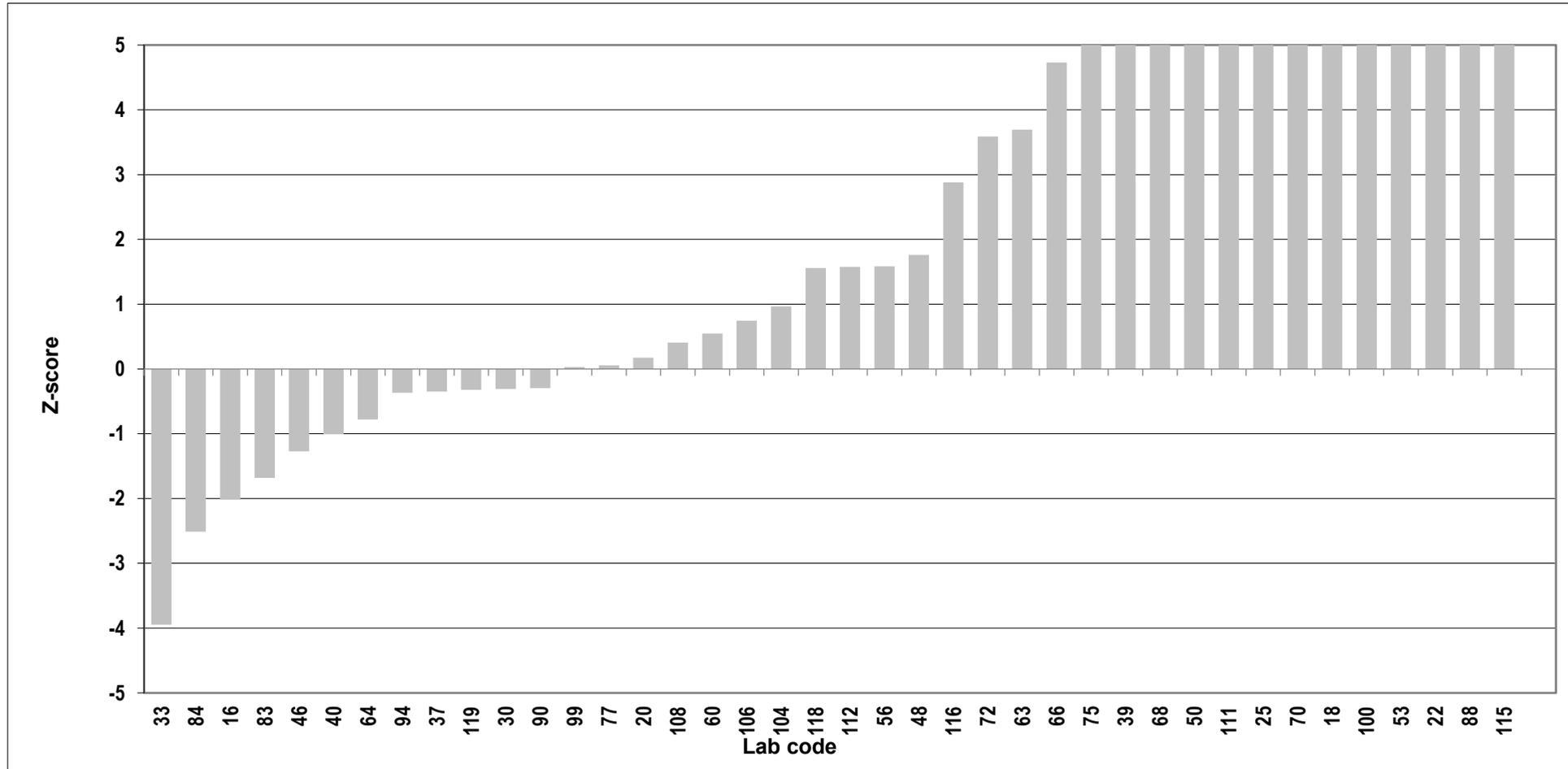
**Z-score Cream, lipid weight; sum PBDE without PBDE-209**



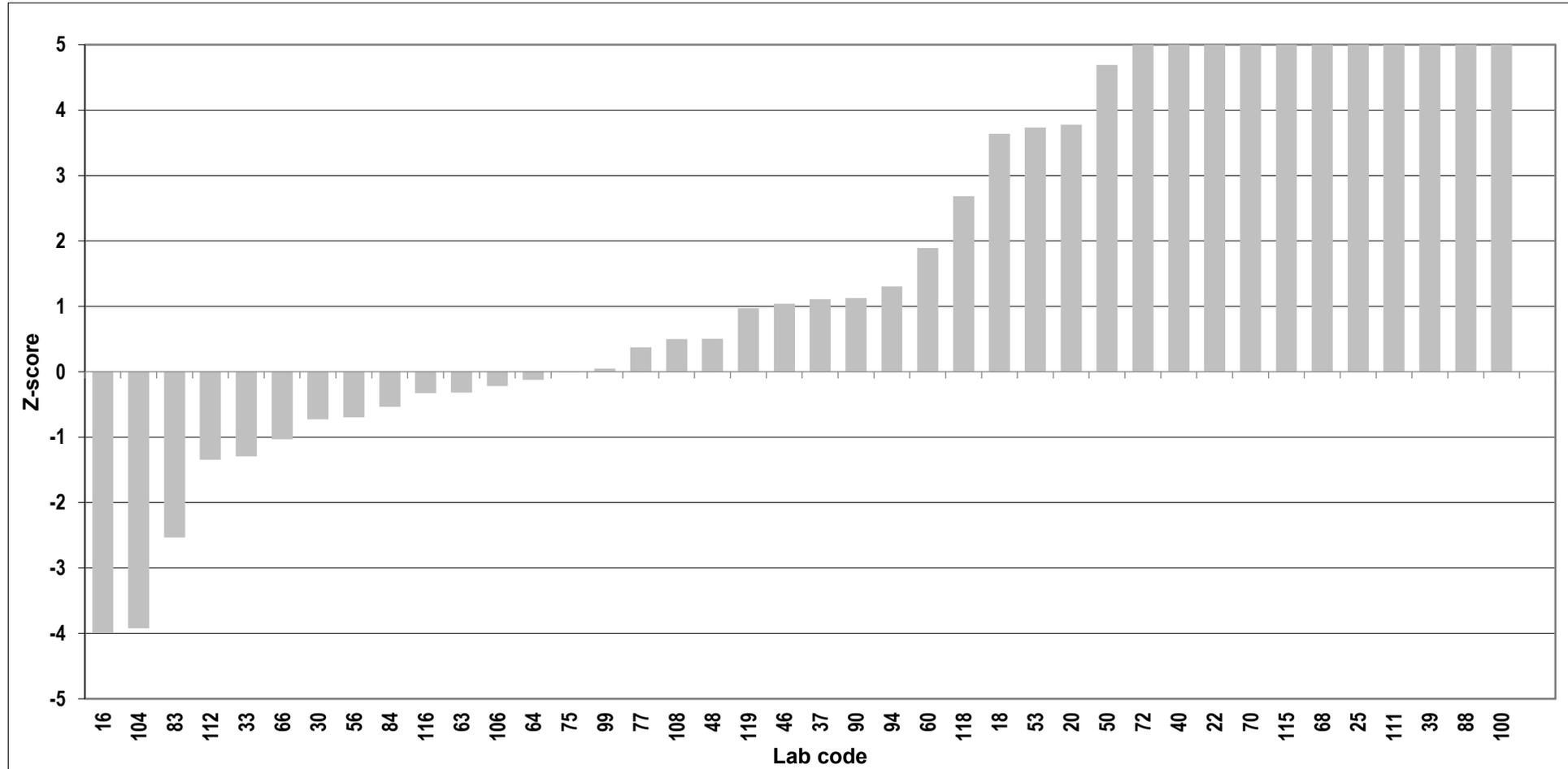
### Z-score Egg yolk, fresh weight; total TEQ



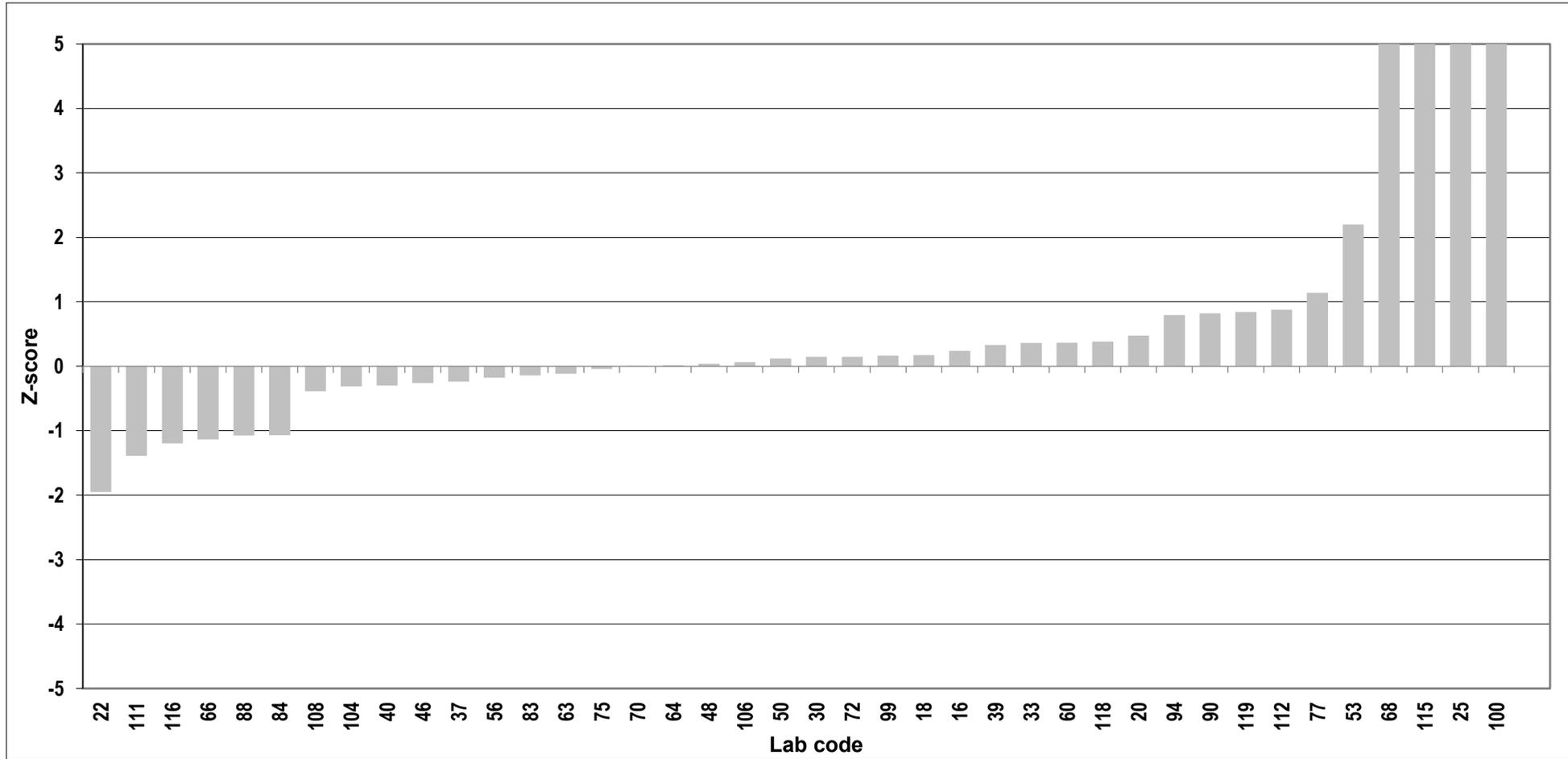
### Z-score Egg yolk, fresh weight; PCDD/PCDF TEQ



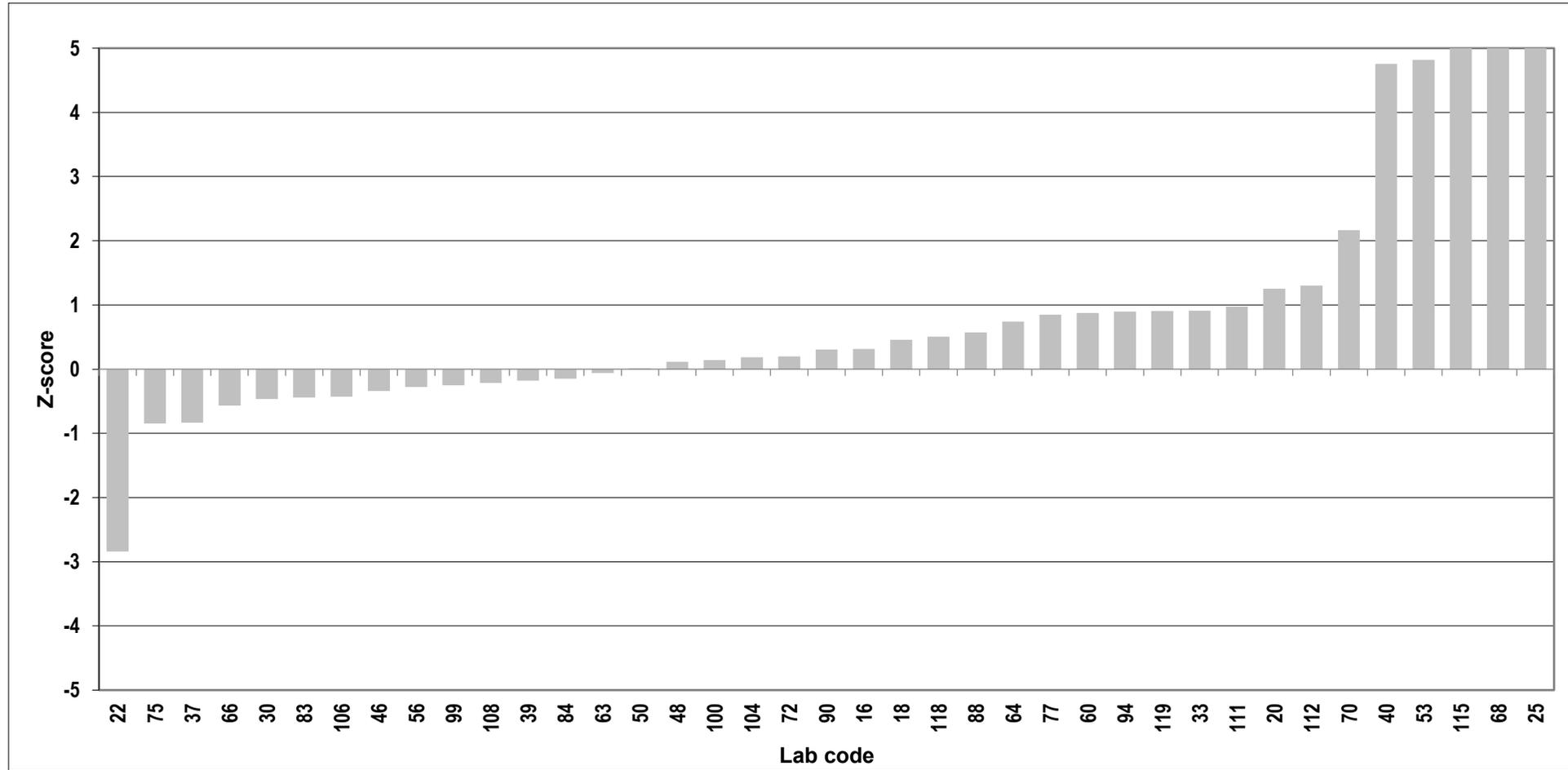
### Z-score Egg yolk, fresh weight; non-ortho PCB TEQ



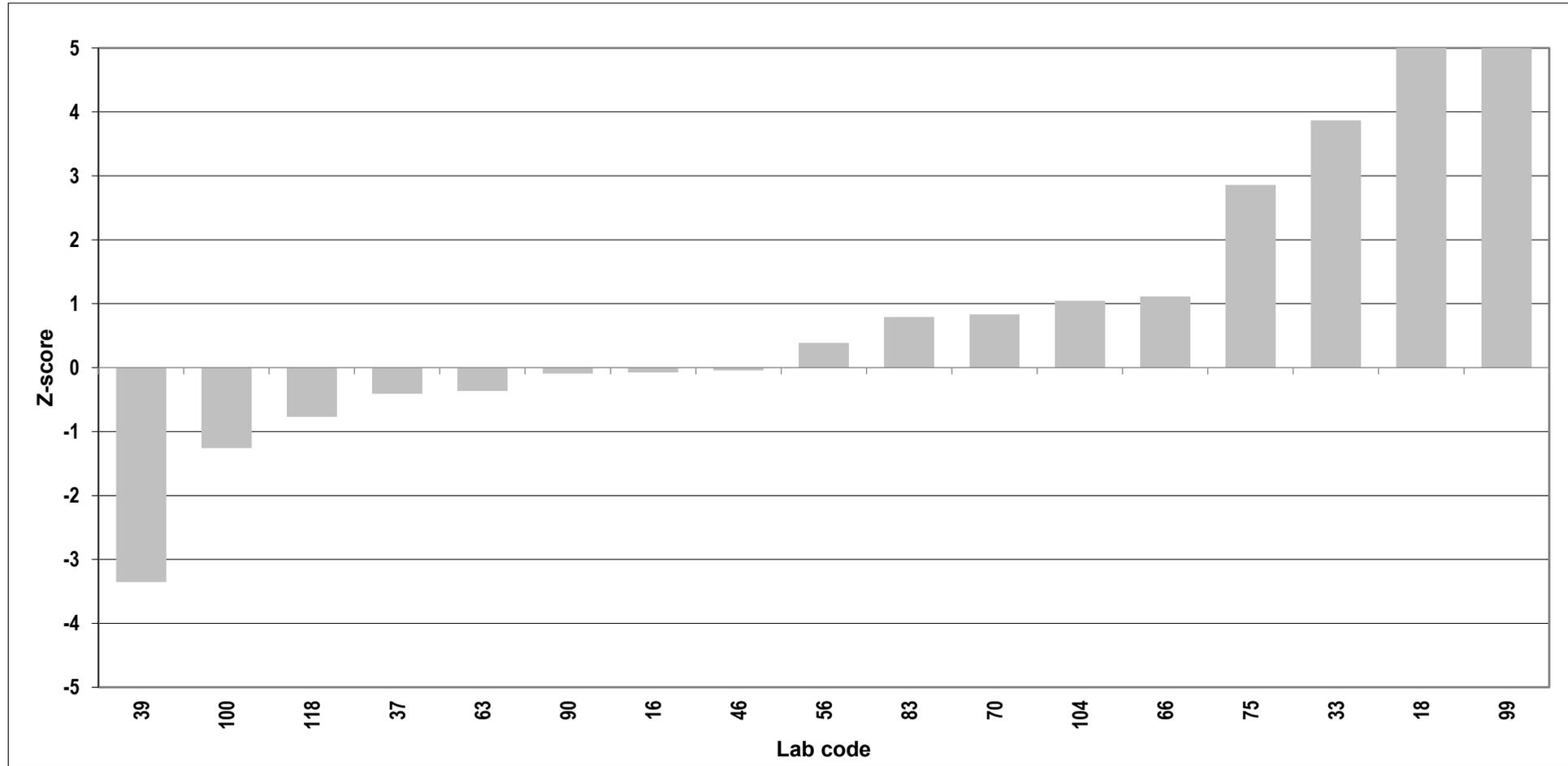
### Z-score Egg yolk, fresh weight; mono-ortho PCB TEQ



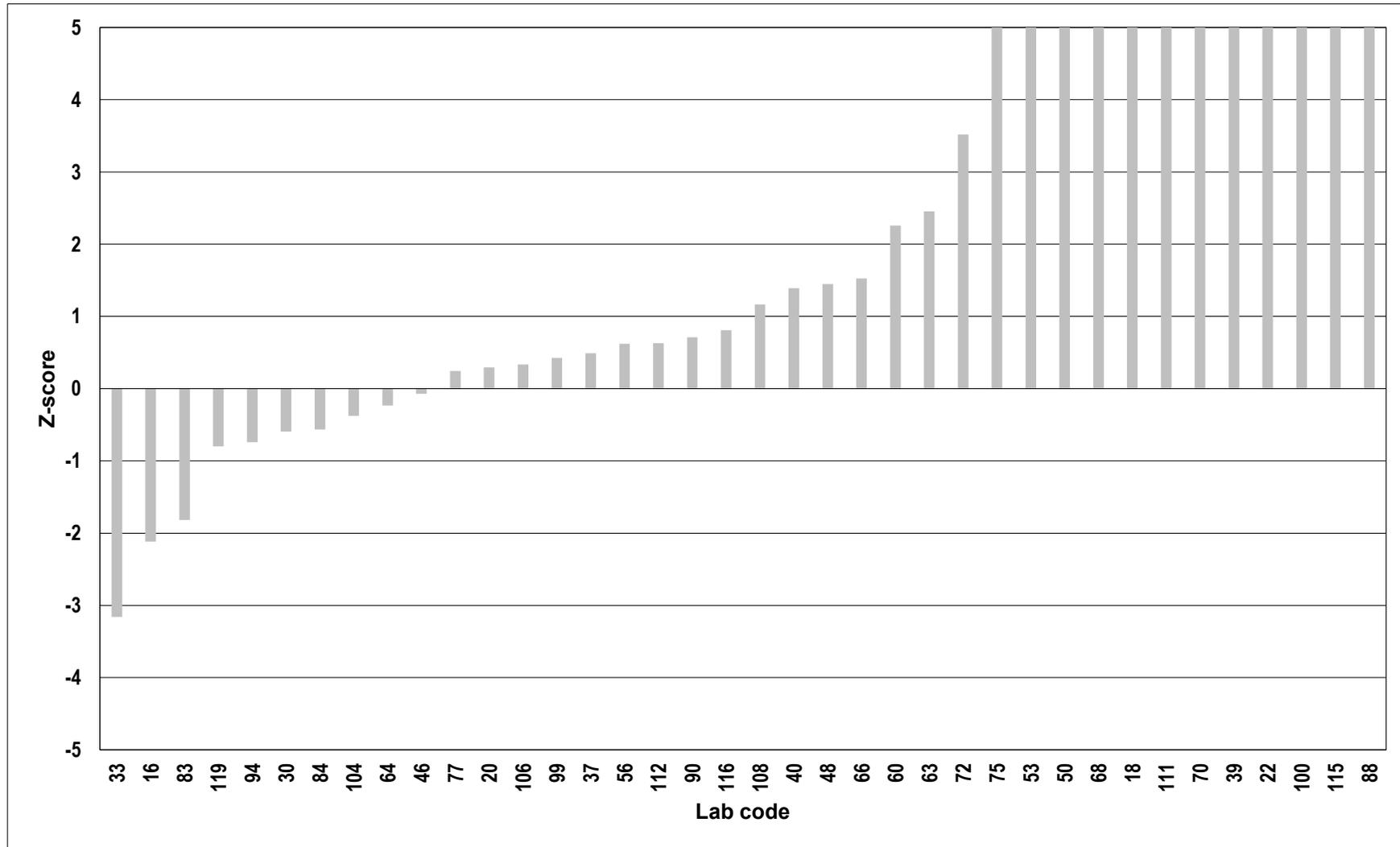
### Z-score Egg yolk, fresh weight; sum indicator PCB



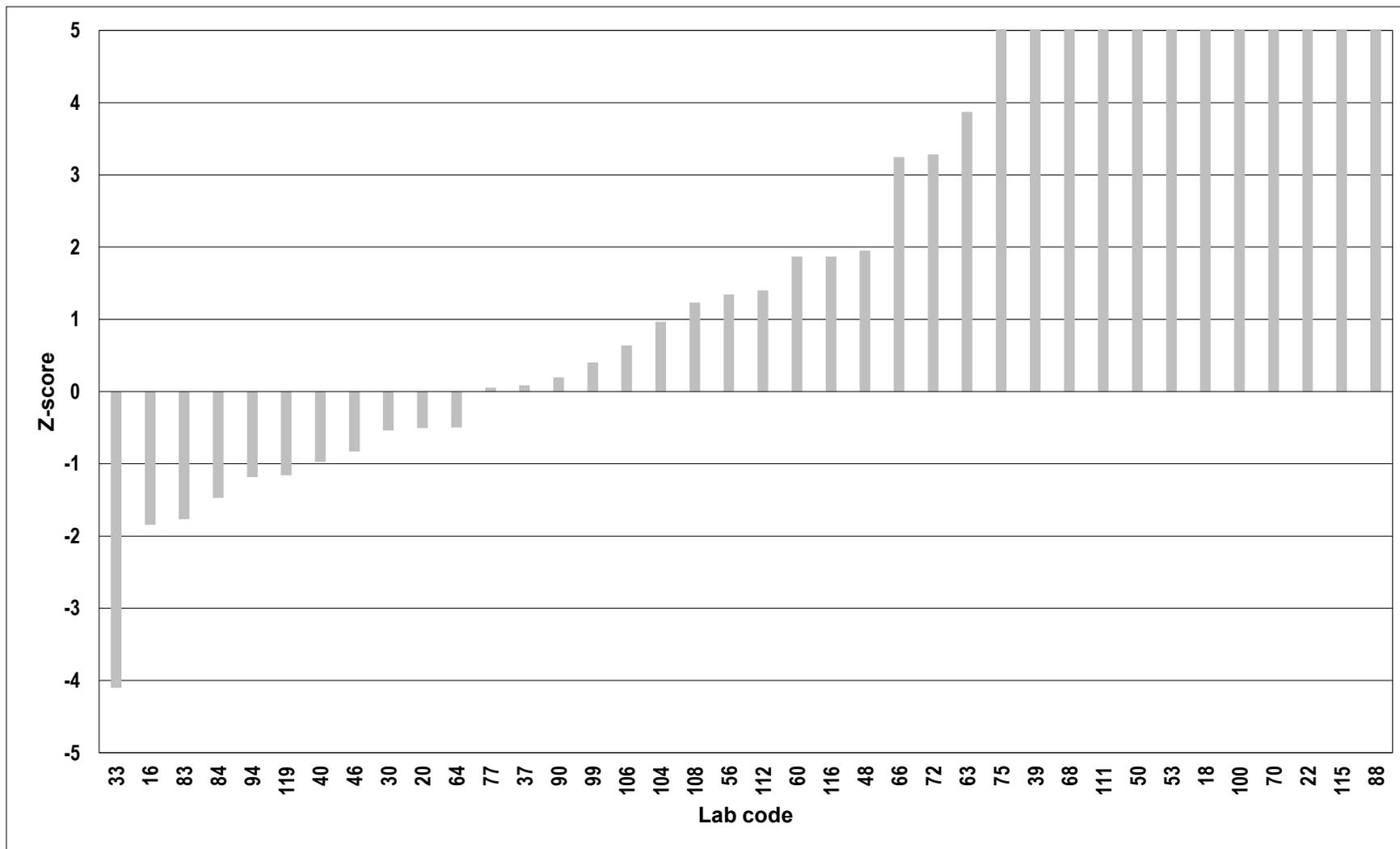
**Z-score Egg yolk, fresh weight; sum PBDE without BDE-209**



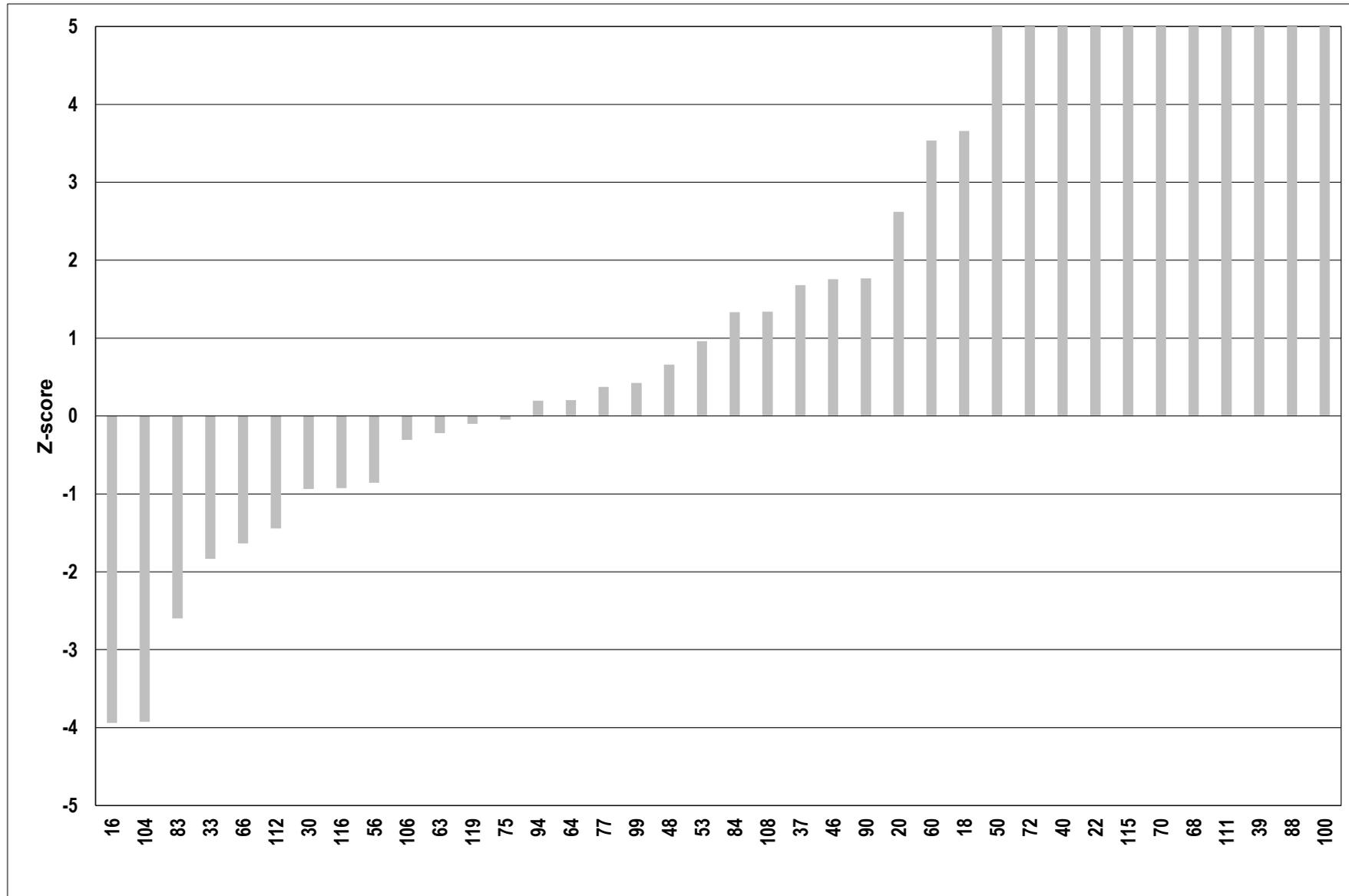
### Z-score Egg yolk, lipid weight; total TEQ



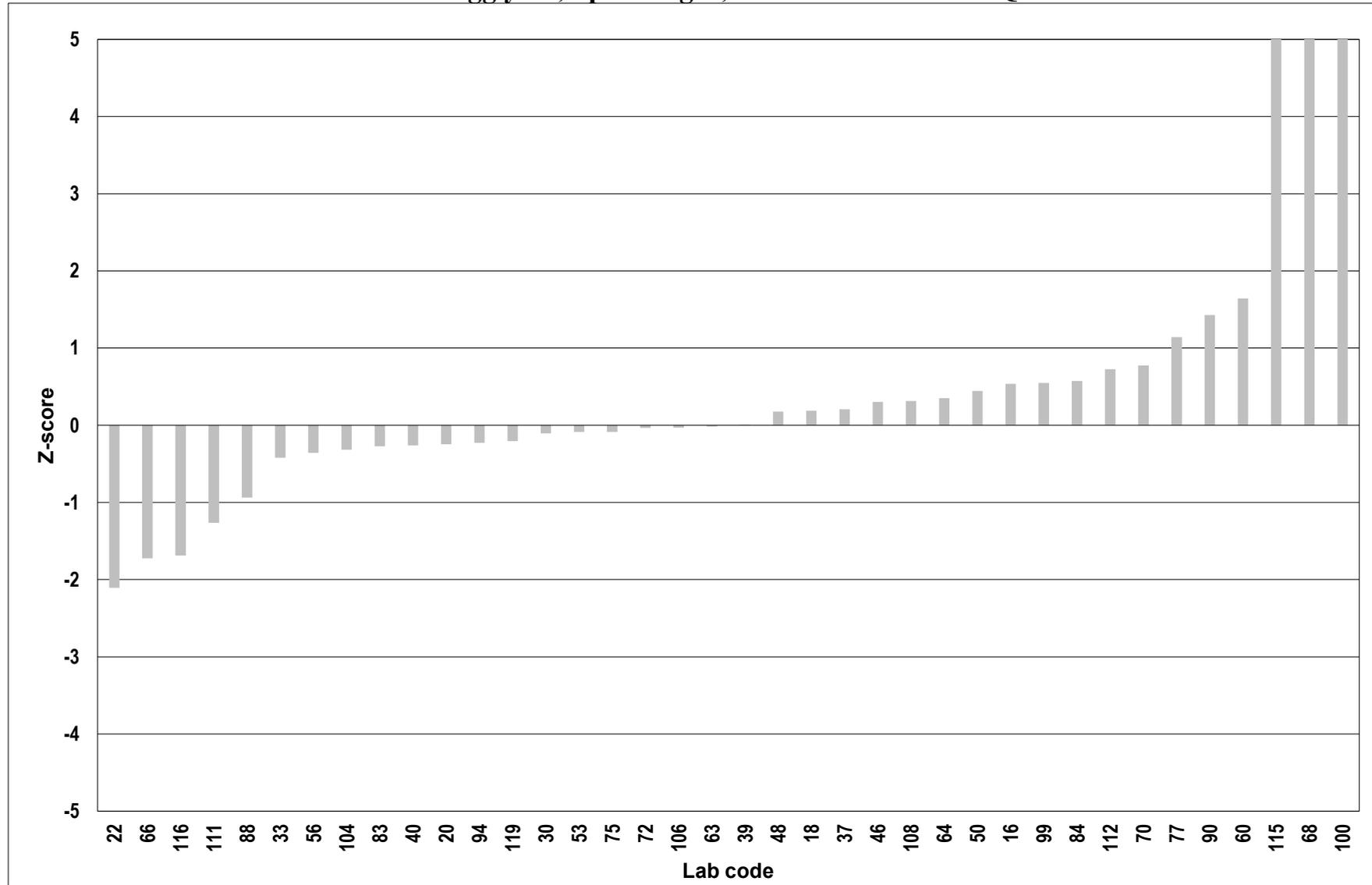
### Z-score Egg yolk, lipid weight; PCDD/PCDF TEQ



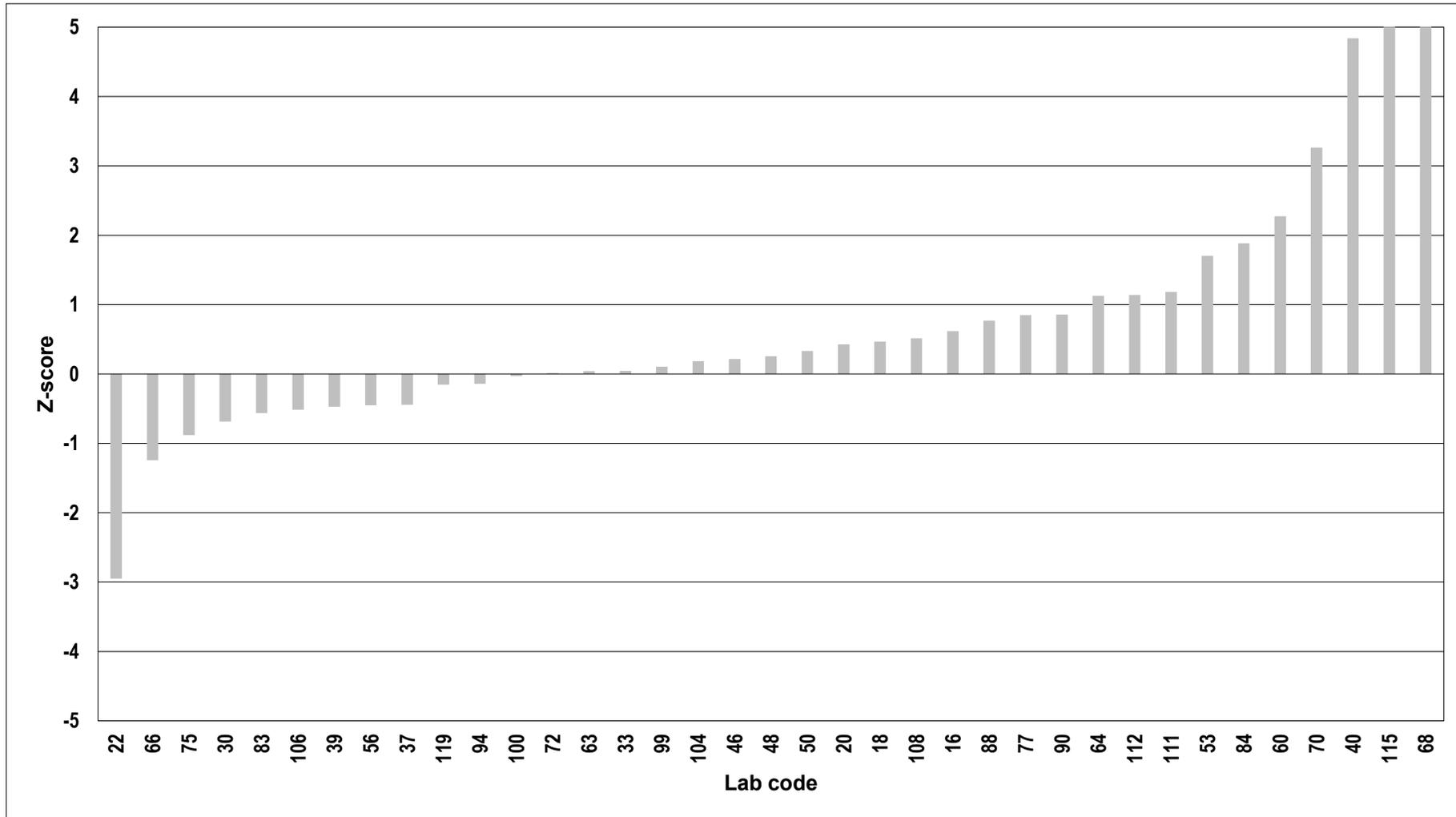
Z-score Egg yolk, lipid weight; non-ortho PCB TEQ



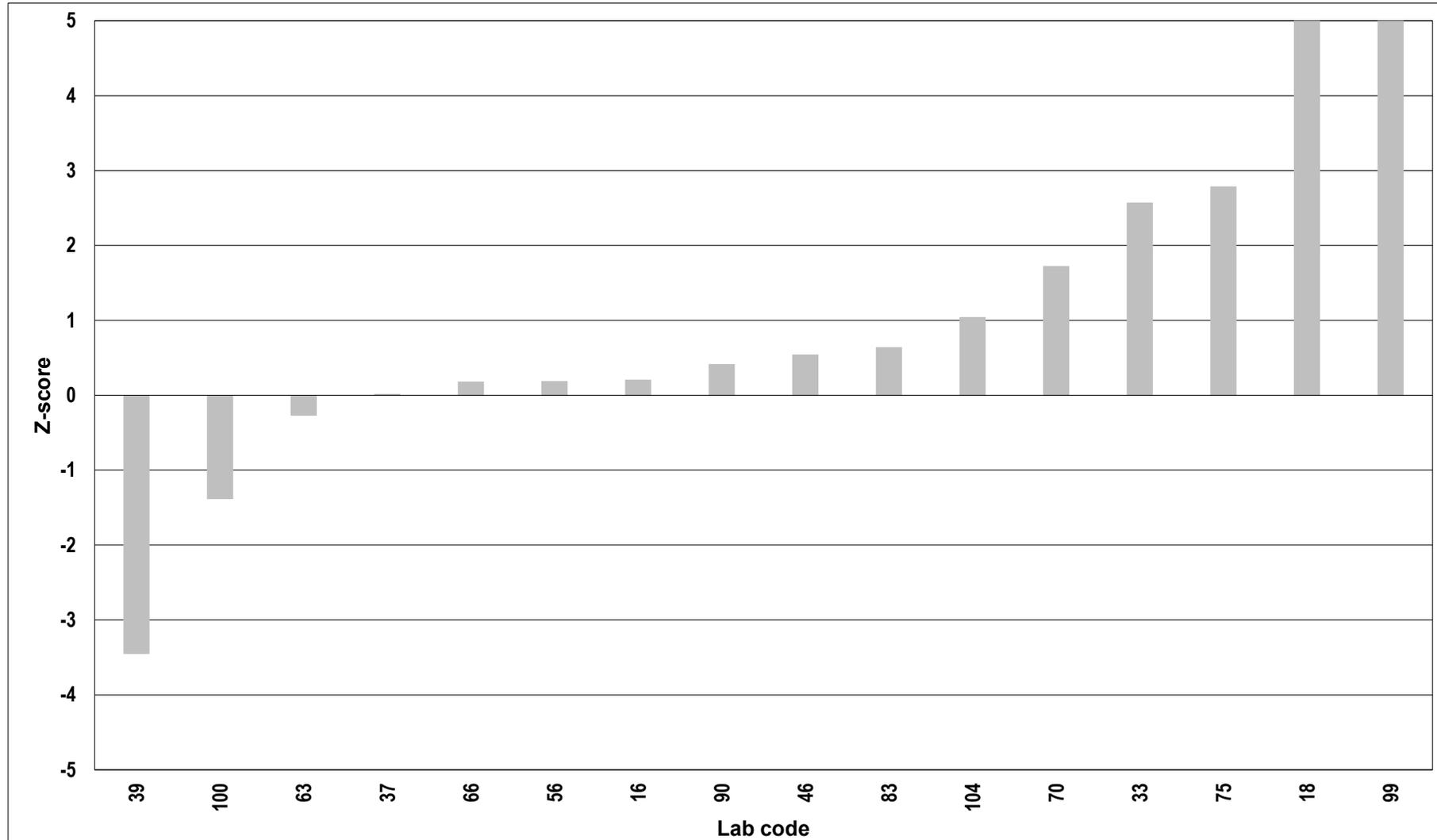
**Z-score Egg yolk, lipid weight; mono-ortho PCB TEQ**



### Z-score Egg yolk, lipid weight; sum indicator PCB



**Z-score Egg yolk, lipid weight; sum PBDE without PBDE-209**





## **Appendix 1:**

Presentation of results  
for analyte solutions



## Appendix 1: Presentation of results: Analyte solution

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

The analyte solution contained

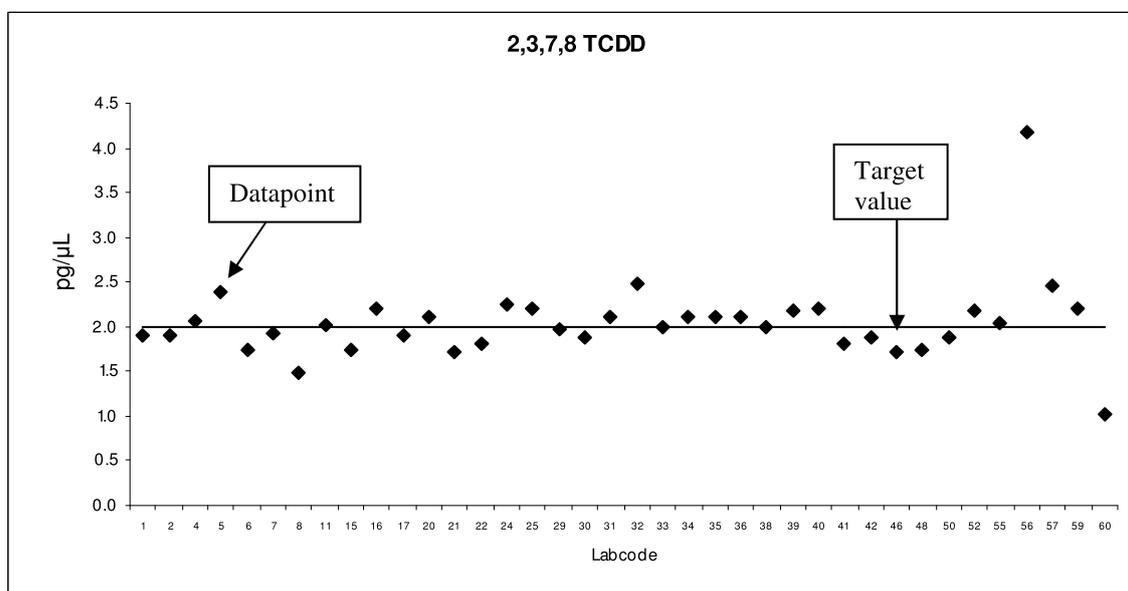
- PCDDs/PCDFs at concentrations of 2:5:10 pg/ $\mu$ l for tetra:penta-hexa-hepta:octa chlorinated dibenzodioxins/furans respectively.
- Non-ortho PCBs at concentration of 10 pg/ $\mu$ l.
- Mono-ortho PCBs and indicator PCBs at concentration of 100 pg/ $\mu$ l.
- PBDE at a concentration of 25 pg/ $\mu$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

These concentrations are called the congeners' target value.

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

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

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



### Z-Scores of individual congeners

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

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

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



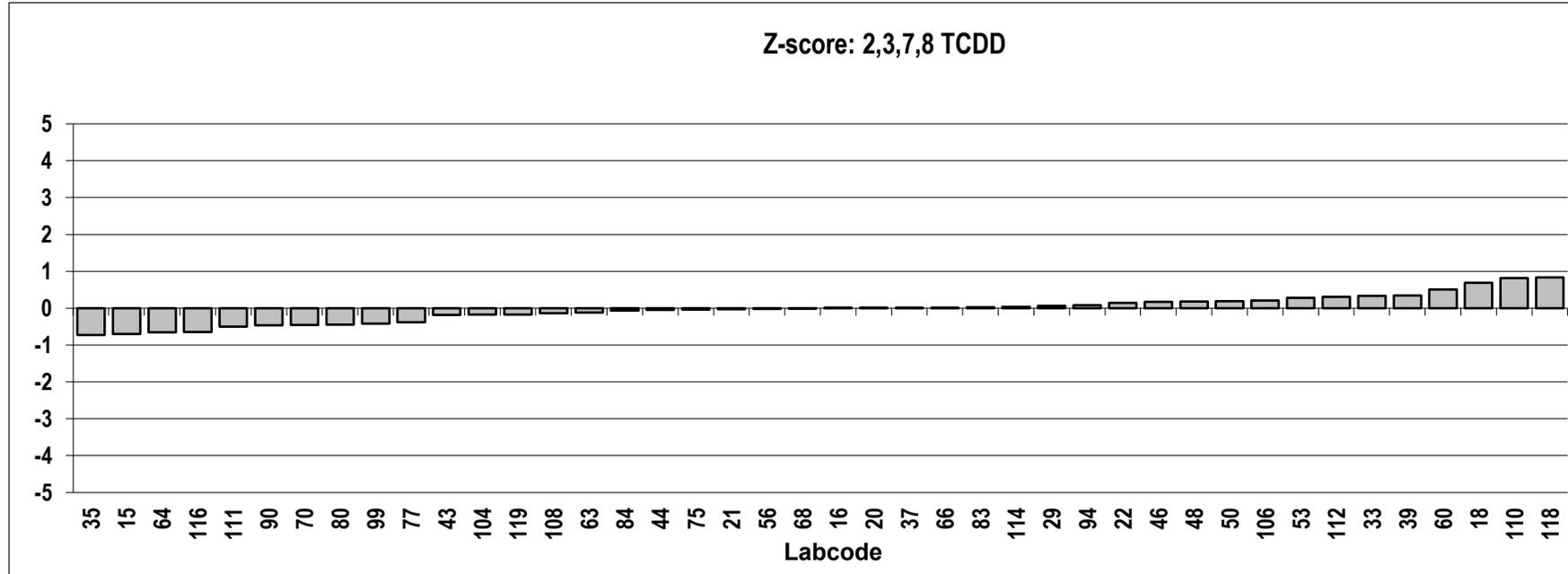
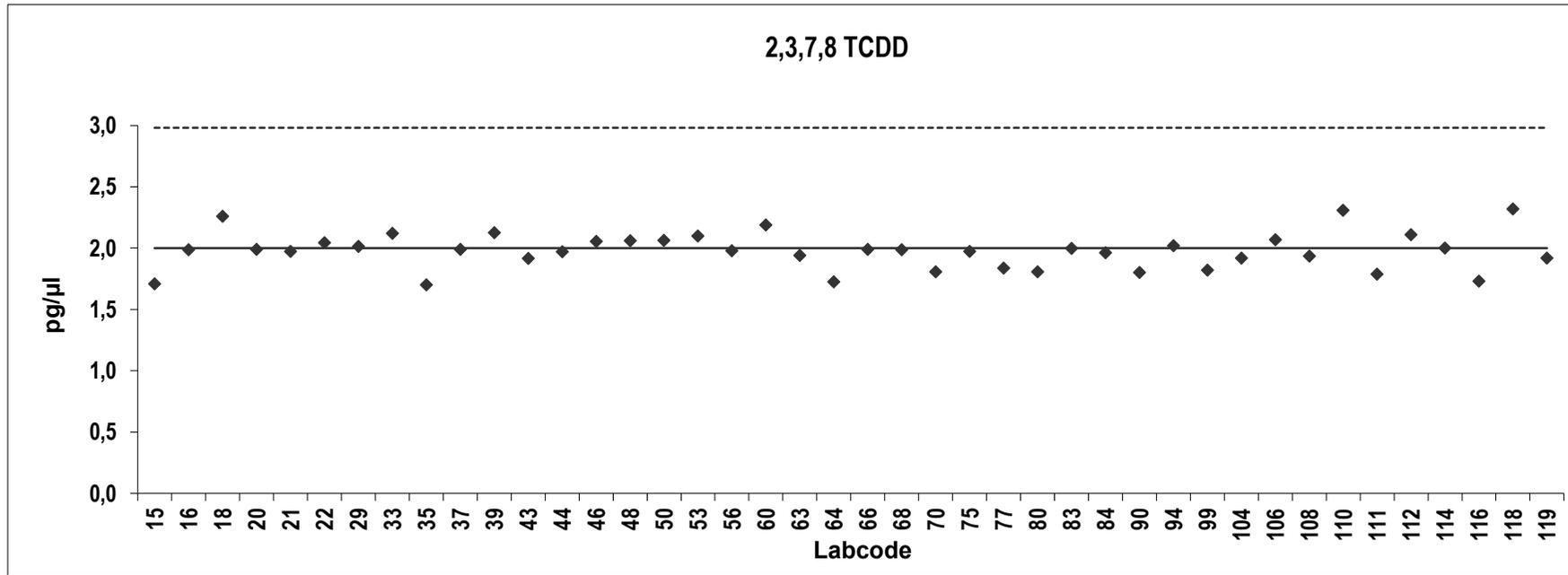
## Analyte solution

Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	1,7	-0,70				
16	2,0	0,0011				
18	2,3	0,69				
20	2,0	0,0062				
21	2,0	-0,033				
22	2,0	0,14				
29	2,0	0,065				
33	2,1	0,33				
35	1,7	-0,72				
37	2,0	0,0062				
39	2,1	0,35				
43	1,9	-0,18				
44	2,0	-0,044				
46	2,1	0,17				
48	2,1	0,18				
50	2,1	0,19				
53	2,1	0,28				
56	2,0	-0,019				
60	2,2	0,50				
63	1,9	-0,12				
64	1,7	-0,66				
66	2,0	0,0074				
68	2,0	-0,0011				
70	1,8	-0,46				
75	2,0	-0,036				
77	1,8	-0,38				
80	1,8	-0,45				
83	2,0	0,025				
84	2,0	-0,061				
90	1,8	-0,47				
94	2,0	0,082				
99	1,8	-0,42				
104	1,9	-0,17				
106	2,1	0,21				
108	1,9	-0,13				
110	2,3	0,81				
111	1,8	-0,50				
112	2,1	0,31				
114	2,0	0,031				
116	1,7	-0,64				
118	2,3	0,84				
119	1,9	-0,17				

### Consensus statistics

Consensus median, pg/μl	2,0
Median all values pg/μl	2,0
Consensus mean, pg/μl	2,0
Standard deviation, pg/μl	0,15
Relative standard deviation, %	7,6
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

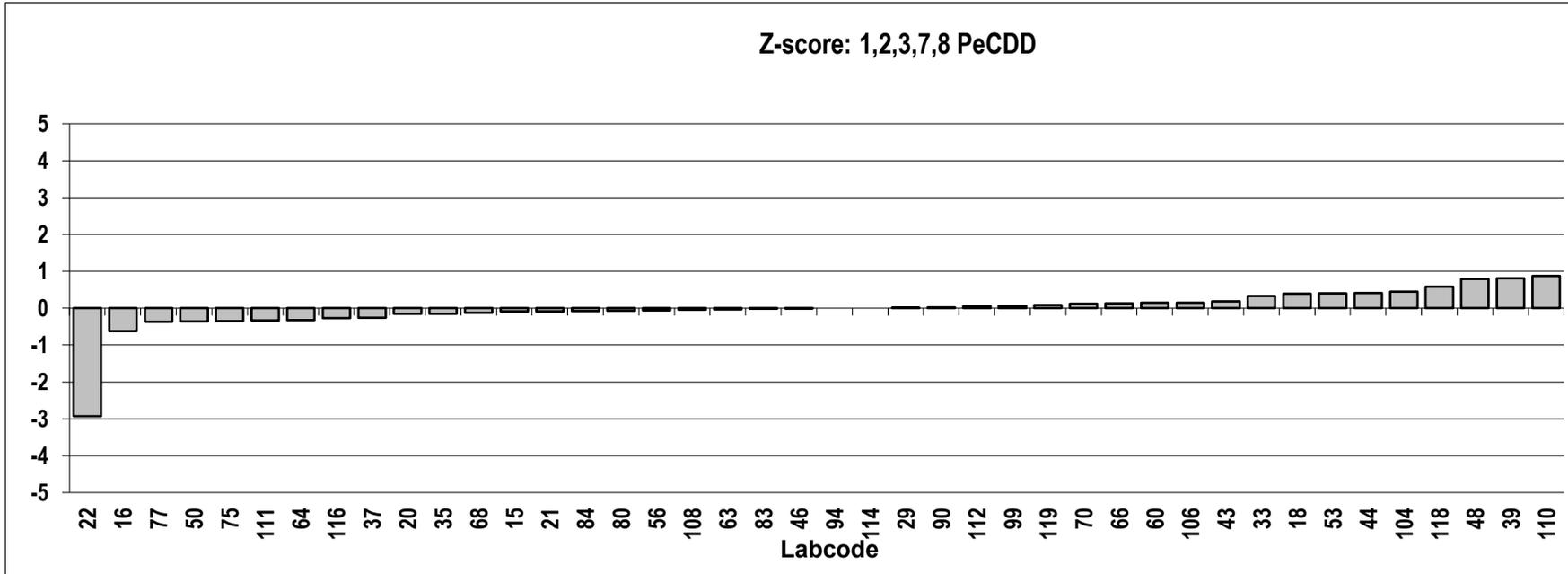
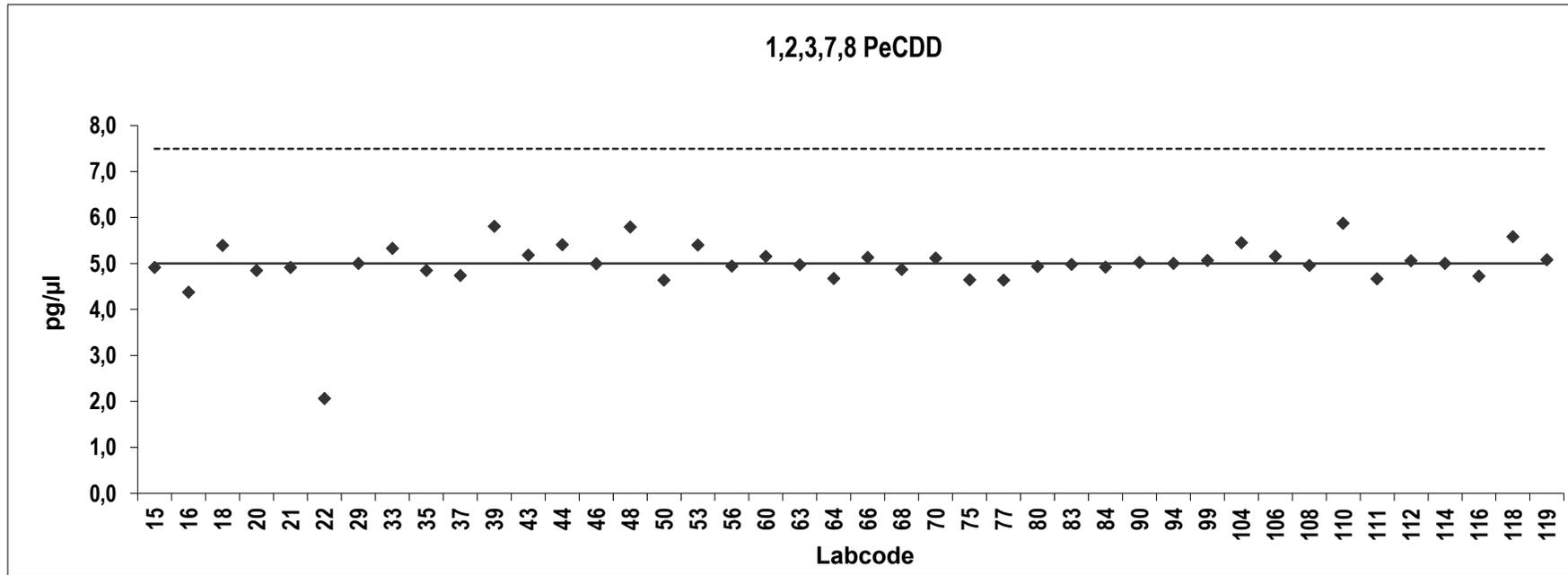


**Analyte solution**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,9	-0,090				
16	4,4	-0,62				
18	5,4	0,39				
20	4,9	-0,15				
21	4,9	-0,088				
22	2,1	-2,9	Outlier			
29	5,0	0,0038				
33	5,3	0,33				
35	4,9	-0,15				
37	4,7	-0,26				
39	5,8	0,81				
43	5,2	0,18				
44	5,4	0,41				
46	5,0	-0,0090				
48	5,8	0,79				
50	4,6	-0,36				
53	5,4	0,40				
56	4,9	-0,060				
60	5,2	0,15				
63	5,0	-0,030				
64	4,7	-0,32				
66	5,1	0,13				
68	4,9	-0,13				
70	5,1	0,12				
75	4,6	-0,35				
77	4,6	-0,37				
80	4,9	-0,068				
83	5,0	-0,019				
84	4,9	-0,080				
90	5,0	0,022				
94	5,0	0,0000				
99	5,1	0,069				
104	5,5	0,45				
106	5,2	0,15				
108	5,0	-0,042				
110	5,9	0,87				
111	4,7	-0,33				
112	5,1	0,060				
114	5,0	0,0000				
116	4,7	-0,27				
118	5,6	0,58				
119	5,1	0,080				

**Consensus statistics**

Consensus median, pg/μl	5,0
Median all values pg/μl	5,0
Consensus mean, pg/μl	5,1
Standard deviation, pg/μl	0,33
Relative standard deviation, %	6,6
No. of values reported	42
No. of values removed	1
No. of reported non-detects	0

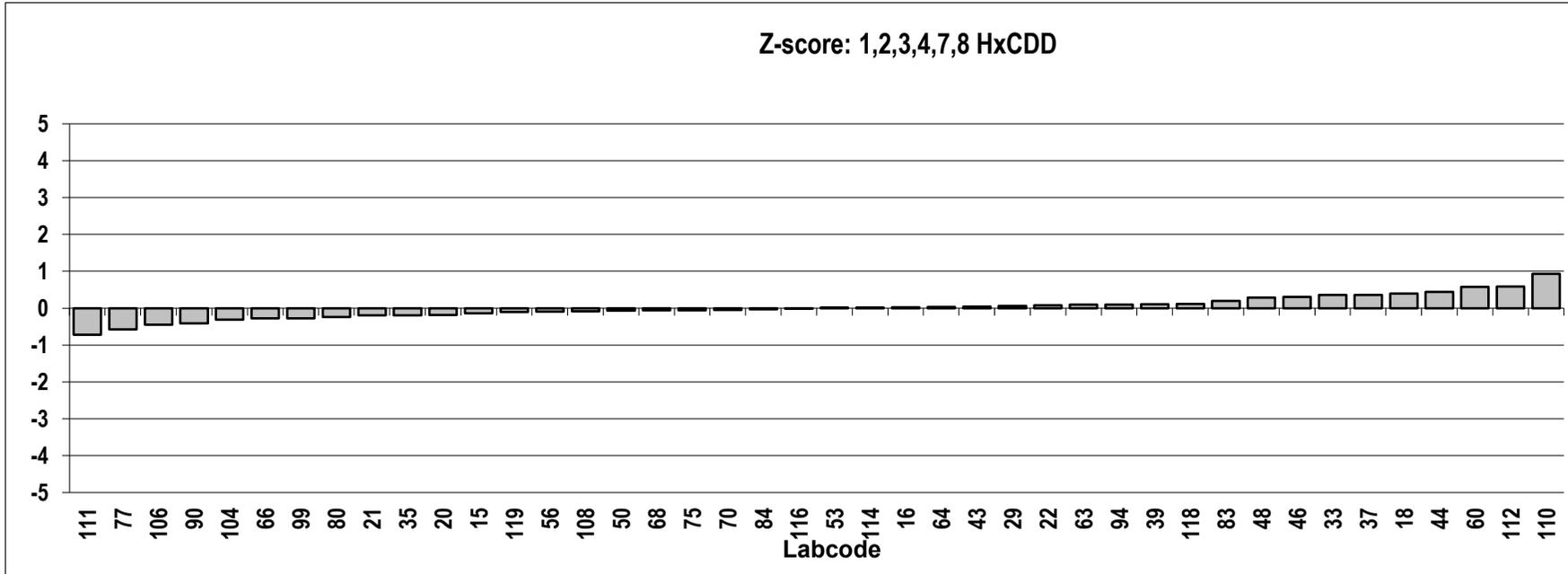
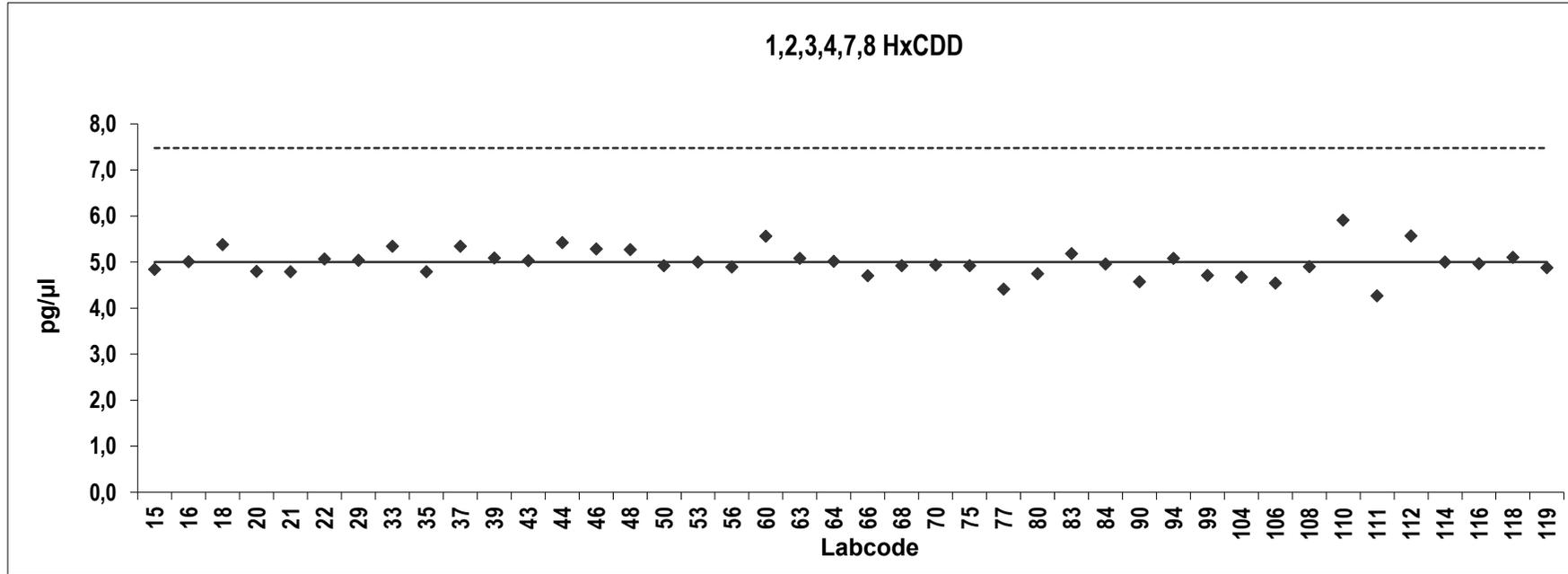


**Analyte solution**  
**Congener: 1,2,3,4,7,8 HxCDD**

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,8	-0,14				
16	5,0	0,027				
18	5,4	0,40				
20	4,8	-0,18				
21	4,8	-0,19				
22	5,1	0,081				
29	5,0	0,056				
33	5,3	0,36				
35	4,8	-0,19				
37	5,3	0,36				
39	5,1	0,10				
43	5,0	0,044				
44	5,4	0,44				
46	5,3	0,30				
48	5,3	0,29				
50	4,9	-0,065				
53	5,0	0,017				
56	4,9	-0,093				
60	5,6	0,58				
63	5,1	0,10				
64	5,0	0,033				
66	4,7	-0,28				
68	4,9	-0,061				
70	4,9	-0,049				
75	4,9	-0,060				
77	4,4	-0,57				
80	4,7	-0,24				
83	5,2	0,20				
84	5,0	-0,030				
90	4,6	-0,41				
94	5,1	0,10				
99	4,7	-0,28				
104	4,7	-0,31				
106	4,5	-0,44				
108	4,9	-0,083				
110	5,9	0,93				
111	4,3	-0,72				
112	5,6	0,59				
114	5,0	0,017				
116	5,0	-0,017				
118	5,1	0,12				
119	4,9	-0,10				

**Consensus statistics**

Consensus median, pg/μl	5,0
Median all values pg/μl	5,0
Consensus mean, pg/μl	5,0
Standard deviation, pg/μl	0,32
Relative standard deviation, %	6,3
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

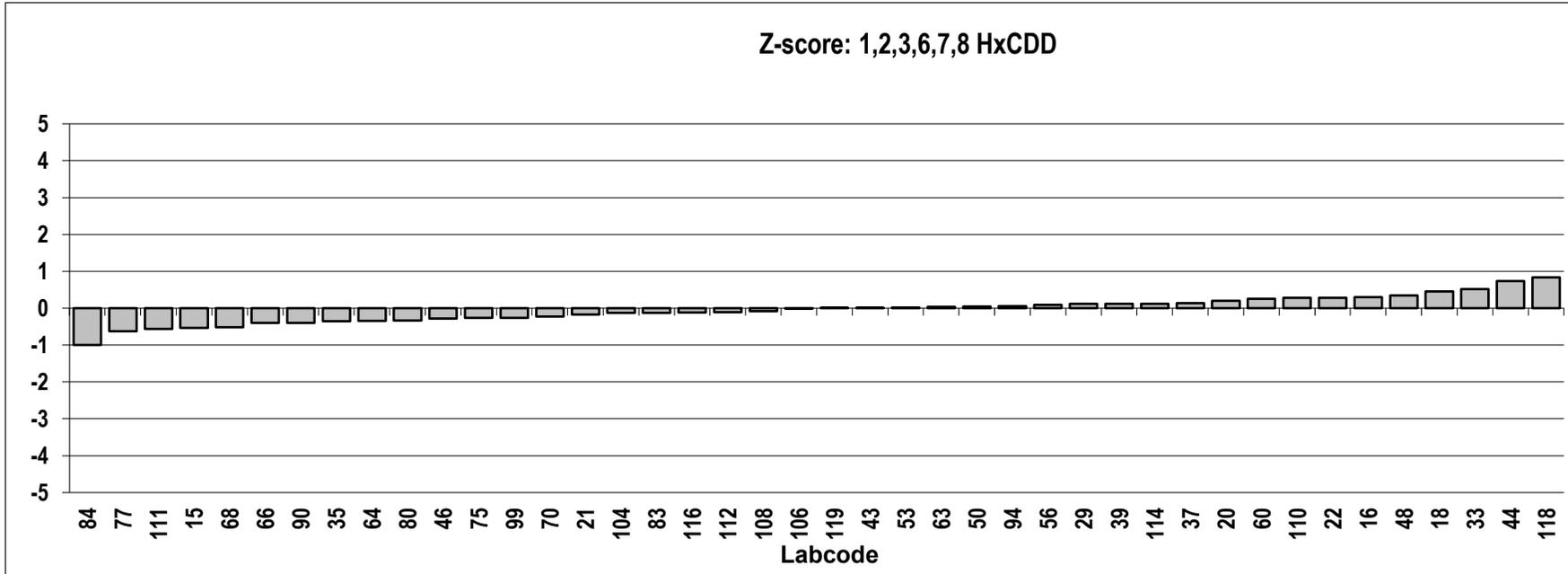
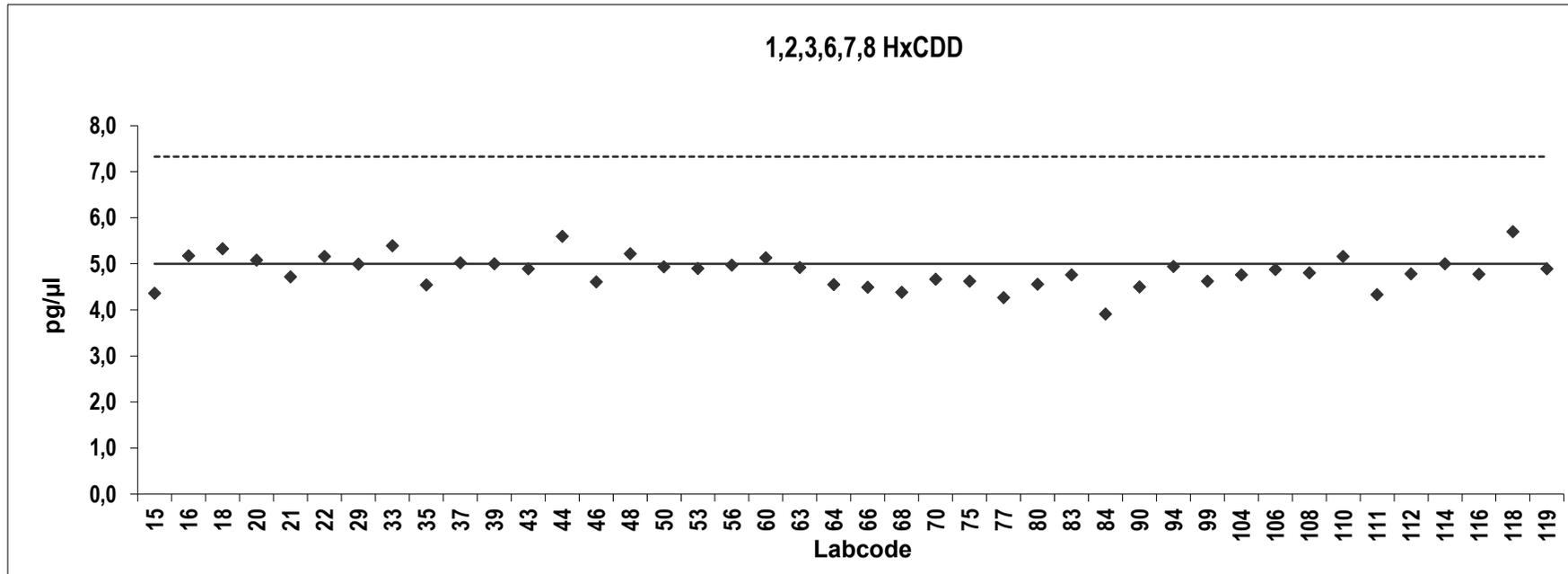


**Analyte solution**  
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,4	-0,54				
16	5,2	0,30				
18	5,3	0,46				
20	5,1	0,20				
21	4,7	-0,17				
22	5,2	0,29				
29	5,0	0,11				
33	5,4	0,52				
35	4,5	-0,35				
37	5,0	0,14				
39	5,0	0,12				
43	4,9	0,010				
44	5,6	0,73				
46	4,6	-0,29				
48	5,2	0,34				
50	4,9	0,049				
53	4,9	0,015				
56	5,0	0,087				
60	5,1	0,25				
63	4,9	0,036				
64	4,6	-0,34				
66	4,5	-0,40				
68	4,4	-0,51				
70	4,7	-0,22				
75	4,6	-0,27				
77	4,3	-0,63				
80	4,6	-0,33				
83	4,8	-0,12				
84	3,9	-1,0				
90	4,5	-0,40				
94	4,9	0,056				
99	4,6	-0,27				
104	4,8	-0,13				
106	4,9	-0,0051				
108	4,8	-0,081				
110	5,2	0,28				
111	4,3	-0,57				
112	4,8	-0,11				
114	5,0	0,12				
116	4,8	-0,12				
118	5,7	0,83				
119	4,9	0,0051				

**Consensus statistics**

Consensus median, pg/μl	4,9
Median all values pg/μl	4,9
Consensus mean, pg/μl	4,8
Standard deviation, pg/μl	0,36
Relative standard deviation, %	7,4
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

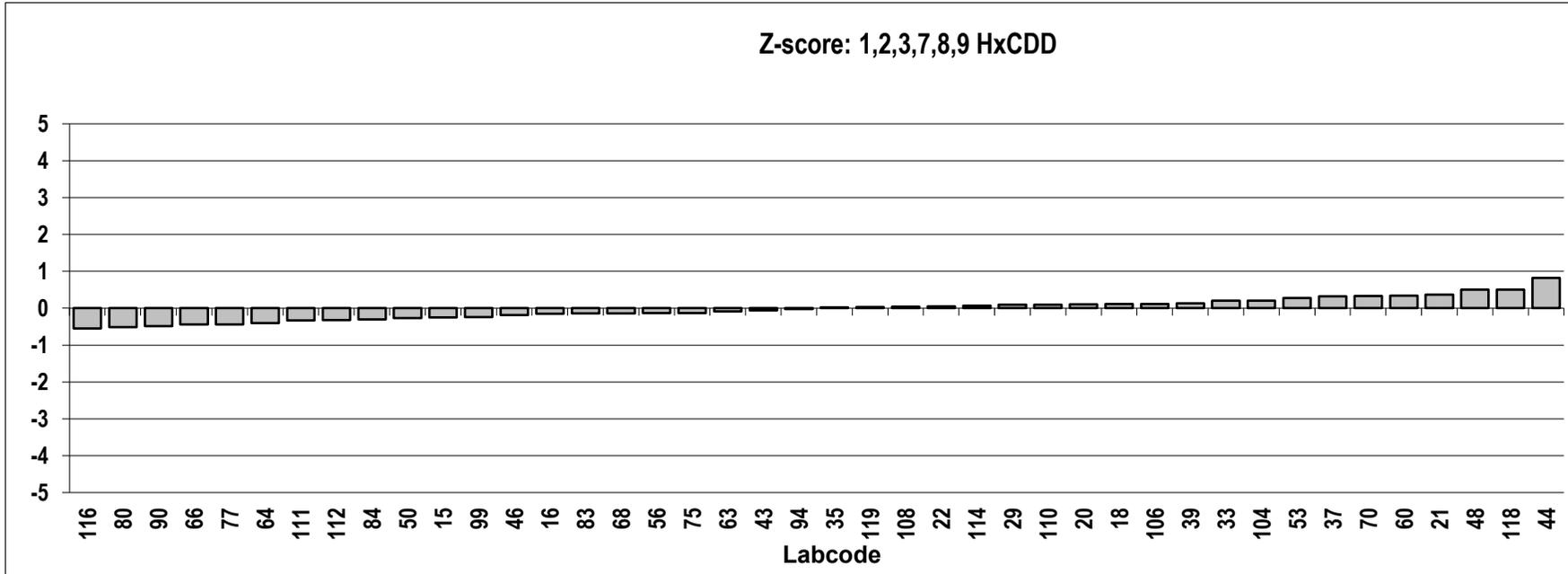
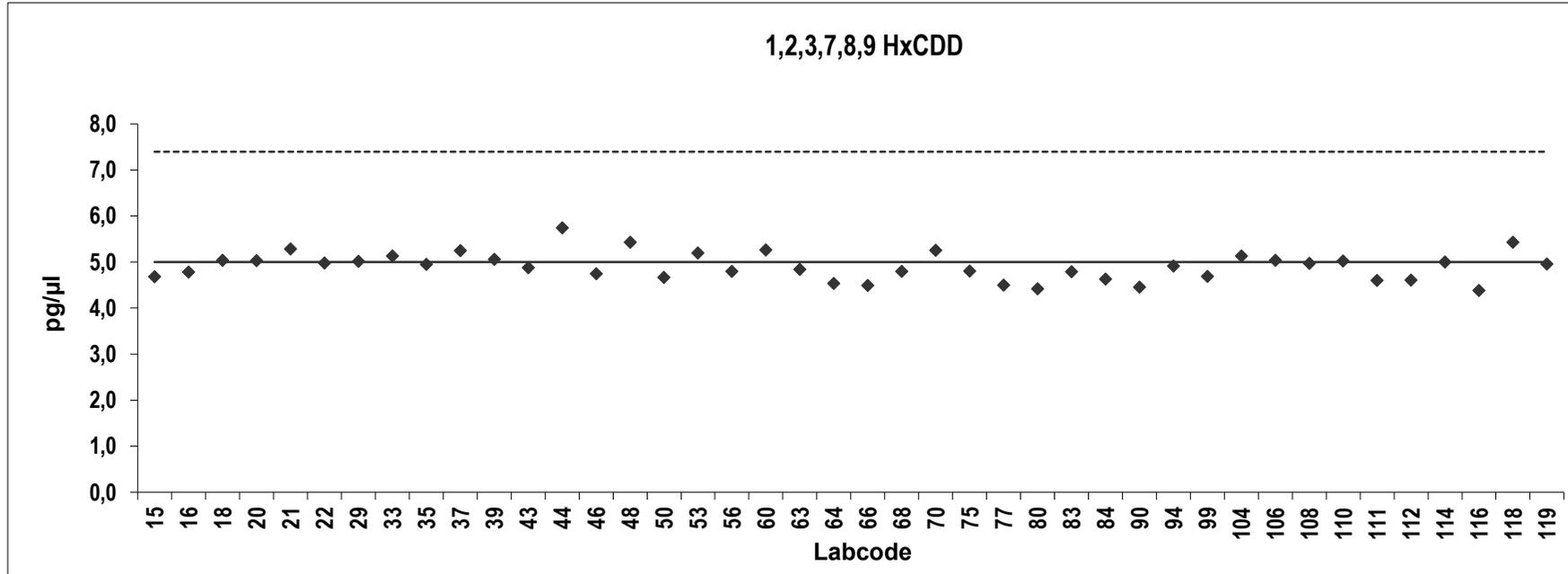


**Analyte solution**  
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,7	-0,25				
16	4,8	-0,15				
18	5,0	0,11				
20	5,0	0,10				
21	5,3	0,36				
22	5,0	0,050				
29	5,0	0,090				
33	5,1	0,20				
35	5,0	0,020				
37	5,3	0,32				
39	5,1	0,13				
43	4,9	-0,057				
44	5,7	0,82				
46	4,7	-0,19				
48	5,4	0,51				
50	4,7	-0,27				
53	5,2	0,27				
56	4,8	-0,13				
60	5,3	0,34				
63	4,8	-0,091				
64	4,5	-0,40				
66	4,5	-0,44				
68	4,8	-0,14				
70	5,3	0,33				
75	4,8	-0,13				
77	4,5	-0,44				
80	4,4	-0,52				
83	4,8	-0,14				
84	4,6	-0,31				
90	4,5	-0,48				
94	4,9	-0,020				
99	4,7	-0,24				
104	5,1	0,20				
106	5,0	0,11				
108	5,0	0,044				
110	5,0	0,091				
111	4,6	-0,33				
112	4,6	-0,32				
114	5,0	0,071				
116	4,4	-0,55				
118	5,4	0,51				
119	5,0	0,030				

**Consensus statistics**

Consensus median, pg/μl	4,9
Median all values pg/μl	4,9
Consensus mean, pg/μl	4,9
Standard deviation, pg/μl	0,30
Relative standard deviation, %	6,2
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

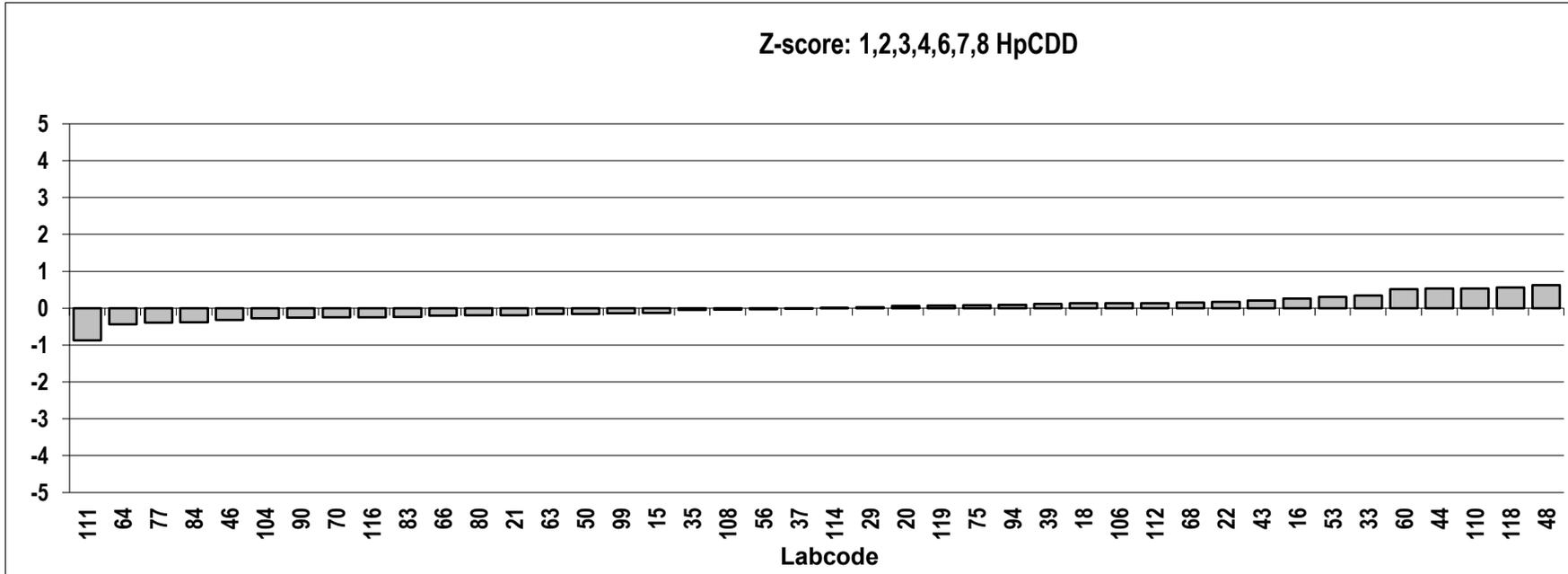
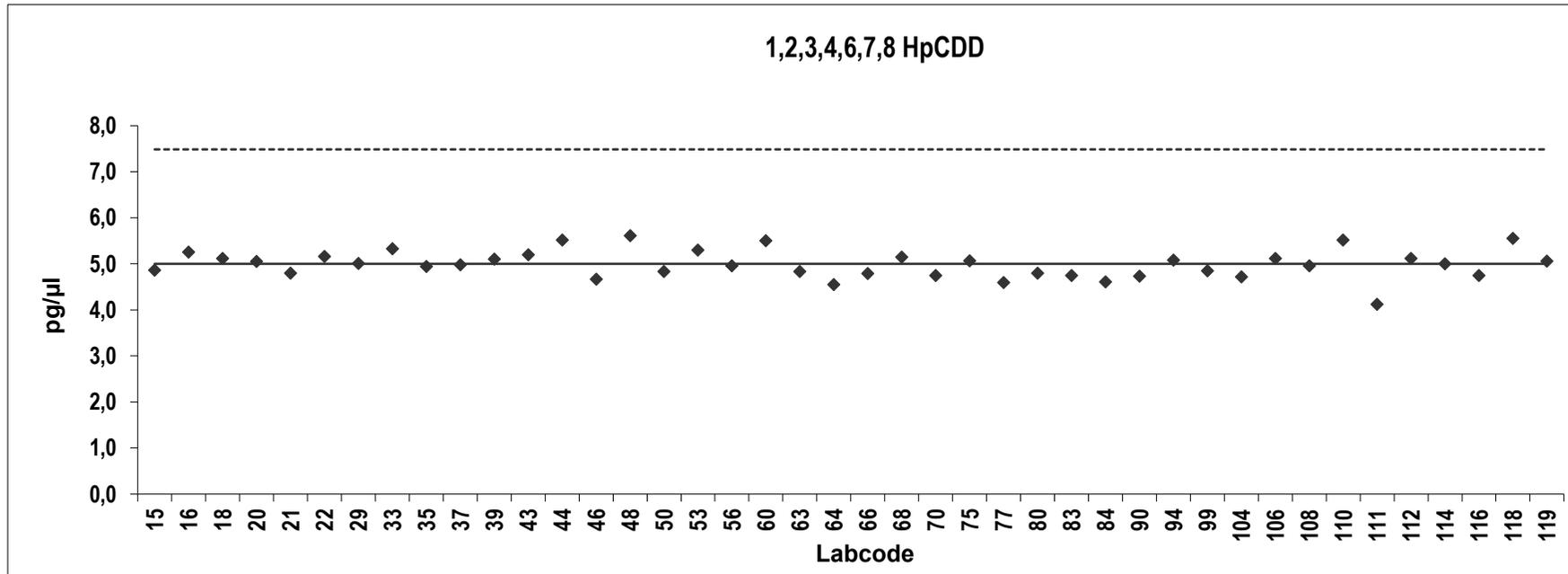


**Analyte solution**  
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,9	-0,13				
16	5,3	0,26				
18	5,1	0,13				
20	5,1	0,060				
21	4,8	-0,20				
22	5,2	0,17				
29	5,0	0,021				
33	5,3	0,34				
35	4,9	-0,050				
37	5,0	-0,010				
39	5,1	0,11				
43	5,2	0,21				
44	5,5	0,53				
46	4,7	-0,32				
48	5,6	0,62				
50	4,8	-0,16				
53	5,3	0,31				
56	5,0	-0,030				
60	5,5	0,51				
63	4,8	-0,16				
64	4,6	-0,44				
66	4,8	-0,20				
68	5,1	0,15				
70	4,7	-0,25				
75	5,1	0,076				
77	4,6	-0,39				
80	4,8	-0,20				
83	4,7	-0,24				
84	4,6	-0,38				
90	4,7	-0,26				
94	5,1	0,090				
99	4,9	-0,14				
104	4,7	-0,27				
106	5,1	0,13				
108	5,0	-0,036				
110	5,5	0,53				
111	4,1	-0,87				
112	5,1	0,13				
114	5,0	0,010				
116	4,7	-0,24				
118	5,6	0,56				
119	5,1	0,070				

**Consensus statistics**

Consensus median, pg/μl	5,0
Median all values pg/μl	5,0
Consensus mean, pg/μl	5,0
Standard deviation, pg/μl	0,31
Relative standard deviation, %	6,2
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



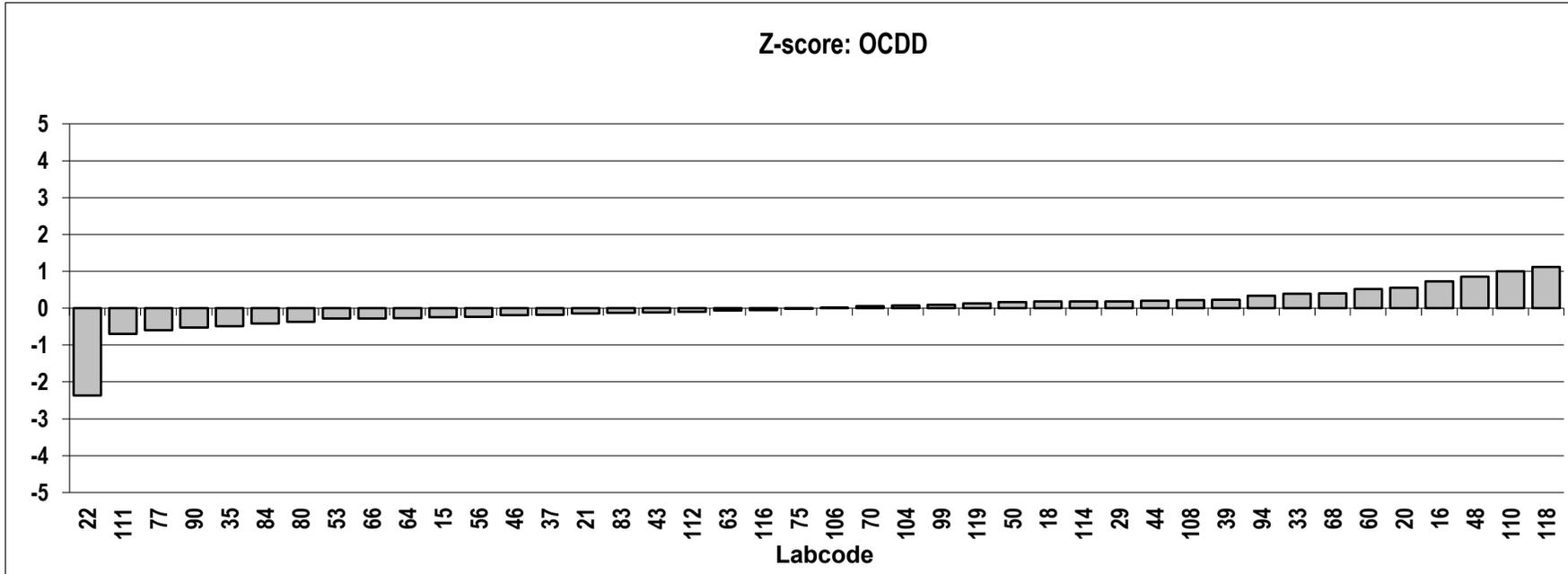
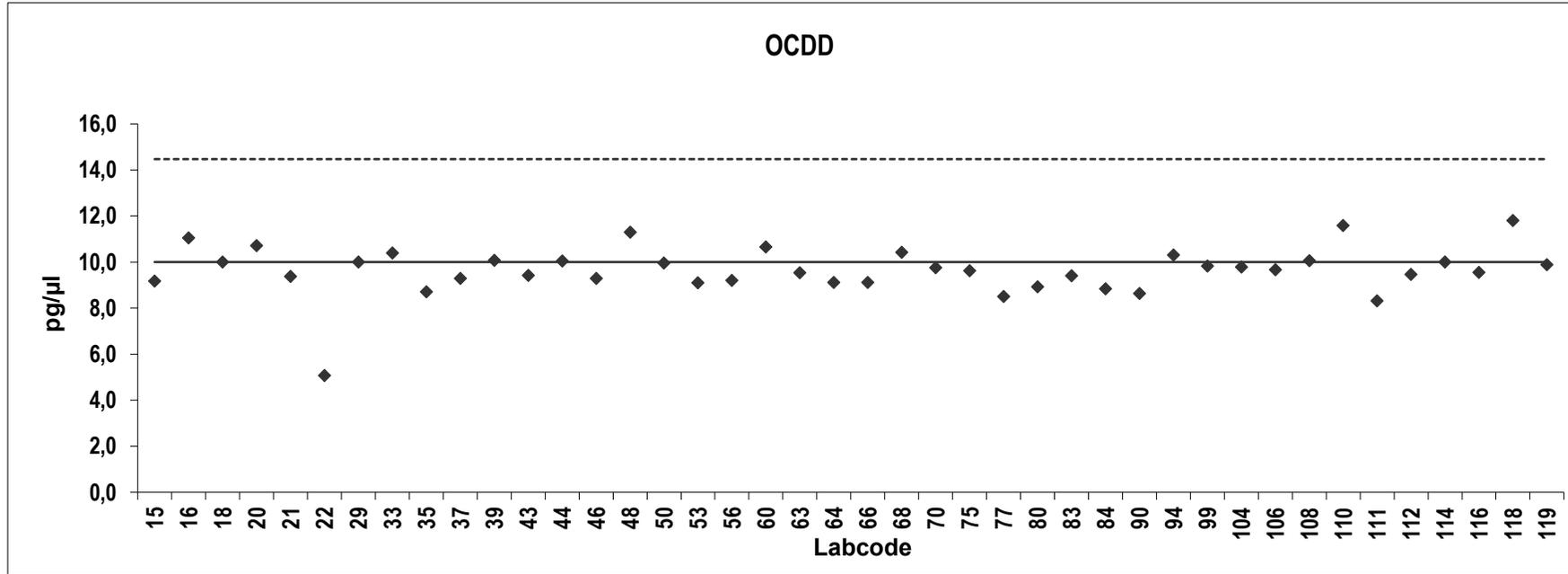
## Analyte solution

Congener: OCDD

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	9,2	-0,25				
16	11	0,73				
18	10	0,18				
20	11	0,55				
21	9,4	-0,14				
22	5,1	-2,4				
29	10	0,19				
33	10	0,39				
35	8,7	-0,49				
37	9,3	-0,18				
39	10	0,22				
43	9,4	-0,12				
44	10	0,20				
46	9,3	-0,19				
48	11	0,85				
50	10	0,16				
53	9,1	-0,28				
56	9,2	-0,23				
60	11	0,52				
63	9,5	-0,060				
64	9,1	-0,28				
66	9,1	-0,28				
68	10	0,40				
70	9,8	0,058				
75	9,6	-0,012				
77	8,5	-0,60				
80	8,9	-0,37				
83	9,4	-0,12				
84	8,8	-0,42				
90	8,6	-0,53				
94	10	0,34				
99	9,8	0,10				
104	9,8	0,075				
106	9,7	0,012				
108	10	0,22				
110	12	1,0				
111	8,3	-0,69				
112	9,5	-0,10				
114	10	0,18				
116	9,5	-0,052				
118	12	1,1				
119	9,9	0,13				

### Consensus statistics

Consensus median, pg/μl	9,6
Median all values pg/μl	9,6
Consensus mean, pg/μl	9,6
Standard deviation, pg/μl	1,1
Relative standard deviation, %	11
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

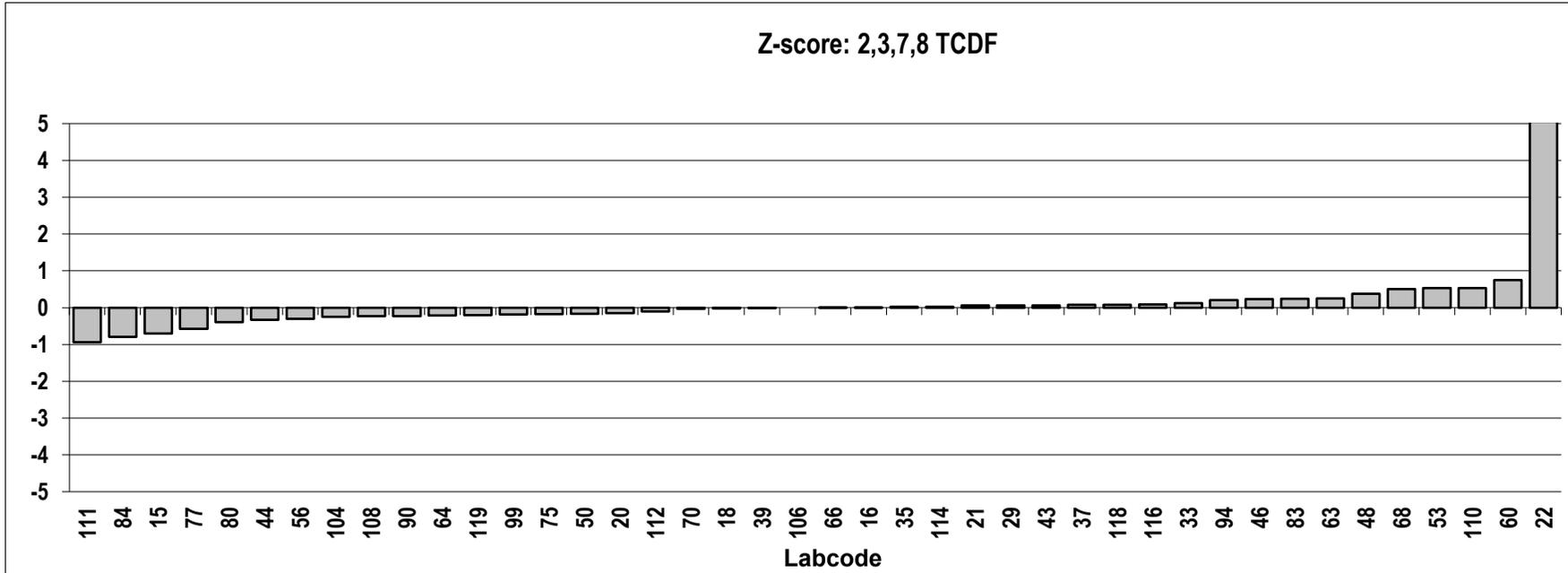
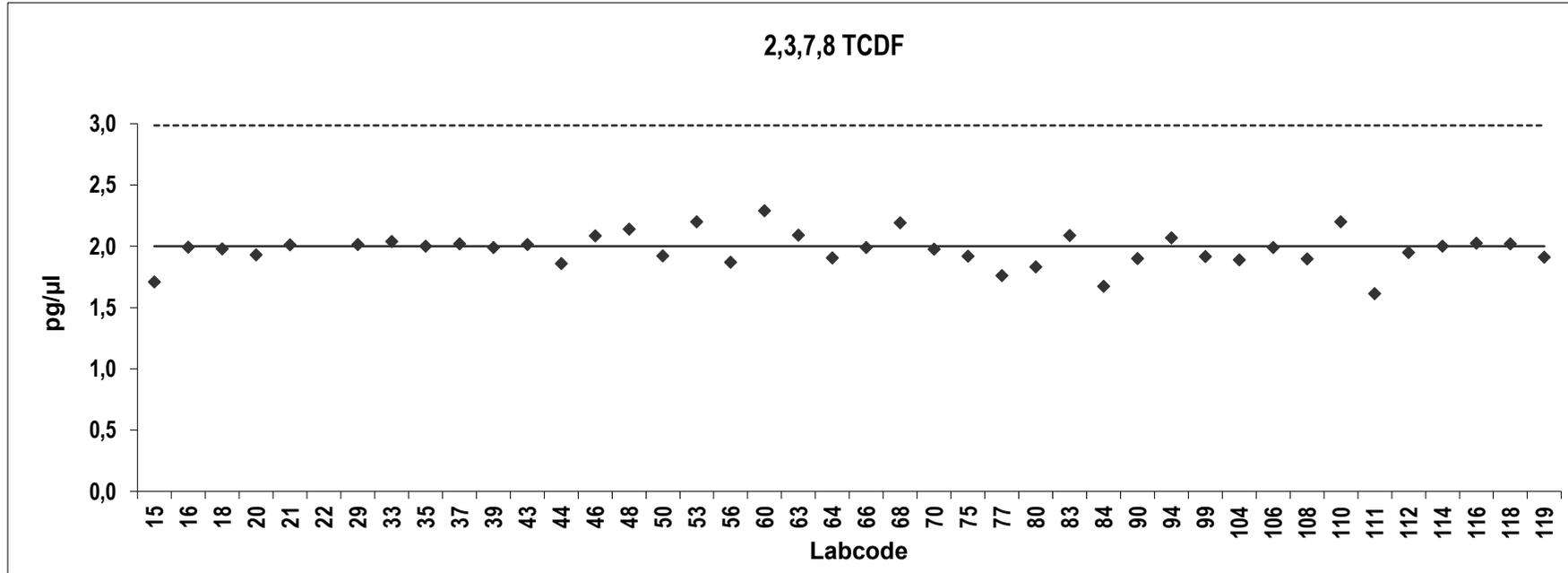


**Analyte solution**  
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	1,7	-0,70				
16	2,0	0,0050				
18	2,0	-0,025				
20	1,9	-0,15				
21	2,0	0,057				
22	5,0	7,6	Outlier			
29	2,0	0,062				
33	2,0	0,13				
35	2,0	0,025				
37	2,0	0,075				
39	2,0	-0,0035				
43	2,0	0,062				
44	1,9	-0,33				
46	2,1	0,24				
48	2,1	0,38				
50	1,9	-0,17				
53	2,2	0,53				
56	1,9	-0,30				
60	2,3	0,75				
63	2,1	0,25				
64	1,9	-0,22				
66	2,0	0,0012				
68	2,2	0,51				
70	2,0	-0,034				
75	1,9	-0,18				
77	1,8	-0,57				
80	1,8	-0,40				
83	2,1	0,24				
84	1,7	-0,79				
90	1,9	-0,23				
94	2,1	0,20				
99	1,9	-0,18				
104	1,9	-0,25				
106	2,0	0,0000				
108	1,9	-0,23				
110	2,2	0,53				
111	1,6	-0,94				
112	2,0	-0,10				
114	2,0	0,025				
116	2,0	0,088				
118	2,0	0,075				
119	1,9	-0,20				

**Consensus statistics**

Consensus median, pg/μl	2,0
Median all values pg/μl	2,0
Consensus mean, pg/μl	2,0
Standard deviation, pg/μl	0,14
Relative standard deviation, %	7,0
No. of values reported	42
No. of values removed	1
No. of reported non-detects	0

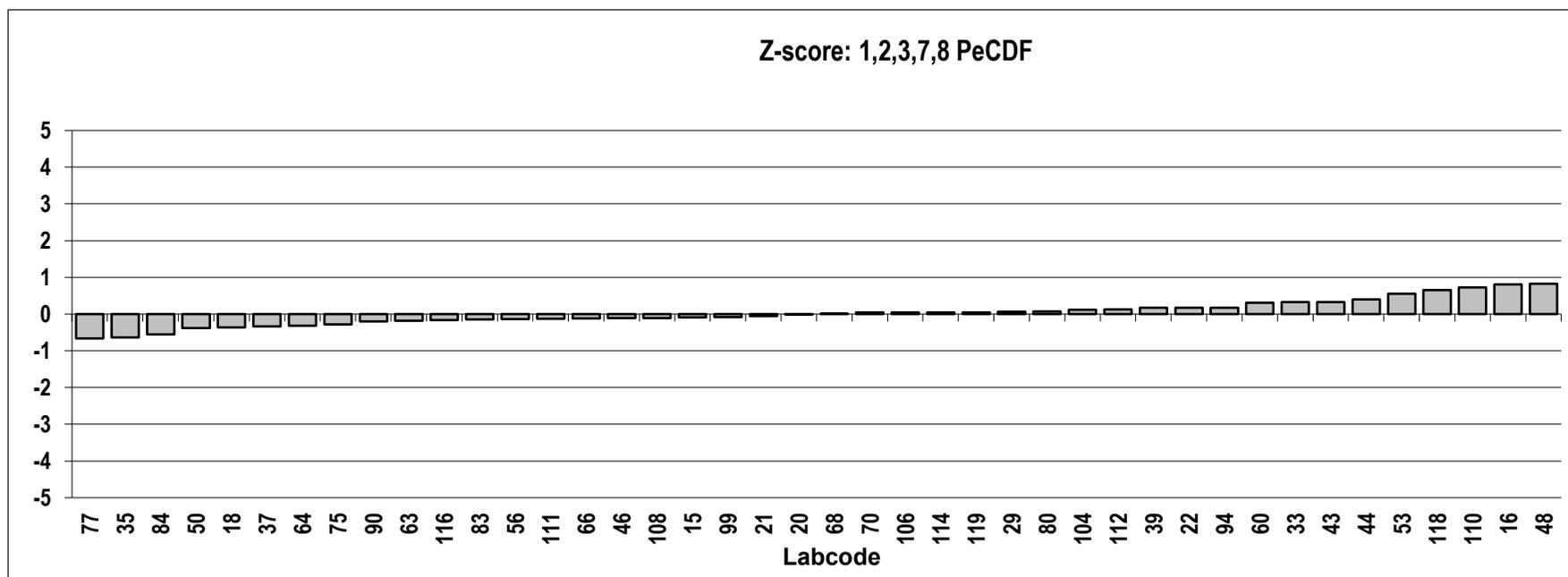
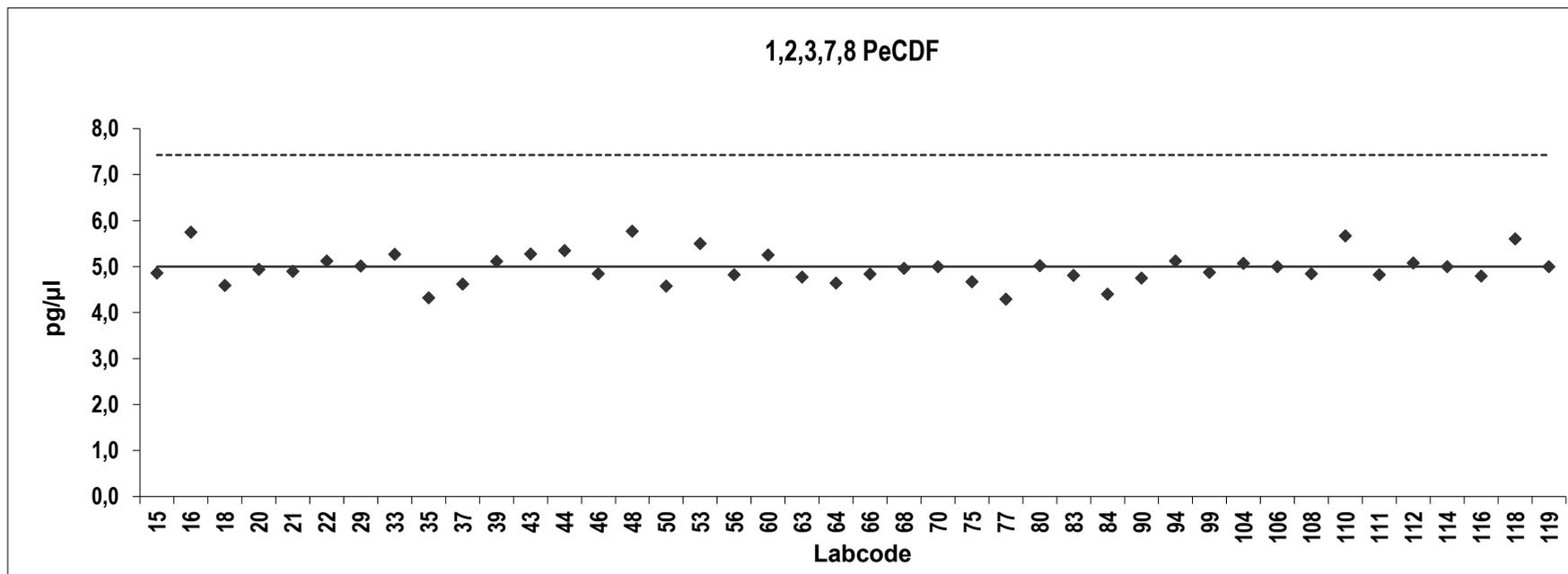


**Analyte solution**  
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,9	-0,092				
16	5,8	0,81				
18	4,6	-0,37				
20	4,9	-0,012				
21	4,9	-0,058				
22	5,1	0,17				
29	5,0	0,065				
33	5,3	0,32				
35	4,3	-0,64				
37	4,6	-0,33				
39	5,1	0,17				
43	5,3	0,33				
44	5,4	0,40				
46	4,8	-0,11				
48	5,8	0,83				
50	4,6	-0,38				
53	5,5	0,55				
56	4,8	-0,13				
60	5,3	0,30				
63	4,8	-0,18				
64	4,6	-0,32				
66	4,8	-0,11				
68	5,0	0,012				
70	5,0	0,046				
75	4,7	-0,28				
77	4,3	-0,67				
80	5,0	0,070				
83	4,8	-0,15				
84	4,4	-0,55				
90	4,8	-0,20				
94	5,1	0,17				
99	4,9	-0,080				
104	5,1	0,12				
106	5,0	0,049				
108	4,8	-0,11				
110	5,7	0,73				
111	4,8	-0,13				
112	5,1	0,13				
114	5,0	0,049				
116	4,8	-0,16				
118	5,6	0,65				
119	5,0	0,049				

**Consensus statistics**

Consensus median, pg/μl	5,0
Median all values pg/μl	5,0
Consensus mean, pg/μl	5,0
Standard deviation, pg/μl	0,35
Relative standard deviation, %	7,0
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

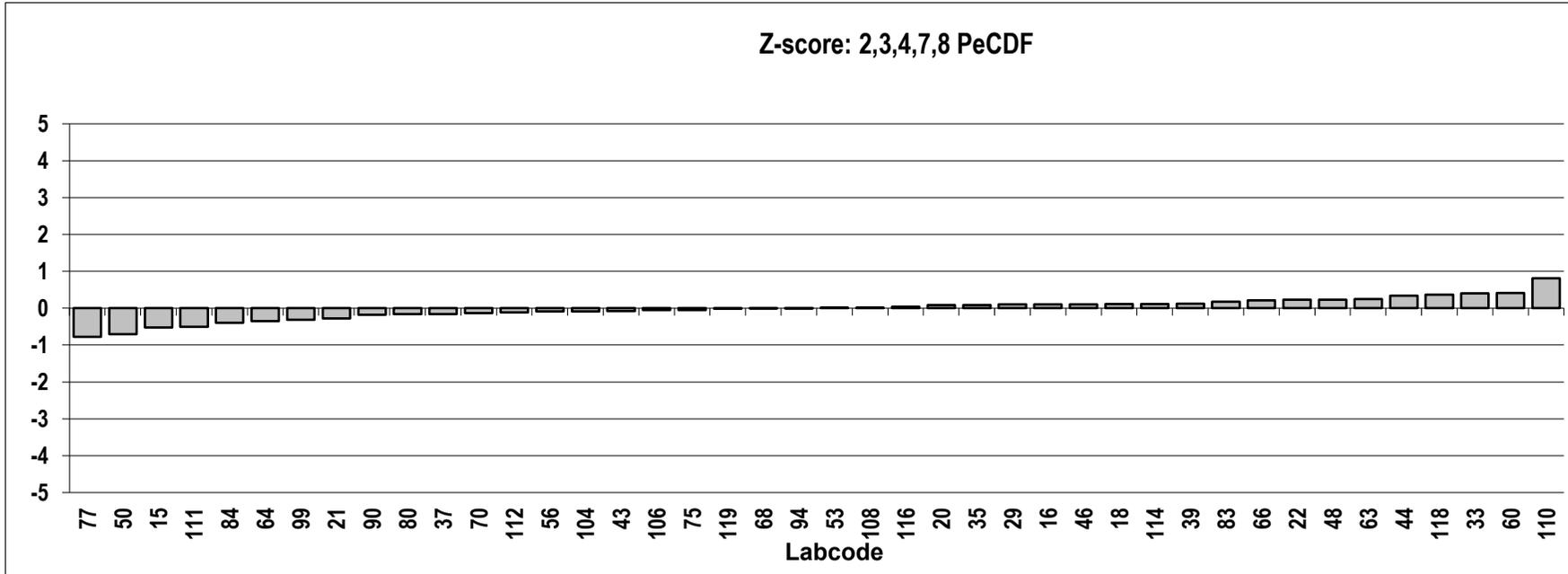
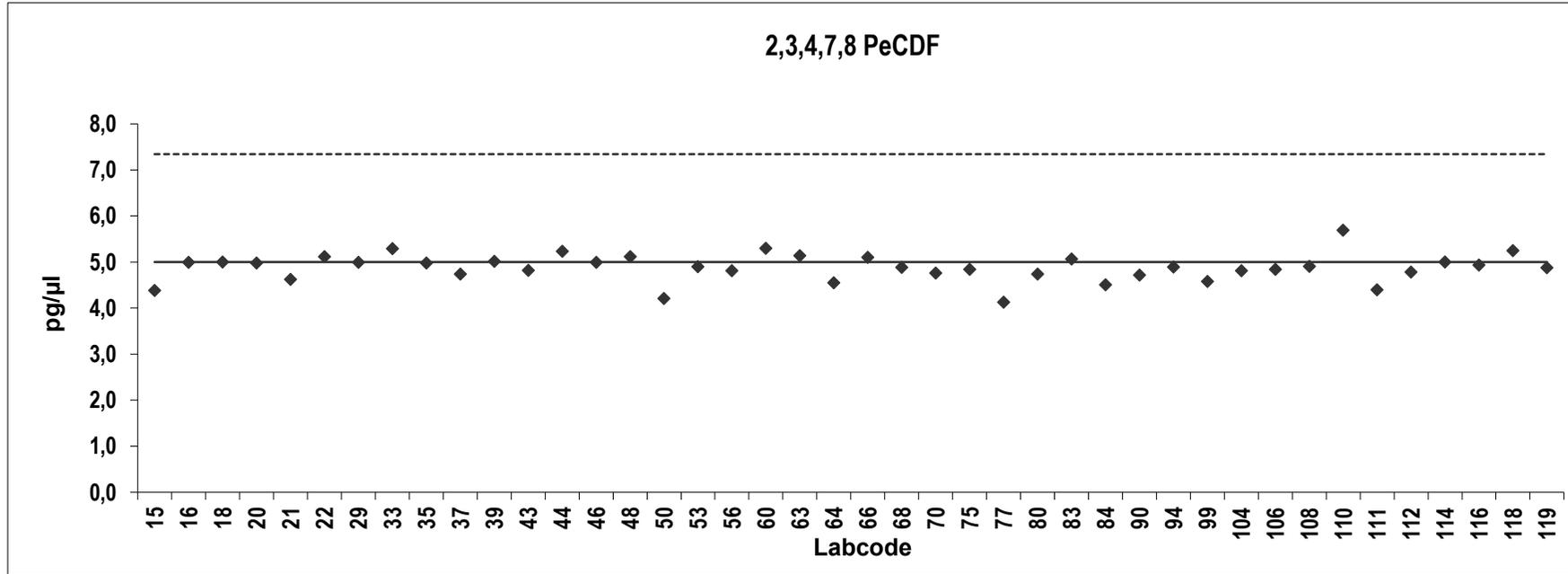


**Analyte solution**  
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,4	-0,53				
16	5,0	0,10				
18	5,0	0,11				
20	5,0	0,087				
21	4,6	-0,28				
22	5,1	0,23				
29	5,0	0,10				
33	5,3	0,40				
35	5,0	0,087				
37	4,7	-0,16				
39	5,0	0,12				
43	4,8	-0,080				
44	5,2	0,34				
46	5,0	0,10				
48	5,1	0,23				
50	4,2	-0,70				
53	4,9	0,0051				
56	4,8	-0,087				
60	5,3	0,41				
63	5,1	0,25				
64	4,5	-0,35				
66	5,1	0,21				
68	4,9	-0,0093				
70	4,8	-0,14				
75	4,8	-0,055				
77	4,1	-0,78				
80	4,7	-0,16				
83	5,1	0,18				
84	4,5	-0,40				
90	4,7	-0,18				
94	4,9	-0,0051				
99	4,6	-0,32				
104	4,8	-0,087				
106	4,8	-0,056				
108	4,9	0,013				
110	5,7	0,81				
111	4,4	-0,51				
112	4,8	-0,12				
114	5,0	0,11				
116	4,9	0,041				
118	5,3	0,36				
119	4,9	-0,015				

**Consensus statistics**

Consensus median, pg/μl	4,9
Median all values pg/μl	4,9
Consensus mean, pg/μl	4,9
Standard deviation, pg/μl	0,30
Relative standard deviation, %	6,1
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

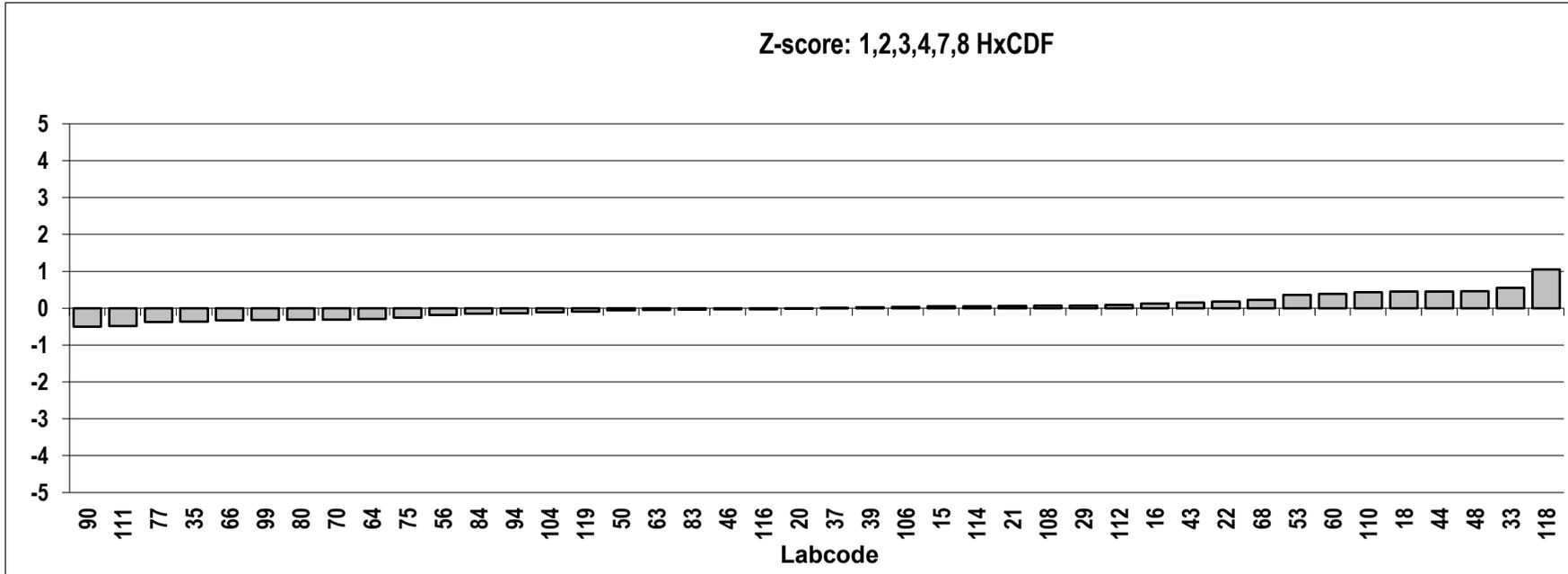
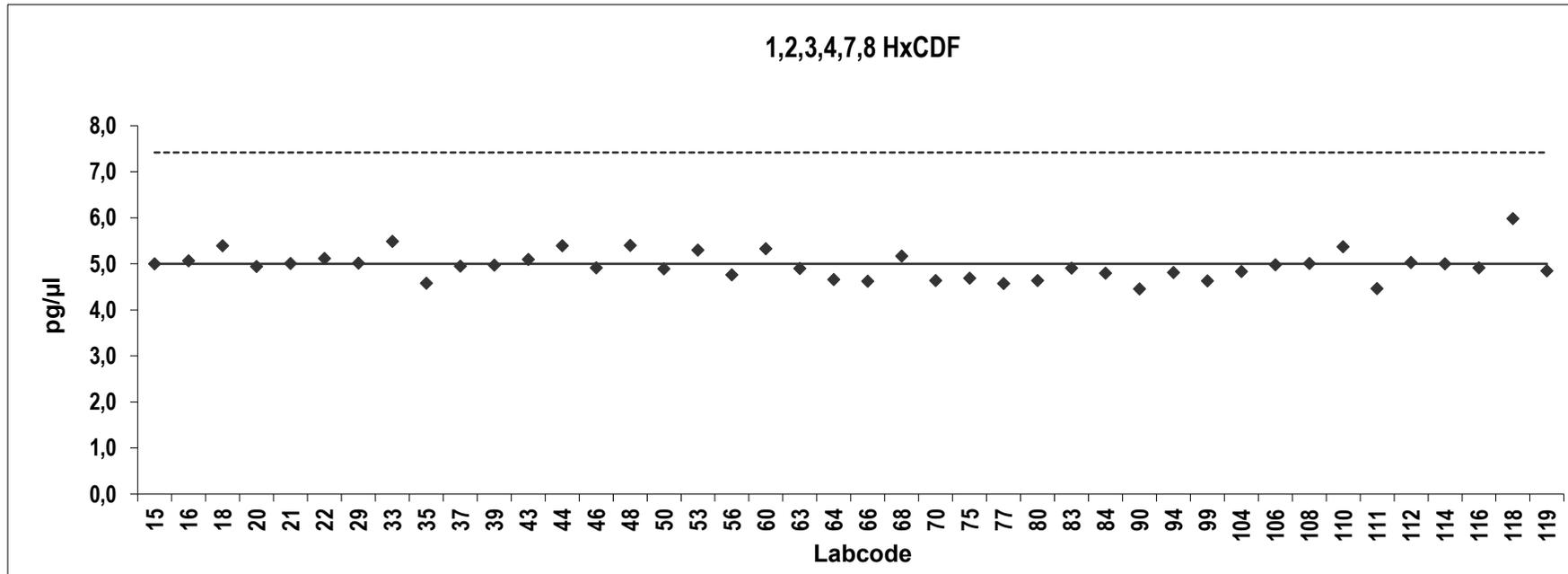


**Analyte solution**  
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	5,0	0,056				
16	5,1	0,12				
18	5,4	0,45				
20	4,9	-0,0051				
21	5,0	0,063				
22	5,1	0,17				
29	5,0	0,073				
33	5,5	0,55				
35	4,6	-0,37				
37	5,0	0,0051				
39	5,0	0,024				
43	5,1	0,15				
44	5,4	0,45				
46	4,9	-0,031				
48	5,4	0,46				
50	4,9	-0,058				
53	5,3	0,36				
56	4,8	-0,19				
60	5,3	0,39				
63	4,9	-0,046				
64	4,7	-0,29				
66	4,6	-0,33				
68	5,2	0,22				
70	4,6	-0,31				
75	4,7	-0,26				
77	4,6	-0,38				
80	4,6	-0,31				
83	4,9	-0,038				
84	4,8	-0,15				
90	4,5	-0,50				
94	4,8	-0,14				
99	4,6	-0,32				
104	4,8	-0,12				
106	5,0	0,035				
108	5,0	0,065				
110	5,4	0,43				
111	4,5	-0,49				
112	5,0	0,086				
114	5,0	0,056				
116	4,9	-0,029				
118	6,0	1,0				
119	4,9	-0,10				

**Consensus statistics**

Consensus median, pg/μl	4,9
Median all values pg/μl	4,9
Consensus mean, pg/μl	5,0
Standard deviation, pg/μl	0,31
Relative standard deviation, %	6,3
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

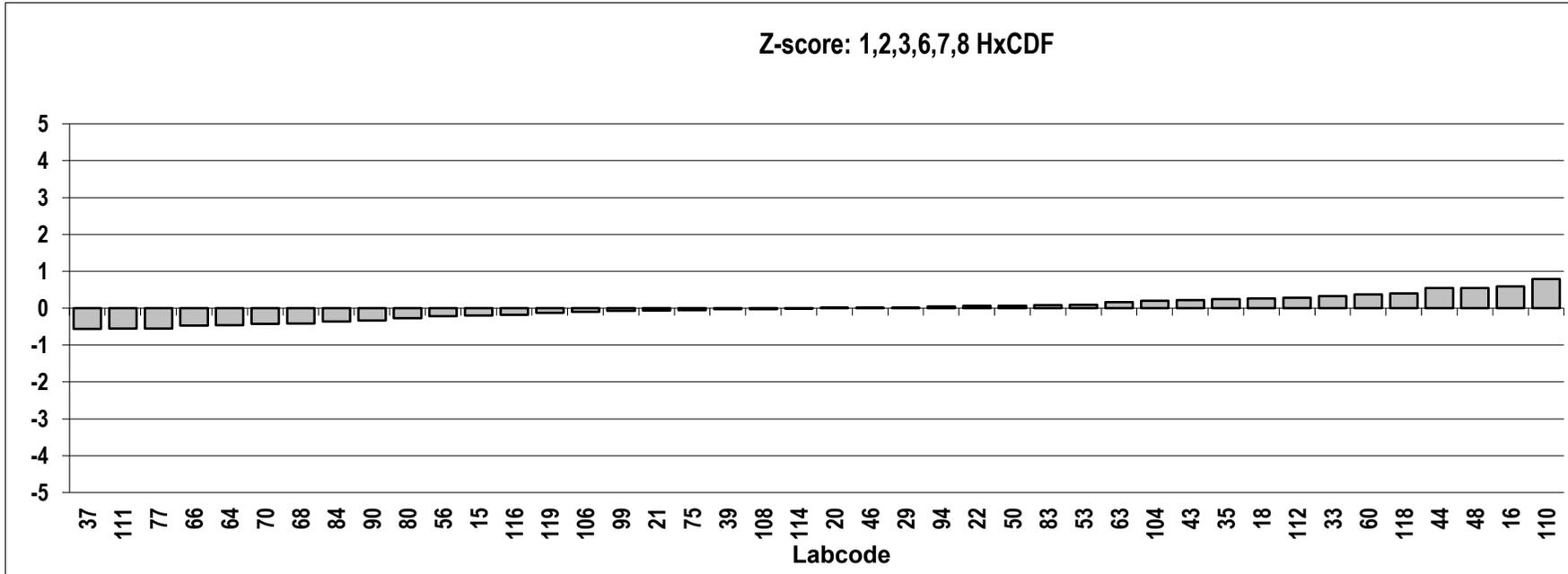
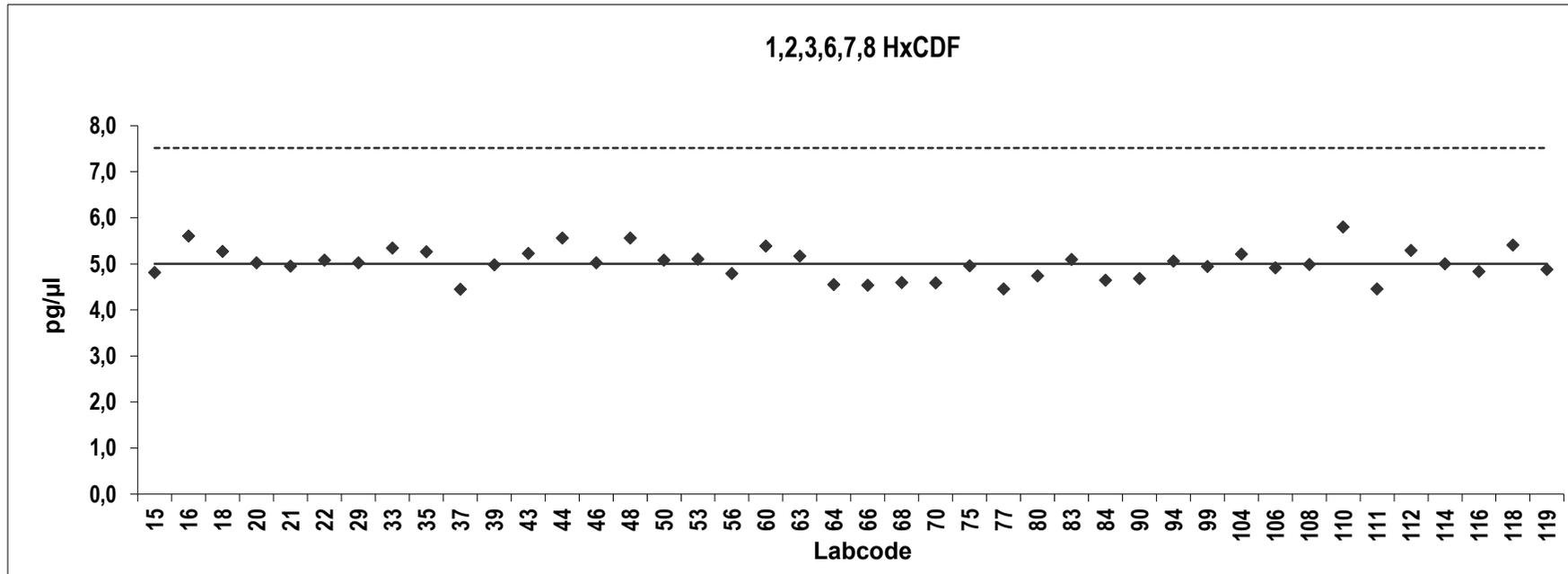


**Analyte solution**  
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,8	-0,20				
16	5,6	0,59				
18	5,3	0,26				
20	5,0	0,010				
21	4,9	-0,062				
22	5,1	0,067				
29	5,0	0,012				
33	5,3	0,33				
35	5,3	0,25				
37	4,5	-0,56				
39	5,0	-0,029				
43	5,2	0,22				
44	5,6	0,55				
46	5,0	0,011				
48	5,6	0,55				
50	5,1	0,068				
53	5,1	0,090				
56	4,8	-0,22				
60	5,4	0,37				
63	5,2	0,16				
64	4,5	-0,46				
66	4,5	-0,48				
68	4,6	-0,42				
70	4,6	-0,42				
75	5,0	-0,053				
77	4,5	-0,56				
80	4,7	-0,27				
83	5,1	0,085				
84	4,6	-0,36				
90	4,7	-0,33				
94	5,1	0,050				
99	4,9	-0,071				
104	5,2	0,20				
106	4,9	-0,10				
108	5,0	-0,022				
110	5,8	0,79				
111	4,5	-0,56				
112	5,3	0,28				
114	5,0	-0,010				
116	4,8	-0,18				
118	5,4	0,40				
119	4,9	-0,13				

**Consensus statistics**

Consensus median, pg/μl	5,0
Median all values pg/μl	5,0
Consensus mean, pg/μl	5,0
Standard deviation, pg/μl	0,33
Relative standard deviation, %	6,6
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

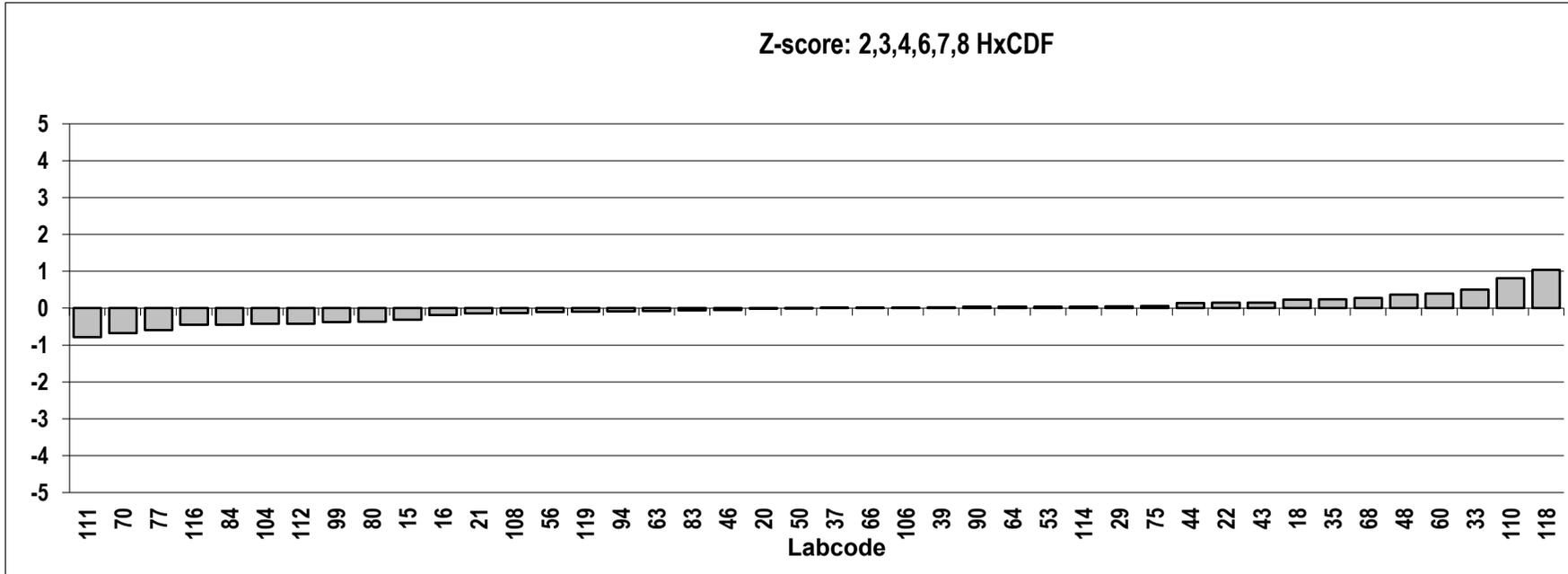
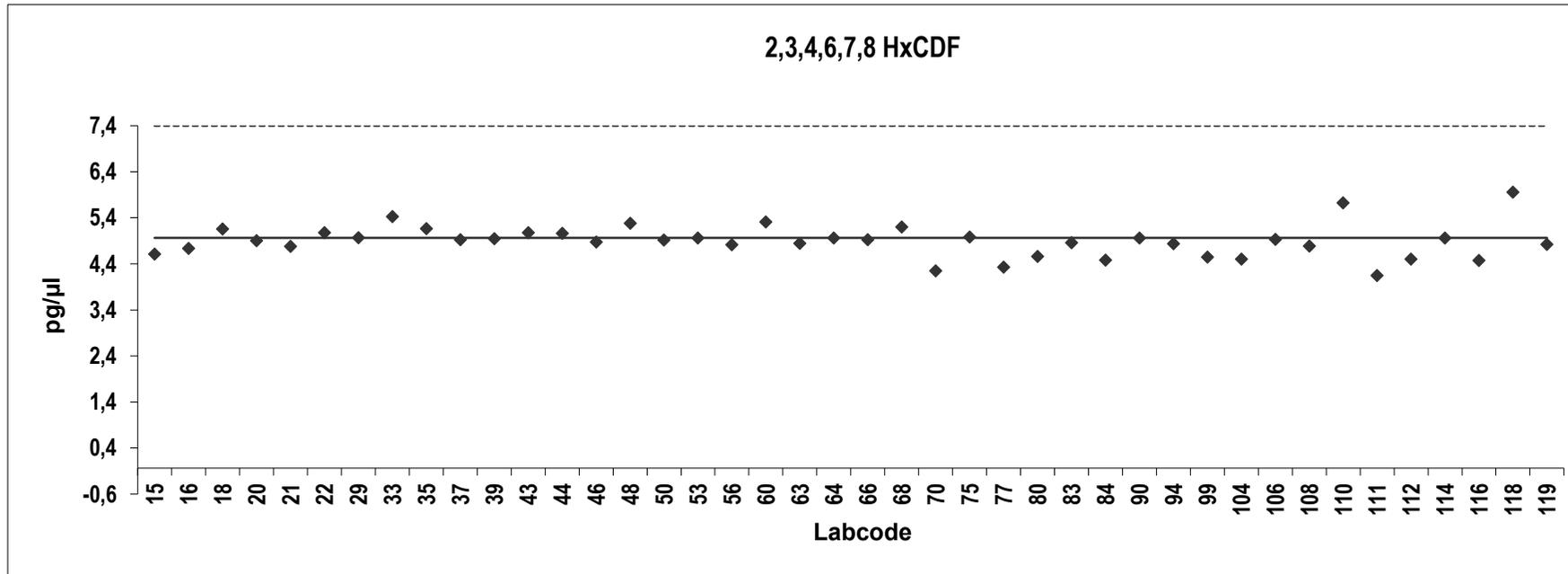


**Analyte solution**  
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,7	-0,31				
16	4,8	-0,19				
18	5,2	0,23				
20	4,9	-0,018				
21	4,8	-0,14				
22	5,1	0,15				
29	5,0	0,047				
33	5,5	0,51				
35	5,2	0,24				
37	5,0	0,0025				
39	5,0	0,023				
43	5,1	0,15				
44	5,1	0,14				
46	4,9	-0,048				
48	5,3	0,37				
50	5,0	-0,0025				
53	5,0	0,043				
56	4,9	-0,11				
60	5,3	0,39				
63	4,9	-0,078				
64	5,0	0,041				
66	5,0	0,0044				
68	5,2	0,28				
70	4,3	-0,68				
75	5,0	0,062				
77	4,4	-0,60				
80	4,6	-0,36				
83	4,9	-0,063				
84	4,5	-0,45				
90	5,0	0,038				
94	4,9	-0,088				
99	4,6	-0,38				
104	4,5	-0,42				
106	5,0	0,013				
108	4,8	-0,14				
110	5,8	0,81				
111	4,2	-0,78				
112	4,5	-0,42				
114	5,0	0,043				
116	4,5	-0,45				
118	6,0	1,0				
119	4,9	-0,10				

**Consensus statistics**

Consensus median, pg/μl	5,0
Median all values pg/μl	5,0
Consensus mean, pg/μl	4,9
Standard deviation, pg/μl	0,35
Relative standard deviation, %	7,2
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

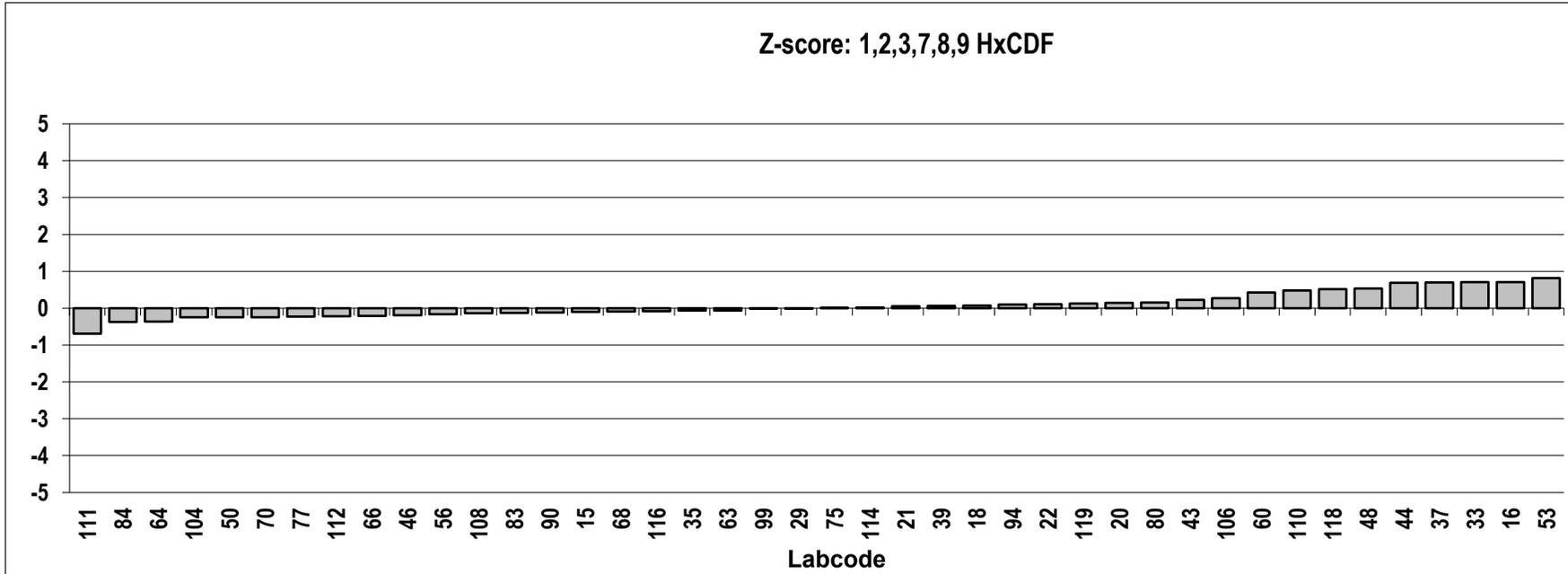
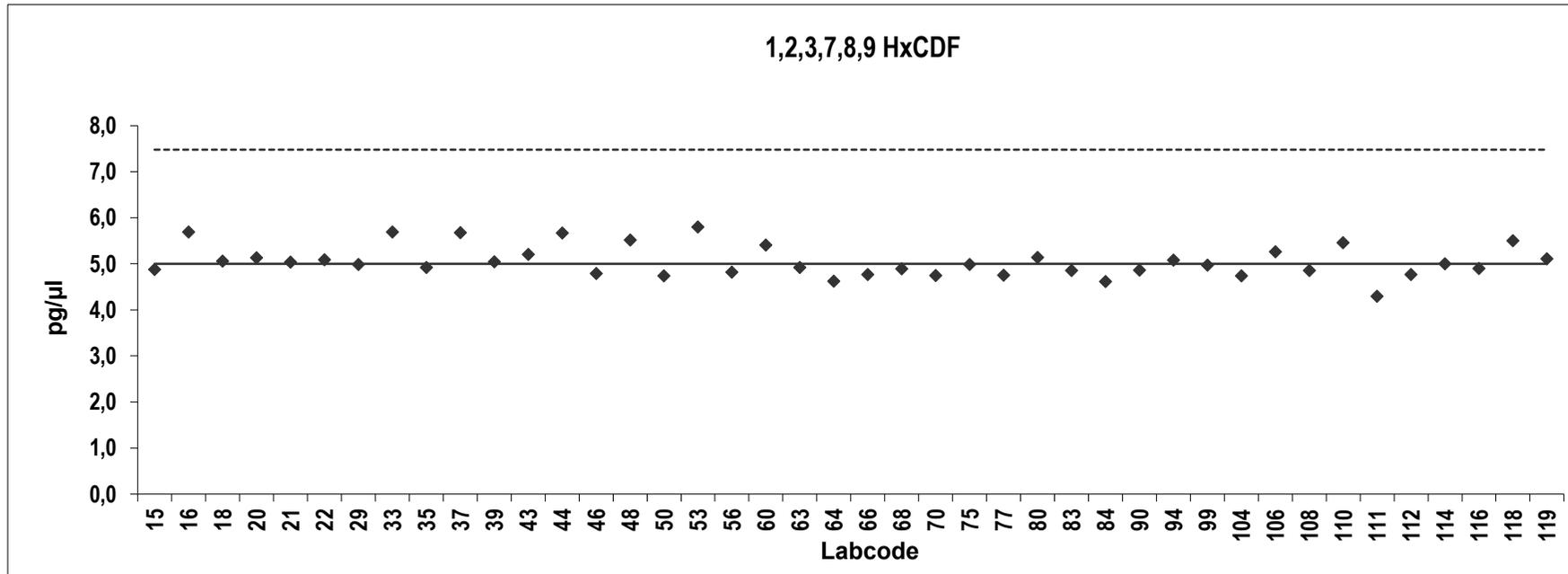


**Analyte solution**  
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,9	-0,11				
16	5,7	0,71				
18	5,1	0,075				
20	5,1	0,14				
21	5,0	0,049				
22	5,1	0,10				
29	5,0	-0,0014				
33	5,7	0,71				
35	4,9	-0,066				
37	5,7	0,70				
39	5,0	0,060				
43	5,2	0,22				
44	5,7	0,69				
46	4,8	-0,20				
48	5,5	0,54				
50	4,7	-0,25				
53	5,8	0,82				
56	4,8	-0,17				
60	5,4	0,42				
63	4,9	-0,066				
64	4,6	-0,37				
66	4,8	-0,21				
68	4,9	-0,091				
70	4,7	-0,24				
75	5,0	0,0014				
77	4,8	-0,23				
80	5,1	0,15				
83	4,9	-0,13				
84	4,6	-0,37				
90	4,9	-0,12				
94	5,1	0,095				
99	5,0	-0,013				
104	4,7	-0,25				
106	5,3	0,28				
108	4,9	-0,13				
110	5,5	0,48				
111	4,3	-0,69				
112	4,8	-0,22				
114	5,0	0,015				
116	4,9	-0,087				
118	5,5	0,52				
119	5,1	0,12				

**Consensus statistics**

Consensus median, pg/μl	5,0
Median all values pg/μl	5,0
Consensus mean, pg/μl	5,1
Standard deviation, pg/μl	0,34
Relative standard deviation, %	6,8
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

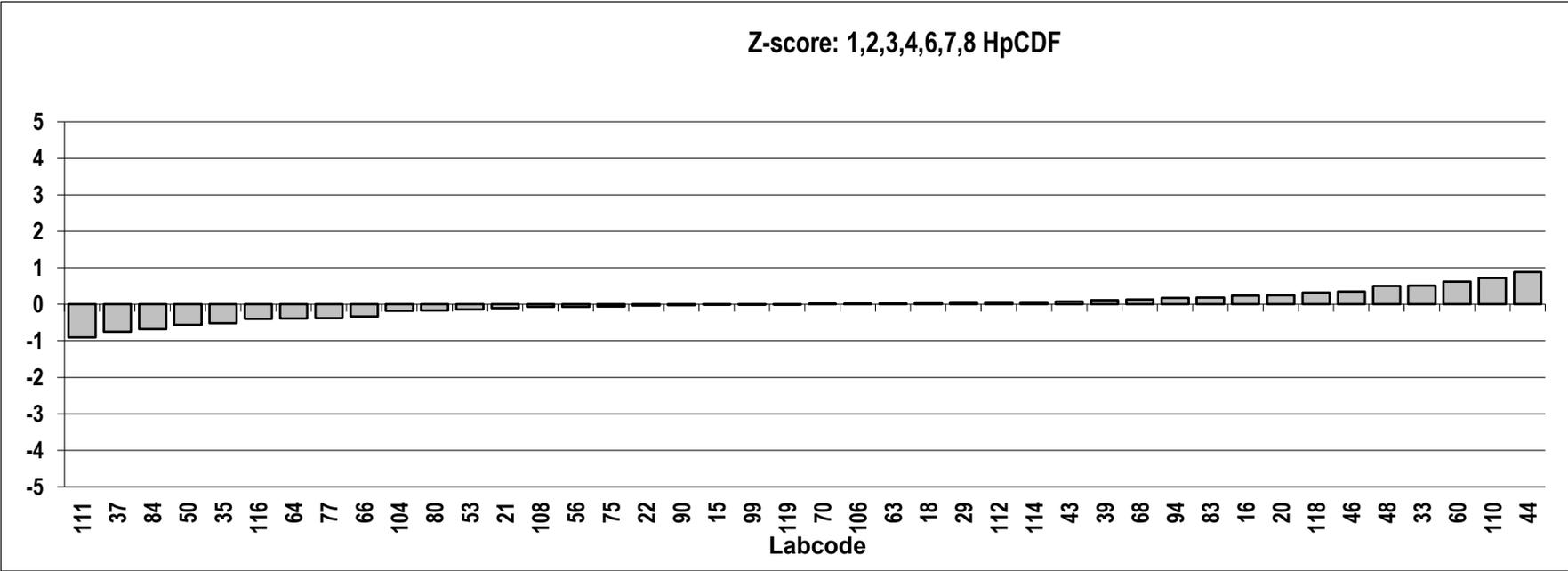
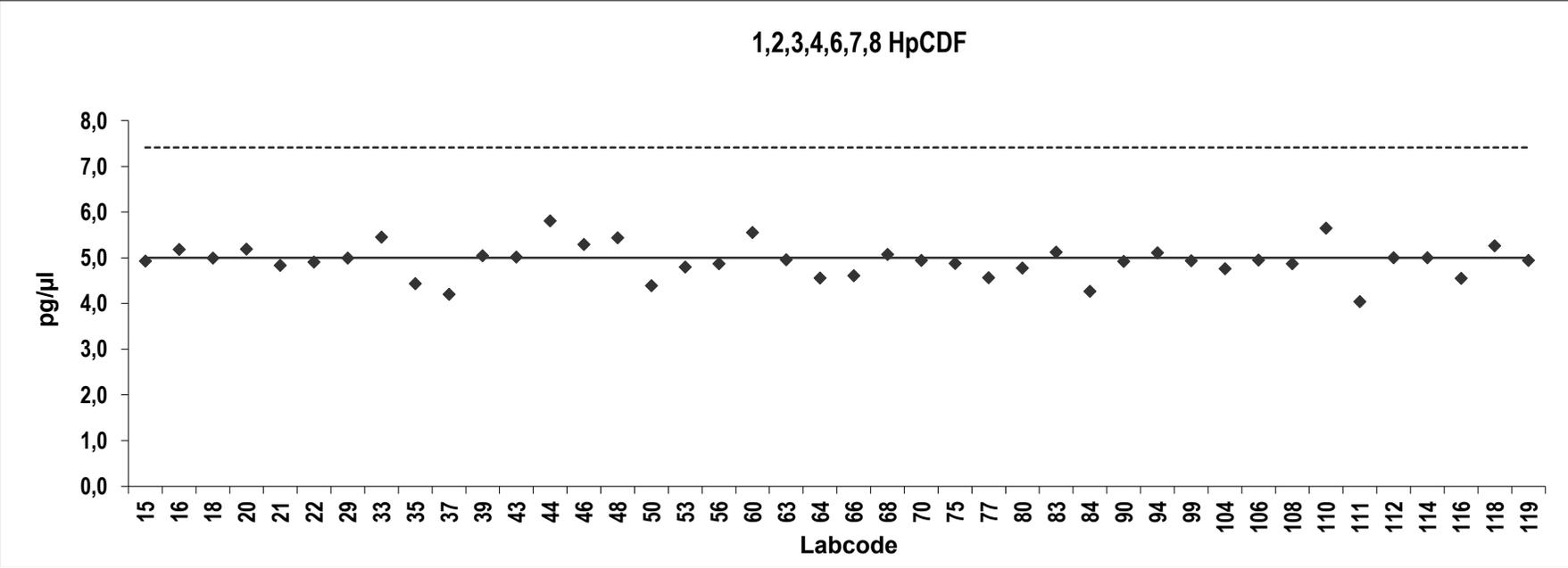


**Analyte solution**  
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,9	-0,012				
16	5,2	0,24				
18	5,0	0,049				
20	5,2	0,25				
21	4,8	-0,11				
22	4,9	-0,032				
29	5,0	0,056				
33	5,5	0,51				
35	4,4	-0,52				
37	4,2	-0,75				
39	5,0	0,11				
43	5,0	0,077				
44	5,8	0,88				
46	5,3	0,35				
48	5,4	0,50				
50	4,4	-0,56				
53	4,8	-0,14				
56	4,9	-0,072				
60	5,6	0,62				
63	5,0	0,019				
64	4,6	-0,39				
66	4,6	-0,34				
68	5,1	0,13				
70	4,9	0,0015				
75	4,9	-0,063				
77	4,6	-0,38				
80	4,8	-0,17				
83	5,1	0,18				
84	4,3	-0,68				
90	4,9	-0,021				
94	5,1	0,17				
99	4,9	-0,0071				
104	4,8	-0,18				
106	5,0	0,0087				
108	4,9	-0,074				
110	5,7	0,72				
111	4,0	-0,91				
112	5,0	0,059				
114	5,0	0,059				
116	4,6	-0,39				
118	5,3	0,32				
119	4,9	-0,0015				

**Consensus statistics**

Consensus median, pg/μl	4,9
Median all values pg/μl	4,9
Consensus mean, pg/μl	4,9
Standard deviation, pg/μl	0,37
Relative standard deviation, %	7,5
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0

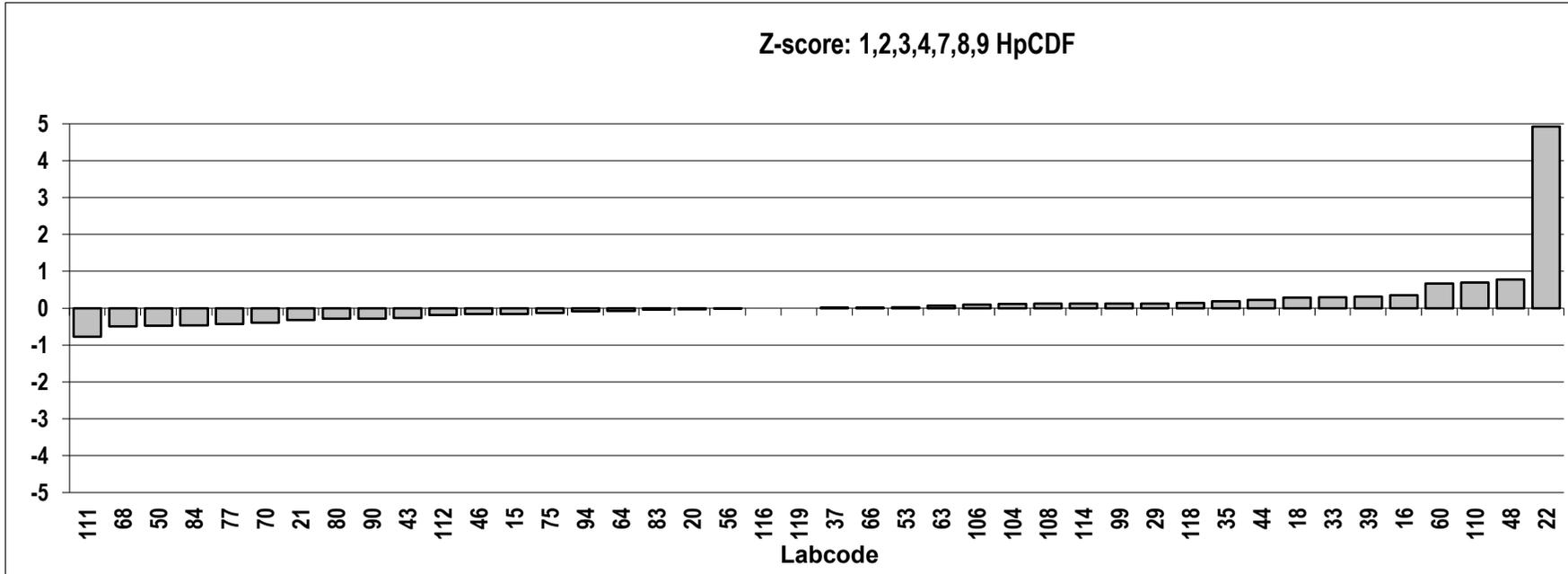
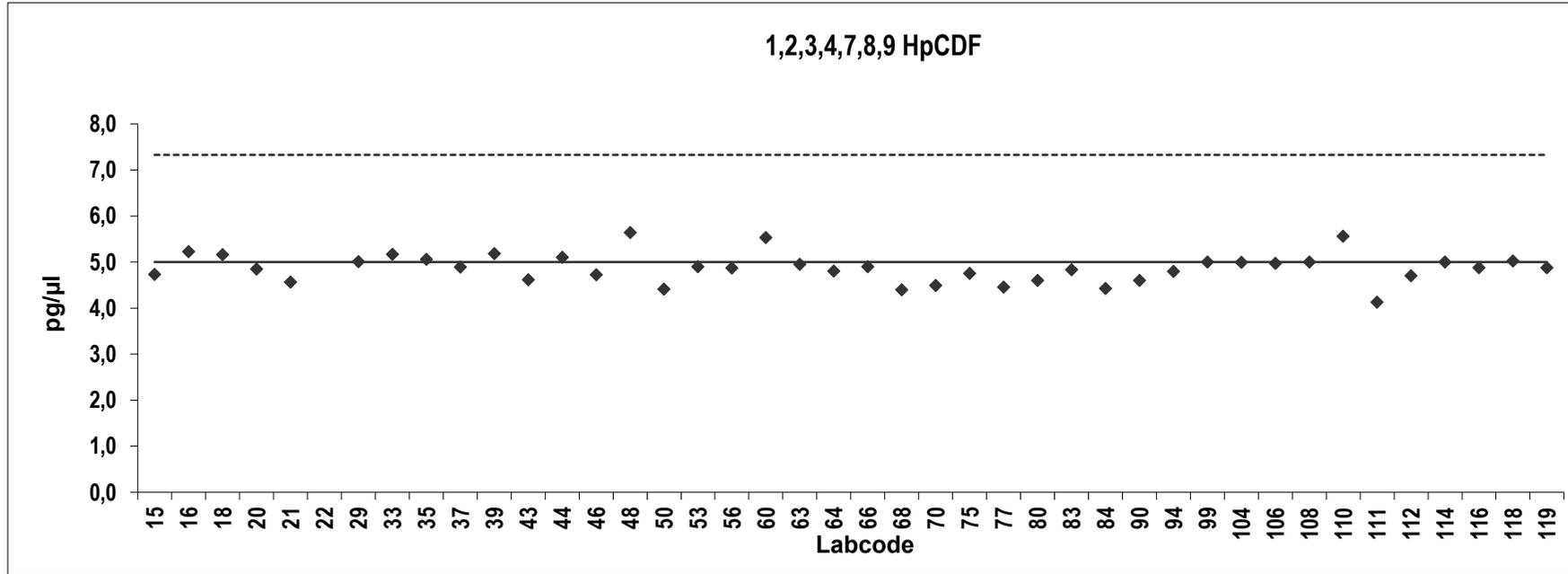


**Analyte solution**  
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	4,7	-0,15				
16	5,2	0,35				
18	5,2	0,29				
20	4,9	-0,031				
21	4,6	-0,32				
22	9,7	4,9	Outlier			
29	5,0	0,13				
33	5,2	0,30				
35	5,1	0,18				
37	4,9	0,010				
39	5,2	0,31				
43	4,6	-0,27				
44	5,1	0,23				
46	4,7	-0,16				
48	5,6	0,78				
50	4,4	-0,48				
53	4,9	0,020				
56	4,9	-0,010				
60	5,5	0,67				
63	5,0	0,072				
64	4,8	-0,077				
66	4,9	0,016				
68	4,4	-0,50				
70	4,5	-0,40				
75	4,8	-0,13				
77	4,5	-0,43				
80	4,6	-0,29				
83	4,8	-0,044				
84	4,4	-0,46				
90	4,6	-0,28				
94	4,8	-0,082				
99	5,0	0,13				
104	5,0	0,11				
106	5,0	0,092				
108	5,0	0,12				
110	5,6	0,70				
111	4,1	-0,77				
112	4,7	-0,18				
114	5,0	0,12				
116	4,9	0,0000				
118	5,0	0,14				
119	4,9	0,0000				

**Consensus statistics**

Consensus median, pg/μl	4,9
Median all values pg/μl	4,9
Consensus mean, pg/μl	4,9
Standard deviation, pg/μl	0,32
Relative standard deviation, %	6,5
No. of values reported	42
No. of values removed	1
No. of reported non-detects	0



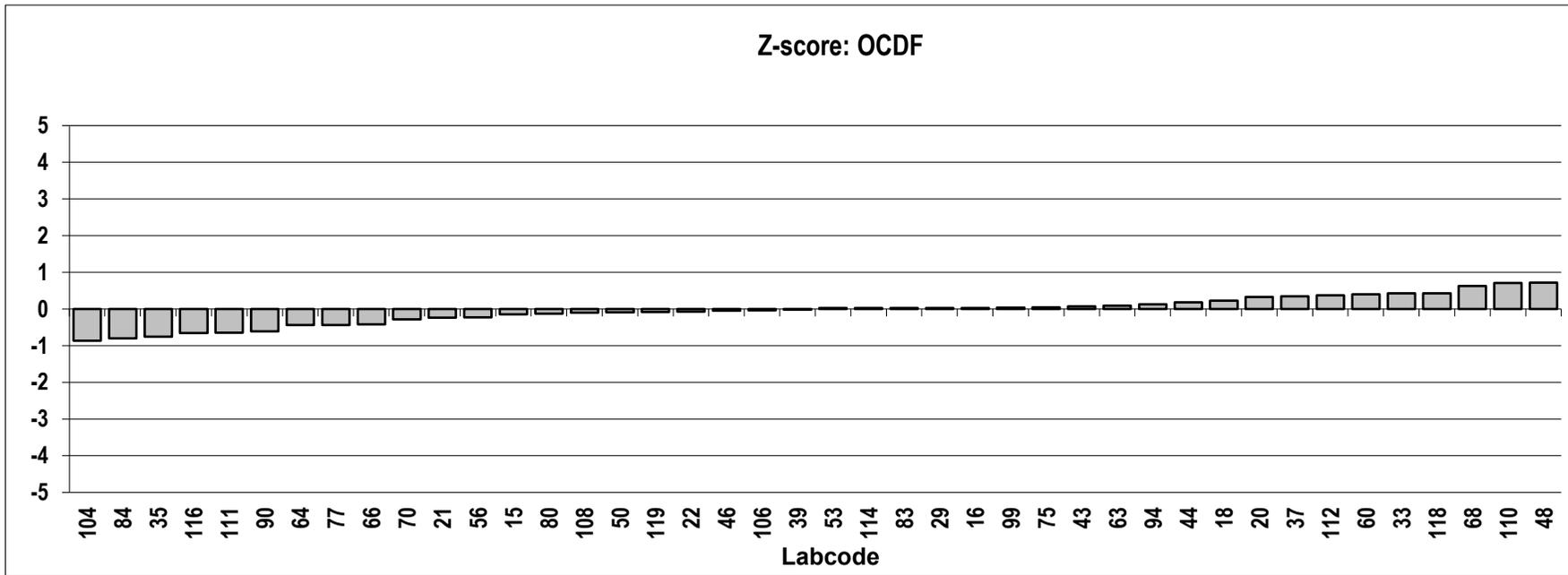
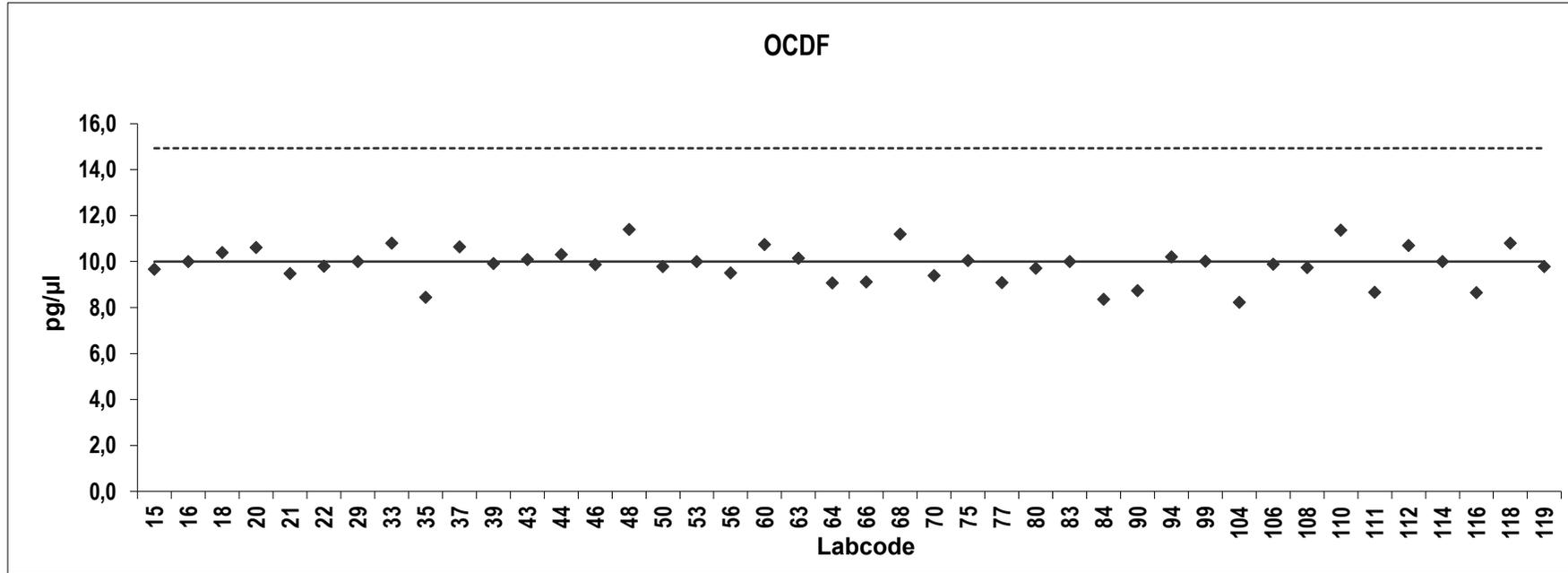
## Analyte solution

Congener: OCDF

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	9,7	-0,15				
16	10	0,026				
18	10	0,22				
20	11	0,33				
21	9,5	-0,24				
22	9,8	-0,075				
29	10	0,025				
33	11	0,43				
35	8,5	-0,76				
37	11	0,34				
39	9,9	-0,023				
43	10	0,071				
44	10	0,18				
46	9,9	-0,044				
48	11	0,72				
50	9,8	-0,089				
53	10	0,023				
56	9,5	-0,23				
60	11	0,40				
63	10	0,094				
64	9,1	-0,44				
66	9,1	-0,42				
68	11	0,63				
70	9,4	-0,28				
75	10	0,048				
77	9,1	-0,44				
80	9,7	-0,13				
83	10	0,025				
84	8,4	-0,80				
90	8,7	-0,61				
94	10	0,12				
99	10	0,031				
104	8,2	-0,87				
106	9,9	-0,037				
108	9,7	-0,11				
110	11	0,71				
111	8,7	-0,65				
112	11	0,37				
114	10	0,023				
116	8,7	-0,65				
118	11	0,43				
119	9,8	-0,087				

### Consensus statistics

Consensus median, pg/μl	10
Median all values pg/μl	10
Consensus mean, pg/μl	9,9
Standard deviation, pg/μl	0,78
Relative standard deviation, %	7,9
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



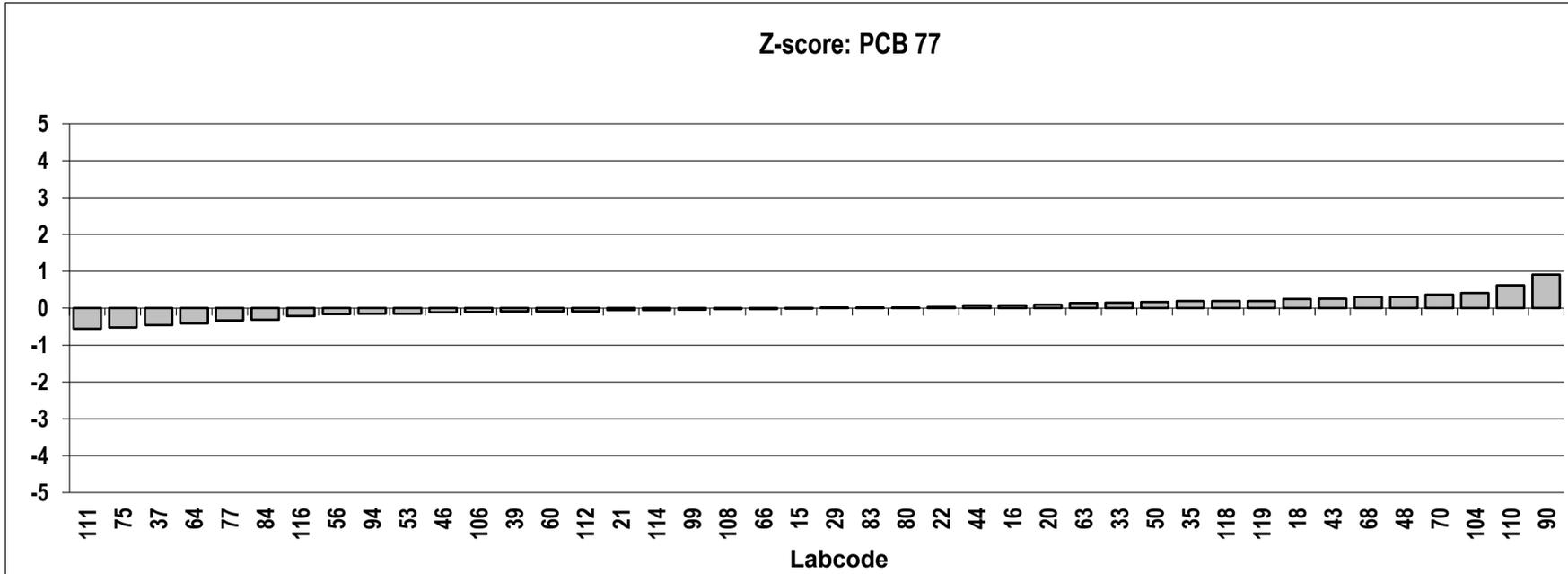
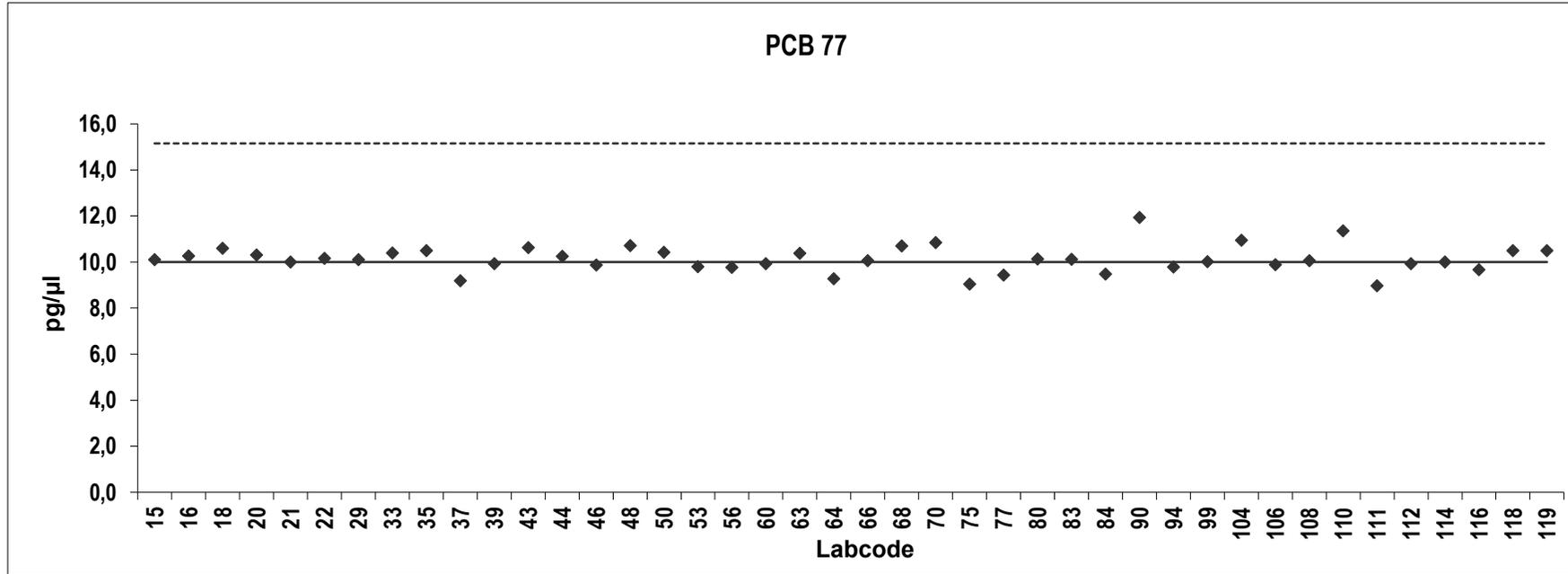
## Analyte solution

Congener: PCB 77

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	10	-0,00033				
16	10	0,080				
18	11	0,25				
20	10	0,10				
21	10	-0,050				
22	10	0,028				
29	10	0,00033				
33	10	0,15				
35	11	0,20				
37	9,2	-0,46				
39	9,9	-0,088				
43	11	0,26				
44	10	0,074				
46	9,9	-0,12				
48	11	0,31				
50	10	0,16				
53	9,8	-0,15				
56	9,8	-0,16				
60	9,9	-0,086				
63	10	0,14				
64	9,3	-0,41				
66	10	-0,022				
68	11	0,30				
70	11	0,37				
75	9,0	-0,52				
77	9,4	-0,33				
80	10	0,014				
83	10	0,012				
84	9,5	-0,31				
90	12	0,91				
94	9,8	-0,15				
99	10	-0,043				
104	11	0,42				
106	9,9	-0,11				
108	10	-0,022				
110	11	0,62				
111	9,0	-0,56				
112	9,9	-0,084				
114	10	-0,050				
116	9,7	-0,22				
118	11	0,20				
119	11	0,20				

### Consensus statistics

Consensus median, pg/μl	10
Median all values pg/μl	10
Consensus mean, pg/μl	10
Standard deviation, pg/μl	0,58
Relative standard deviation, %	5,7
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



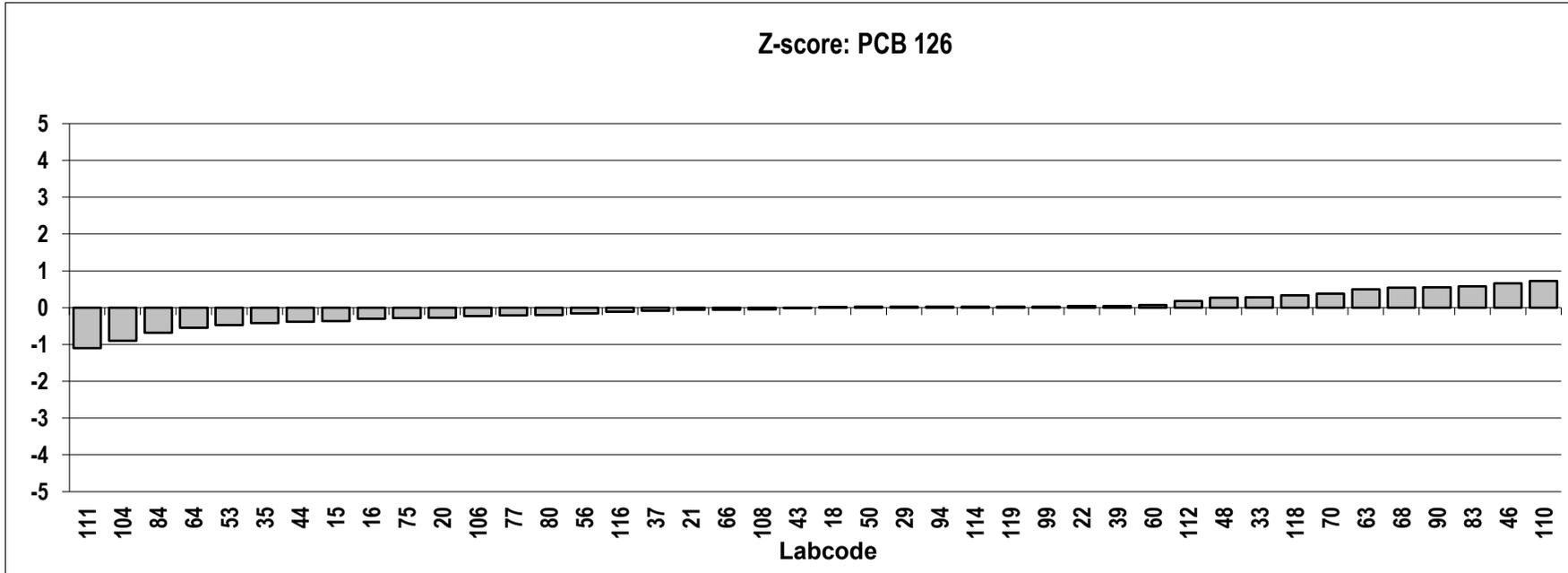
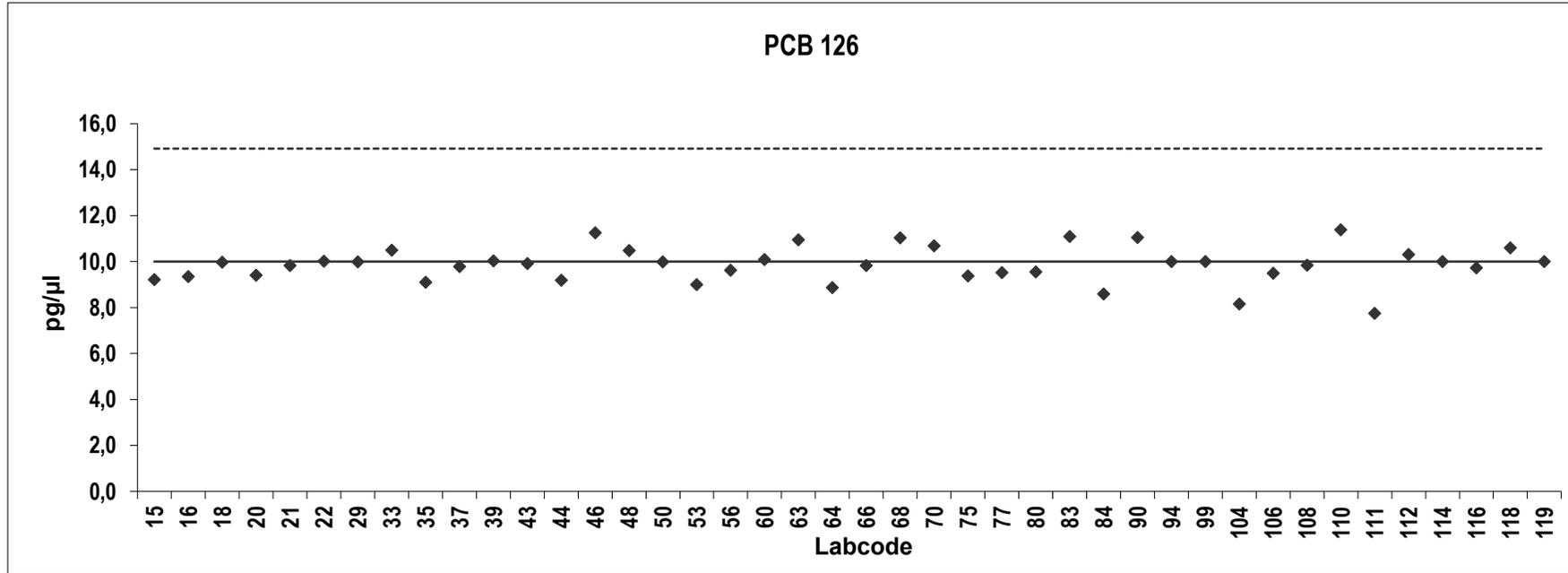
## Analyte solution

Congener: PCB 126

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	9,2	-0,36				
16	9,3	-0,30				
18	10	0,014				
20	9,4	-0,27				
21	9,8	-0,059				
22	10	0,040				
29	10	0,025				
33	11	0,28				
35	9,1	-0,42				
37	9,8	-0,082				
39	10	0,047				
43	9,9	-0,014				
44	9,2	-0,38				
46	11	0,66				
48	10	0,27				
50	10	0,022				
53	9,0	-0,47				
56	9,6	-0,16				
60	10	0,074				
63	11	0,50				
64	8,9	-0,54				
66	9,8	-0,058				
68	11	0,55				
70	11	0,37				
75	9,4	-0,29				
77	9,5	-0,21				
80	9,5	-0,20				
83	11	0,58				
84	8,6	-0,68				
90	11	0,55				
94	10	0,029				
99	10	0,029				
104	8,2	-0,90				
106	9,5	-0,23				
108	9,8	-0,051				
110	11	0,72				
111	7,7	-1,1				
112	10	0,18				
114	10	0,029				
116	9,7	-0,11				
118	11	0,33				
119	10	0,029				

### Consensus statistics

Consensus median, pg/μl	9,9
Median all values pg/μl	9,9
Consensus mean, pg/μl	9,9
Standard deviation, pg/μl	0,79
Relative standard deviation, %	8,0
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



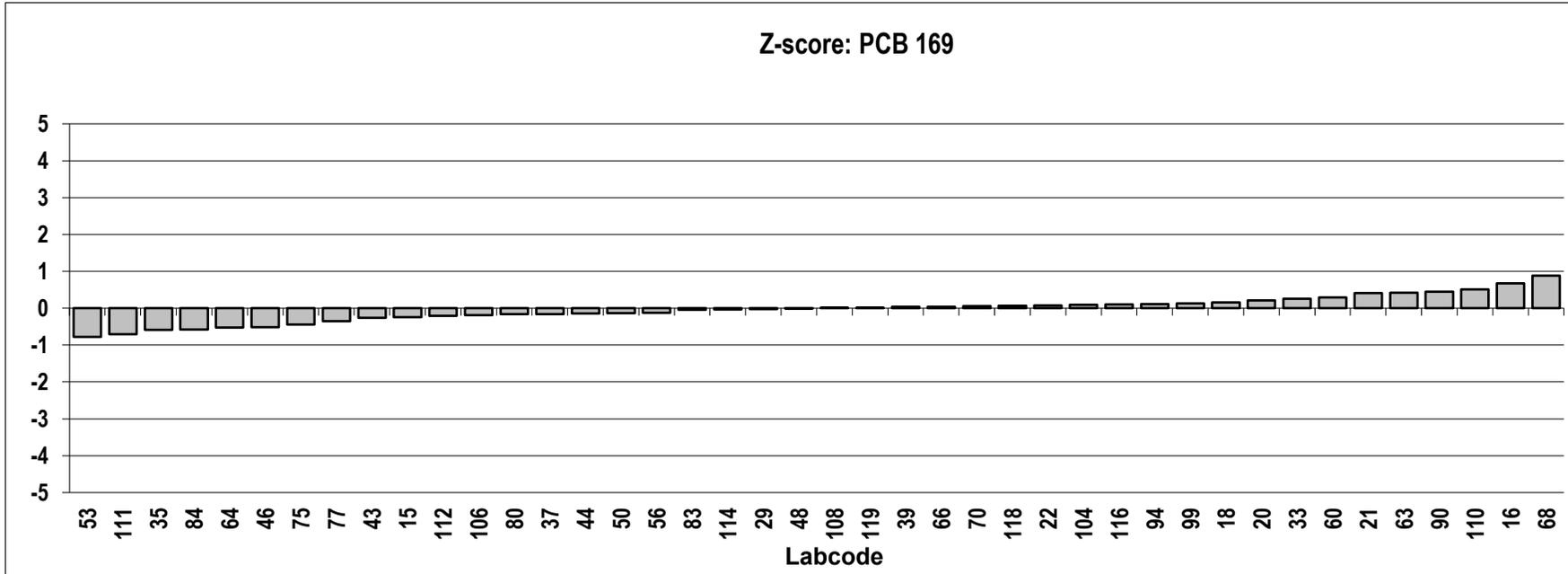
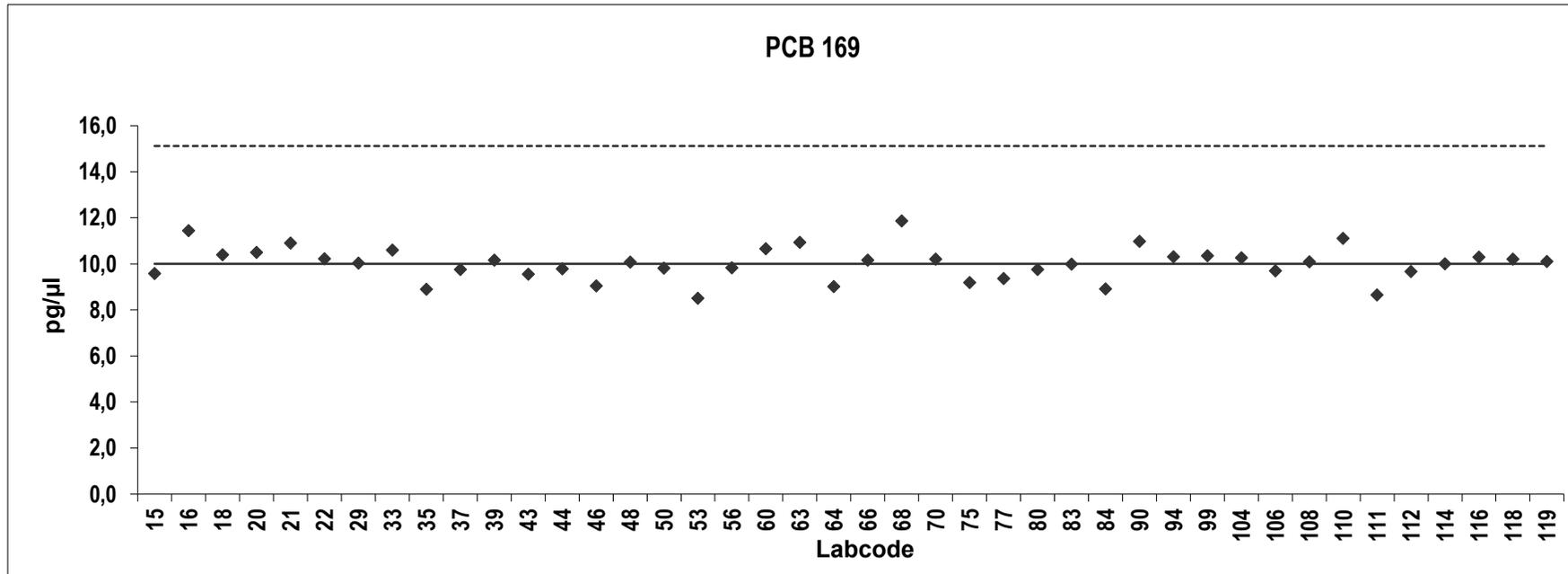
## Analyte solution

Congener: PCB 169

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	9,6	-0,25				
16	11	0,68				
18	10	0,16				
20	11	0,21				
21	11	0,41				
22	10	0,073				
29	10	-0,024				
33	11	0,26				
35	8,9	-0,58				
37	9,8	-0,16				
39	10	0,041				
43	9,5	-0,26				
44	9,8	-0,14				
46	9,0	-0,52				
48	10	-0,0040				
50	9,8	-0,13				
53	8,5	-0,78				
56	9,8	-0,13				
60	11	0,29				
63	11	0,42				
64	9,0	-0,53				
66	10	0,042				
68	12	0,88				
70	10	0,060				
75	9,2	-0,44				
77	9,4	-0,35				
80	9,8	-0,16				
83	10	-0,047				
84	8,9	-0,58				
90	11	0,45				
94	10	0,11				
99	10	0,13				
104	10	0,10				
106	9,7	-0,19				
108	10	0,0040				
110	11	0,51				
111	8,7	-0,71				
112	9,7	-0,21				
114	10	-0,039				
116	10	0,10				
118	10	0,060				
119	10	0,01				

### Consensus statistics

Consensus median, pg/μl	10
Median all values pg/μl	10
Consensus mean, pg/μl	10
Standard deviation, pg/μl	0,72
Relative standard deviation, %	7,2
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



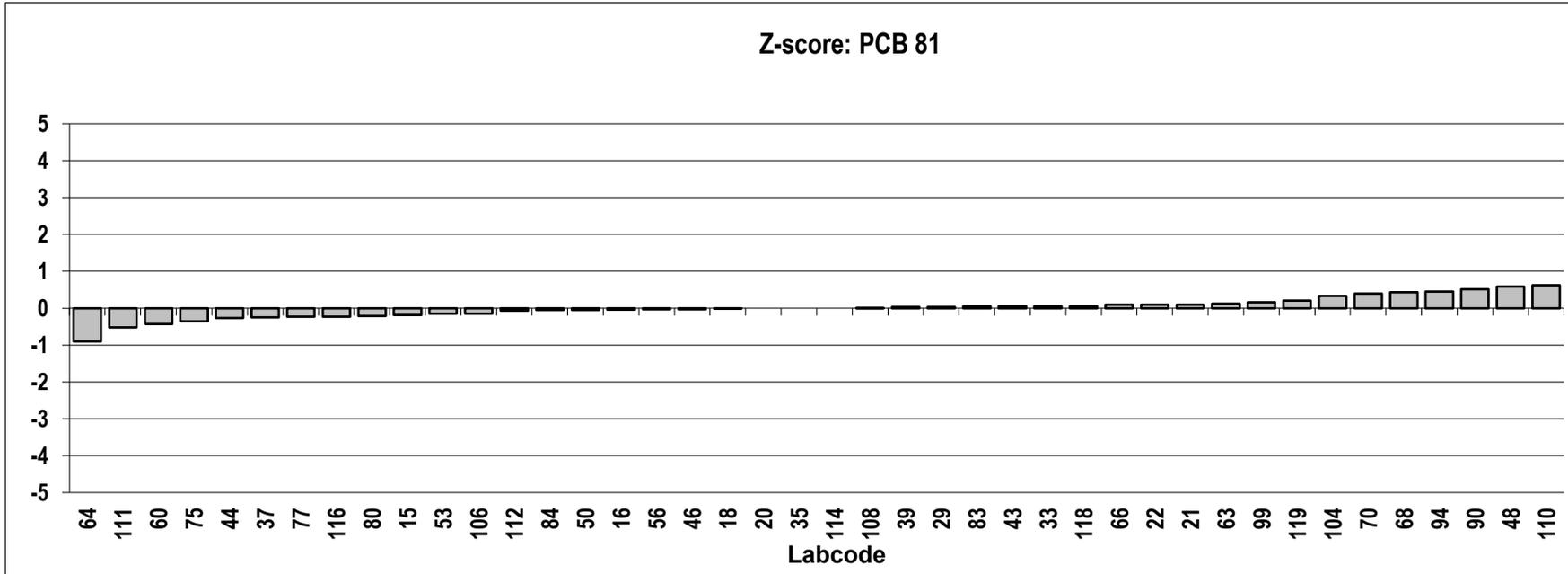
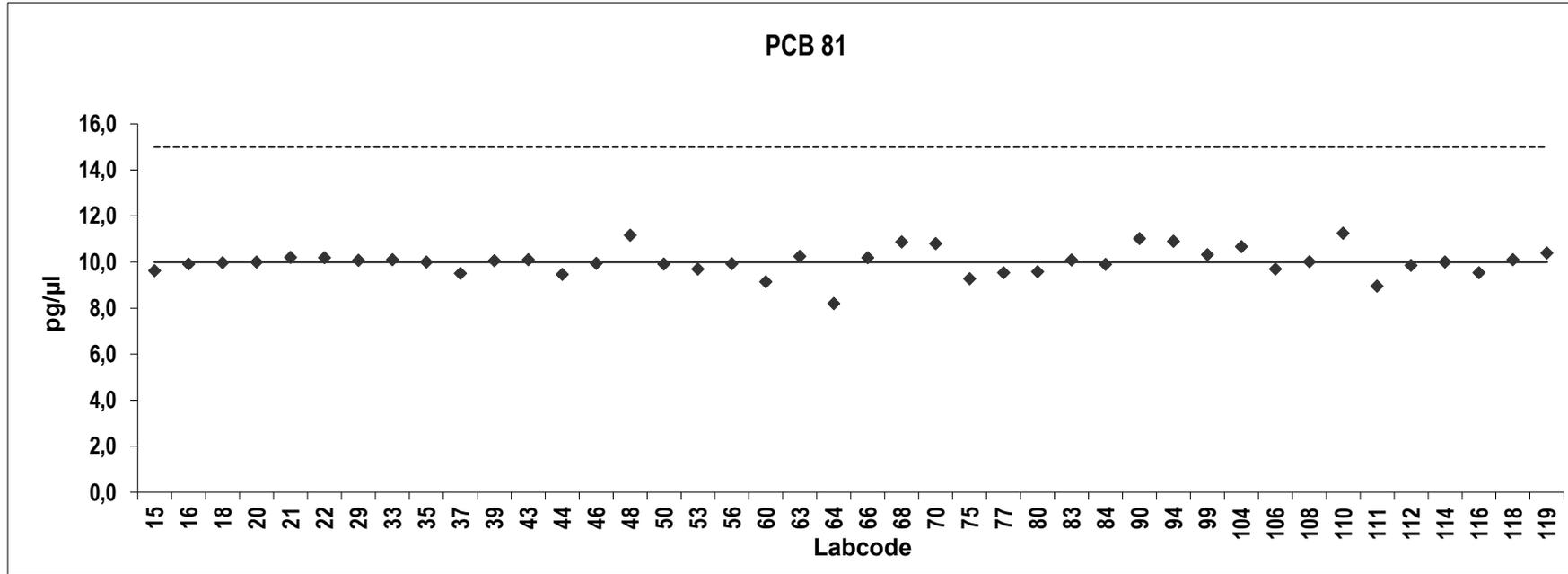
## Analyte solution

Congener: PCB 81

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	9,6	-0,19				
16	9,9	-0,045				
18	10	-0,015				
20	10	0,00000				
21	10	0,10				
22	10	0,10				
29	10	0,035				
33	10	0,050				
35	10	0,00000				
37	9,5	-0,25				
39	10	0,033				
43	10	0,050				
44	9,5	-0,27				
46	9,9	-0,031				
48	11	0,59				
50	9,9	-0,045				
53	9,7	-0,15				
56	9,9	-0,035				
60	9,1	-0,43				
63	10	0,13				
64	8,2	-0,90				
66	10	0,10				
68	11	0,44				
70	11	0,40				
75	9,3	-0,36				
77	9,5	-0,23				
80	9,6	-0,21				
83	10	0,047				
84	9,9	-0,048				
90	11	0,51				
94	11	0,45				
99	10	0,16				
104	11	0,34				
106	9,7	-0,15				
108	10	0,0085				
110	11	0,63				
111	9,0	-0,52				
112	9,9	-0,070				
114	10	0,00000				
116	9,5	-0,23				
118	10	0,050				
119	10	0,20				

### Consensus statistics

Consensus median, pg/μl	10
Median all values pg/μl	10
Consensus mean, pg/μl	10
Standard deviation, pg/μl	0,59
Relative standard deviation, %	5,9
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



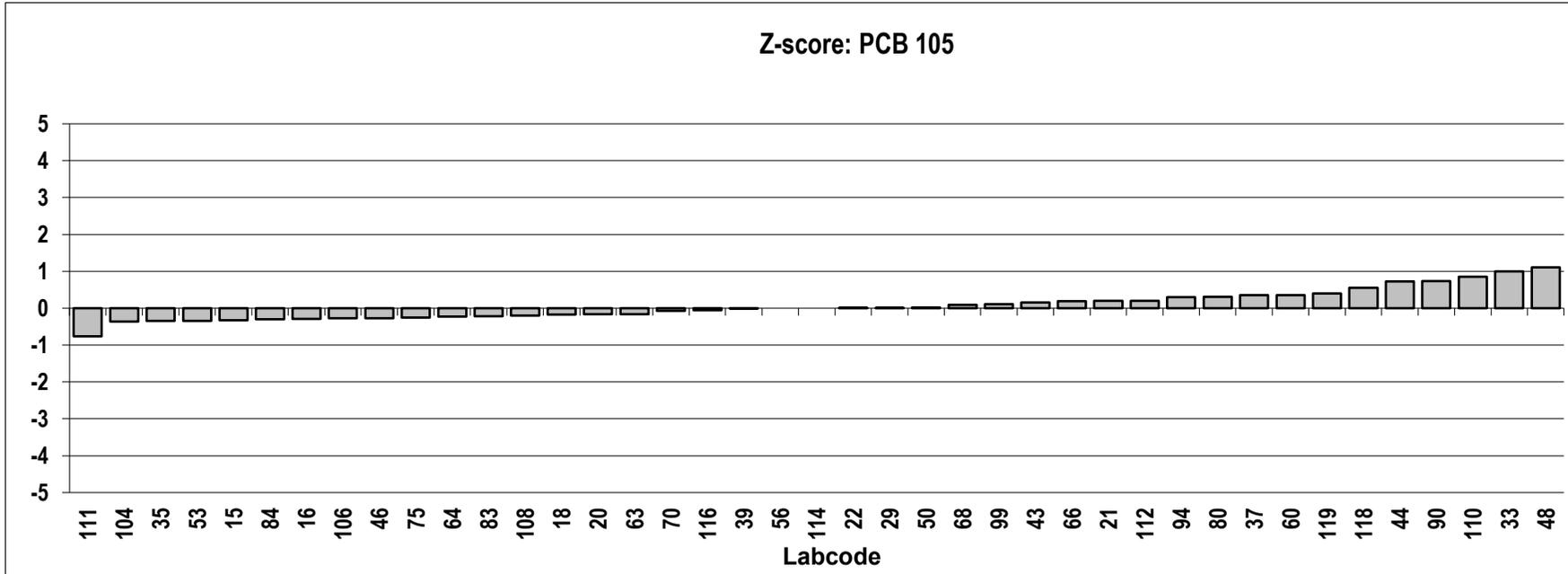
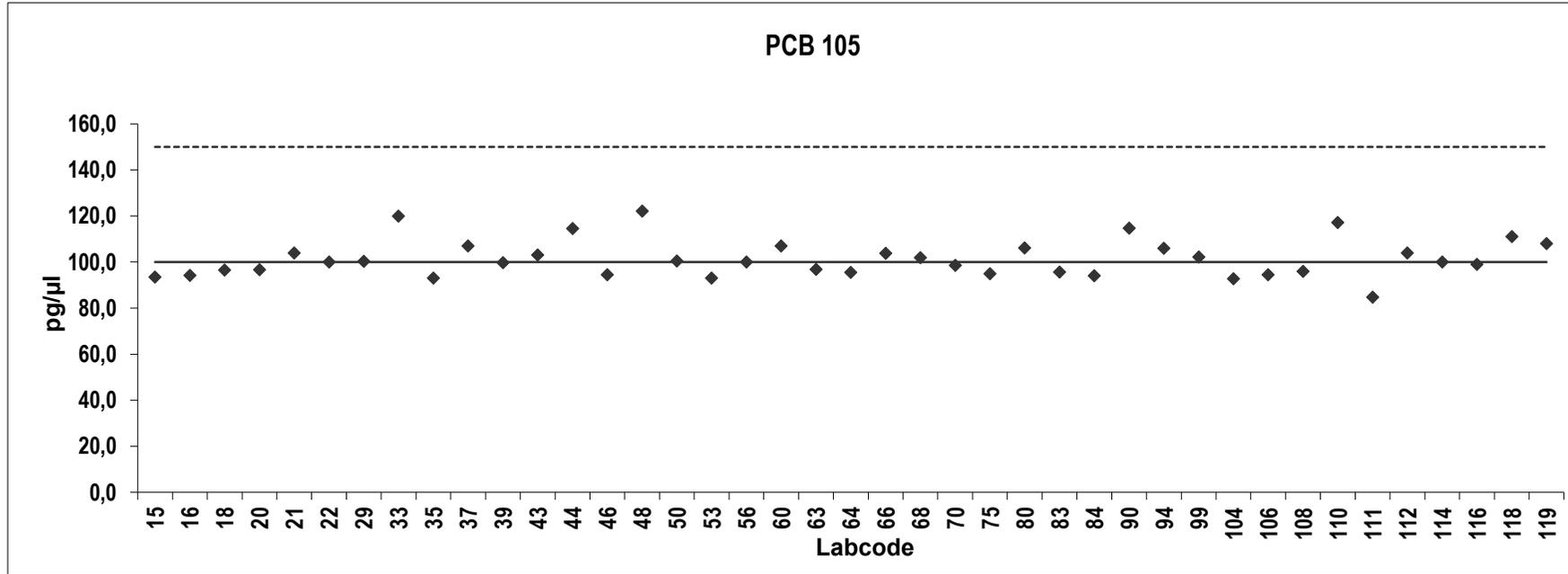
## Analyte solution

Congener: PCB 105

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	93	-0,33				
16	94	-0,29				
18	97	-0,18				
20	97	-0,17				
21	104	0,20				
22	100	0,00093				
29	100	0,013				
33	120	1,0				
35	93	-0,35				
37	107	0,35				
39	100	-0,014				
43	103	0,15				
44	115	0,73				
46	95	-0,27				
48	122	1,1				
50	100	0,020				
53	93	-0,35				
56	100	0,00000				
60	107	0,35				
63	97	-0,16				
64	96	-0,22				
66	104	0,19				
68	102	0,094				
70	99	-0,070				
75	95	-0,25				
80	106	0,31				
83	96	-0,22				
84	94	-0,30				
90	115	0,73				
94	106	0,30				
99	102	0,11				
104	93	-0,37				
106	95	-0,28				
108	96	-0,20				
110	117	0,86				
111	85	-0,76				
112	104	0,20				
114	100	0,00000				
116	99	-0,054				
118	111	0,55				
119	108	0,40				

### Consensus statistics

Consensus median, pg/μl	100
Median all values pg/μl	100
Consensus mean, pg/μl	101
Standard deviation, pg/μl	8,1
Relative standard deviation, %	8,0
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



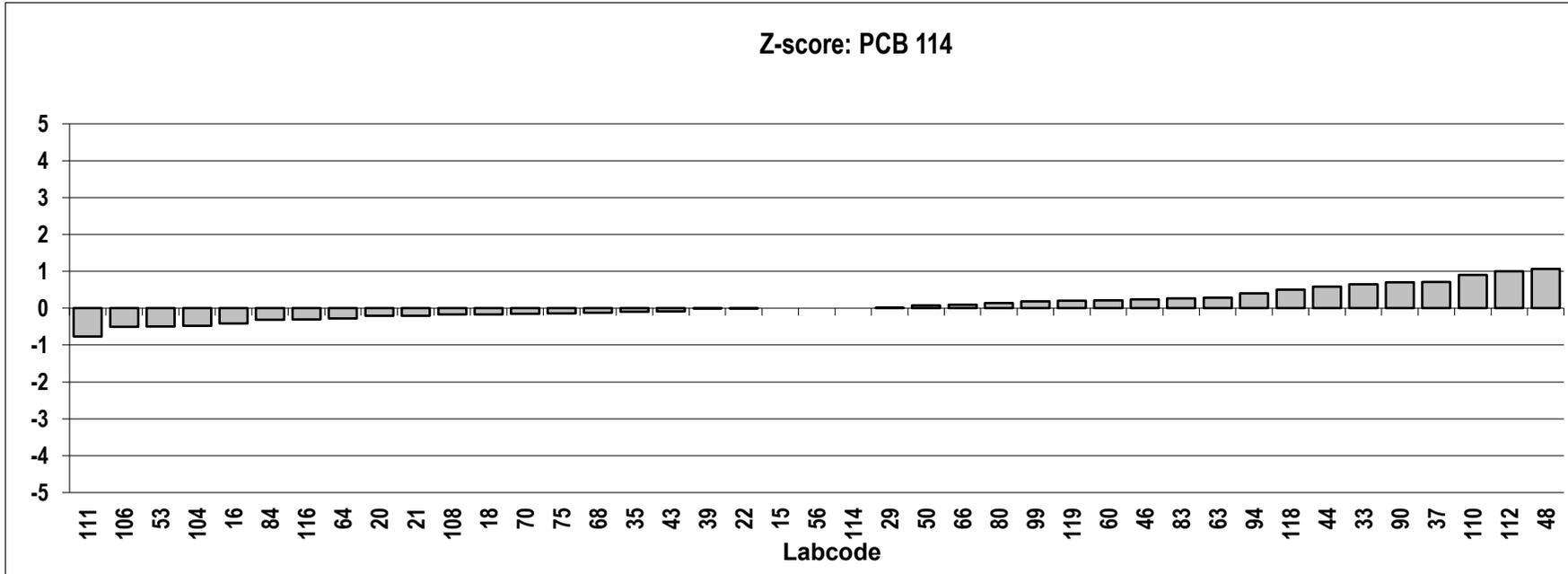
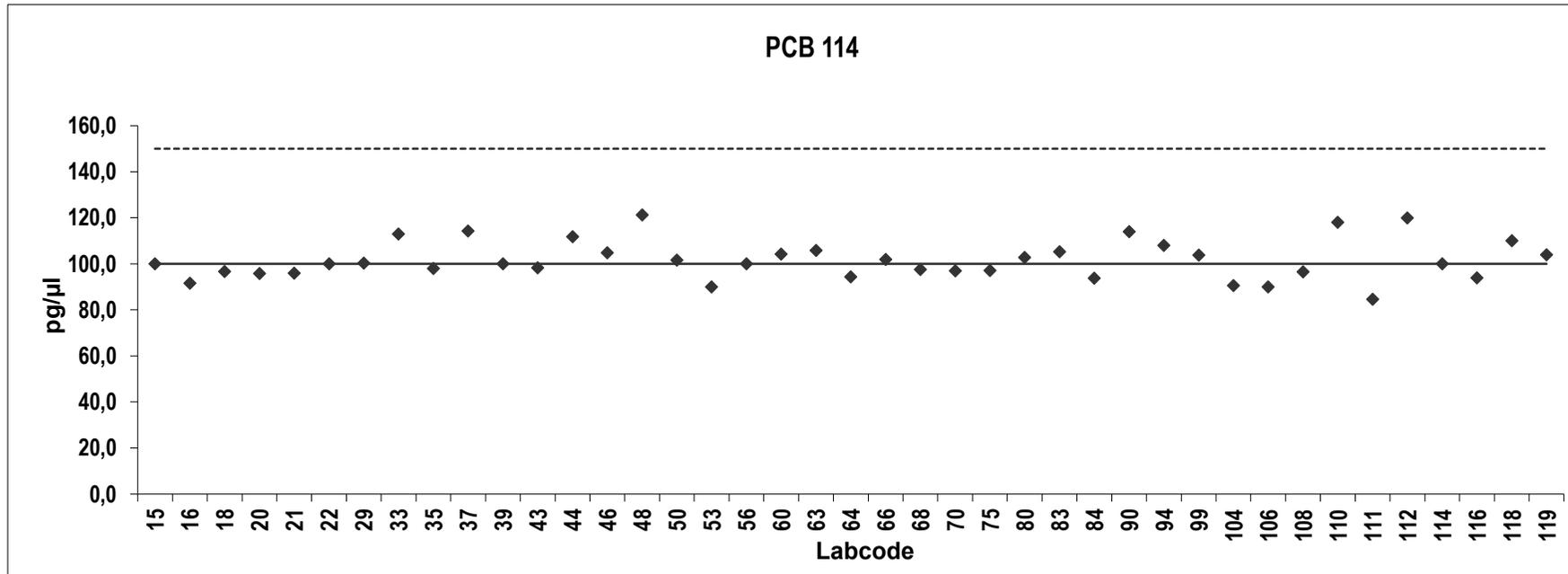
## Analyte solution

Congener: PCB 114

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	100	0,00000				
16	92	-0,42				
18	97	-0,17				
20	96	-0,21				
21	96	-0,21				
22	100	-0,00067				
29	100	0,016				
33	113	0,65				
35	98	-0,10				
37	114	0,71				
39	100	-0,0015				
43	98	-0,087				
44	112	0,59				
46	105	0,24				
48	121	1,1				
50	102	0,078				
53	90	-0,50				
56	100	0,00000				
60	104	0,21				
63	106	0,29				
64	94	-0,28				
66	102	0,10				
68	98	-0,12				
70	97	-0,15				
75	97	-0,14				
80	103	0,14				
83	105	0,26				
84	94	-0,31				
90	114	0,70				
94	108	0,40				
99	104	0,19				
104	91	-0,48				
106	90	-0,50				
108	97	-0,17				
110	118	0,90				
111	85	-0,77				
112	120	1,0				
114	100	0,00000				
116	94	-0,31				
118	110	0,50				
119	104	0,20				

### Consensus statistics

Consensus median, pg/μl	100
Median all values pg/μl	100
Consensus mean, pg/μl	102
Standard deviation, pg/μl	8,5
Relative standard deviation, %	8,3
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



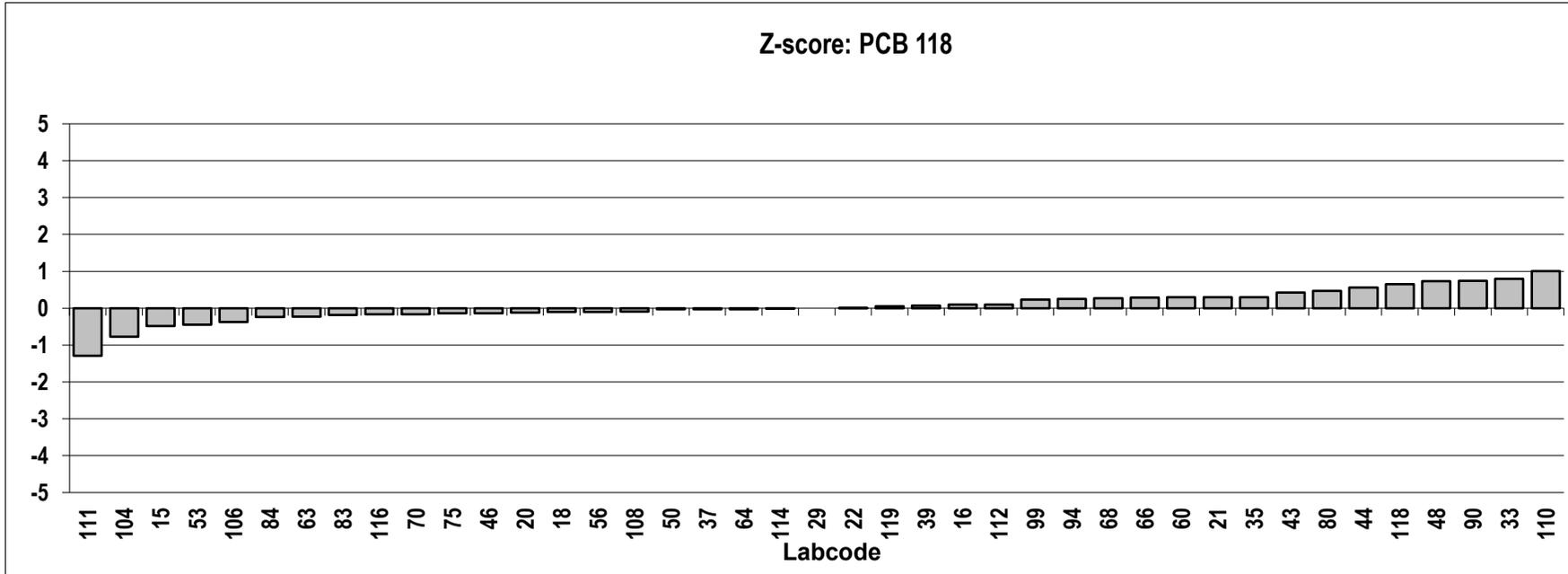
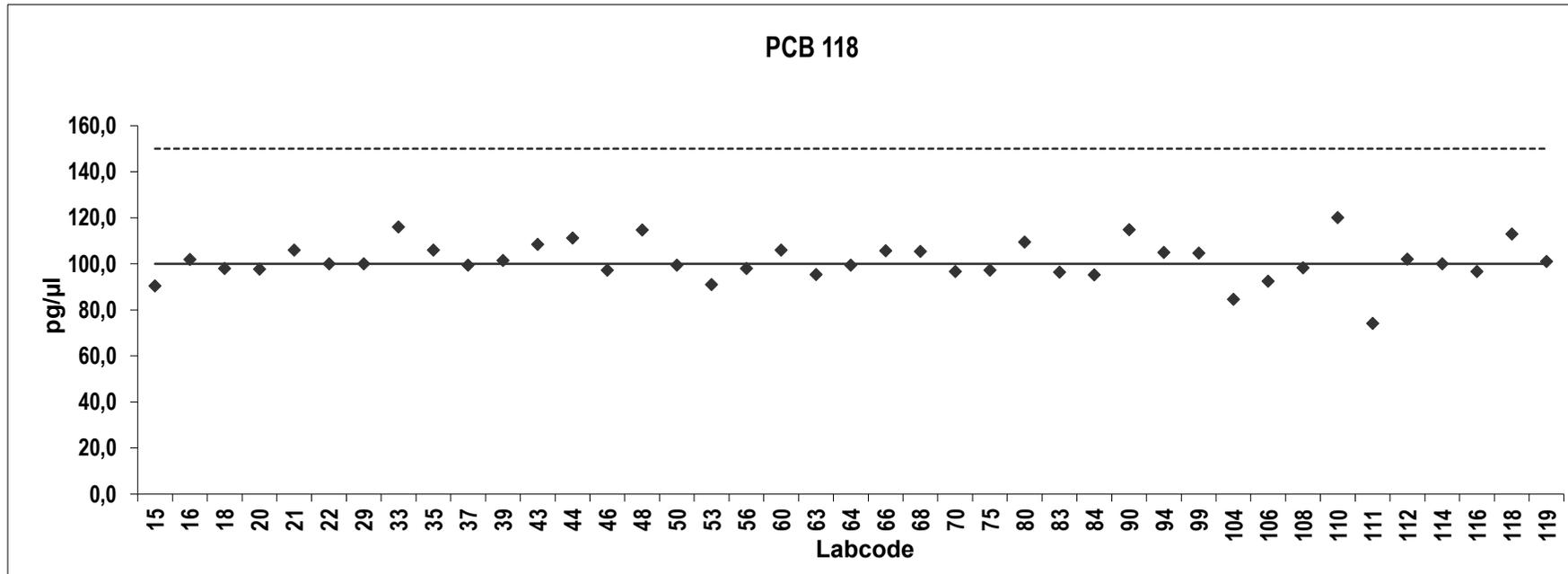
## Analyte solution

Congener: PCB 118

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	90	-0,48				
16	102	0,095				
18	98	-0,10				
20	98	-0,12				
21	106	0,30				
22	100	0,0027				
29	100	0,00000				
33	116	0,80				
35	106	0,30				
37	99	-0,027				
39	101	0,073				
43	108	0,42				
44	111	0,56				
46	97	-0,14				
48	115	0,73				
50	99	-0,028				
53	91	-0,45				
56	98	-0,10				
60	106	0,29				
63	95	-0,23				
64	99	-0,026				
66	106	0,29				
68	105	0,27				
70	97	-0,17				
75	97	-0,14				
80	109	0,47				
83	96	-0,18				
84	95	-0,24				
90	115	0,74				
94	105	0,25				
99	105	0,24				
104	85	-0,77				
106	93	-0,38				
108	98	-0,090				
110	120	1,0				
111	74	-1,3				
112	102	0,10				
114	100	-0,00025				
116	97	-0,17				
118	113	0,65				
119	101	0,050				

### Consensus statistics

Consensus median, pg/μl	100
Median all values pg/μl	100
Consensus mean, pg/μl	101
Standard deviation, pg/μl	8,6
Relative standard deviation, %	8,5
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



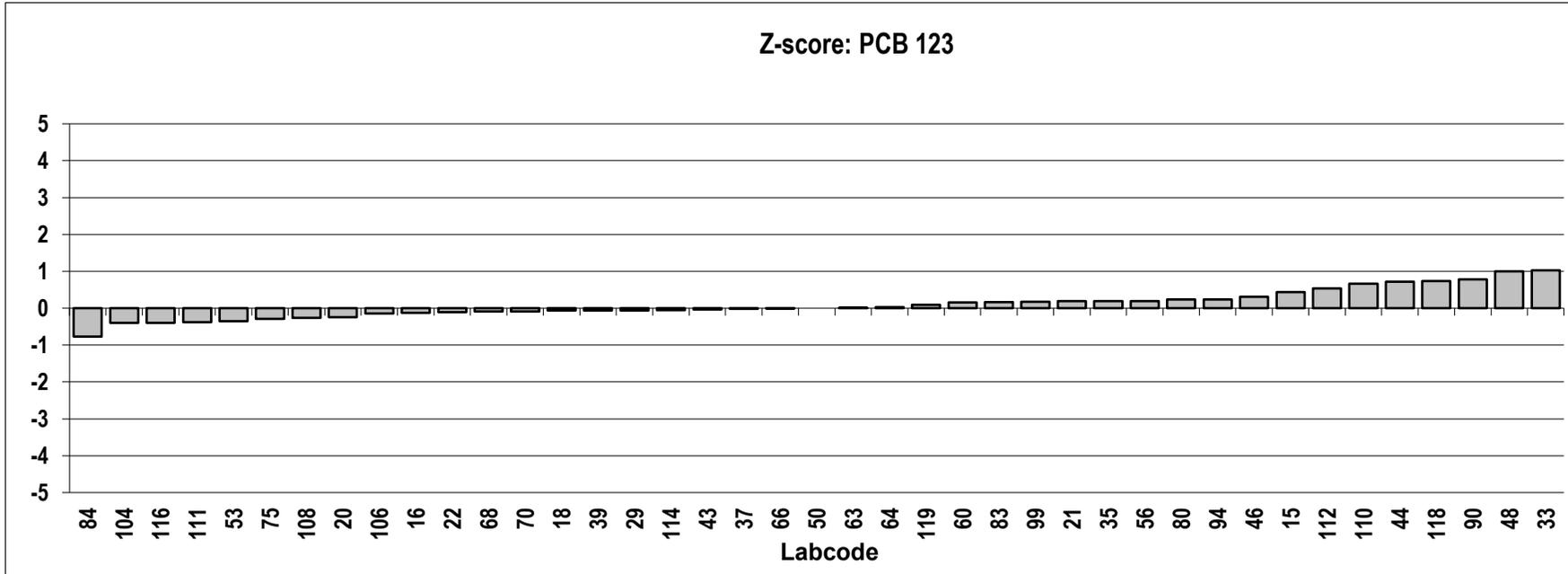
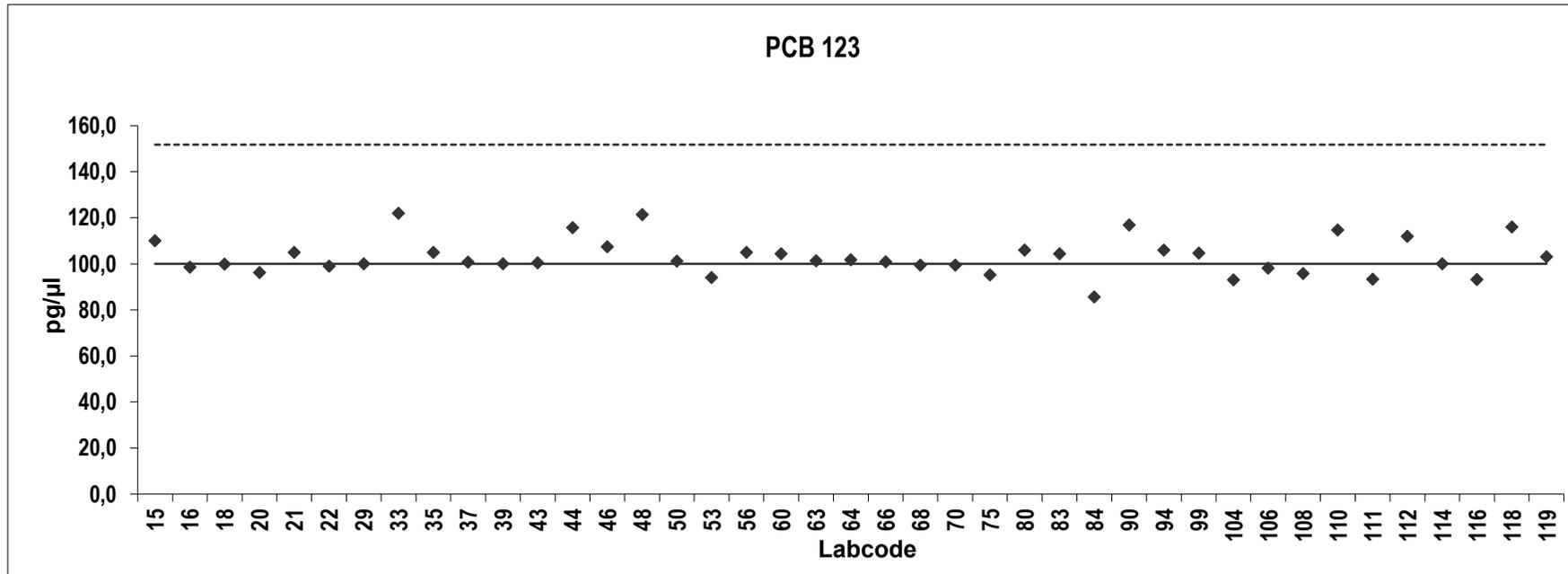
## Analyte solution

Congener: PCB 123

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	110	0,44				
16	99	-0,13				
18	100	-0,063				
20	96	-0,24				
21	105	0,19				
22	99	-0,10				
29	100	-0,059				
33	122	1,0				
35	105	0,19				
37	101	-0,020				
39	100	-0,060				
43	100	-0,039				
44	116	0,72				
46	107	0,31				
48	121	1,0				
50	101	0,00000				
53	94	-0,35				
56	105	0,19				
60	104	0,16				
63	101	0,011				
64	102	0,026				
66	101	-0,011				
68	99	-0,086				
70	99	-0,086				
75	95	-0,29				
80	106	0,24				
83	104	0,16				
84	86	-0,77				
90	117	0,78				
94	106	0,24				
99	105	0,17				
104	93	-0,40				
106	98	-0,15				
108	96	-0,26				
110	115	0,67				
111	93	-0,38				
112	112	0,54				
114	100	-0,058				
116	93	-0,40				
118	116	0,73				
119	103	0,091				

### Consensus statistics

Consensus median, pg/μl	101
Median all values pg/μl	101
Consensus mean, pg/μl	103
Standard deviation, pg/μl	7,9
Relative standard deviation, %	7,7
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



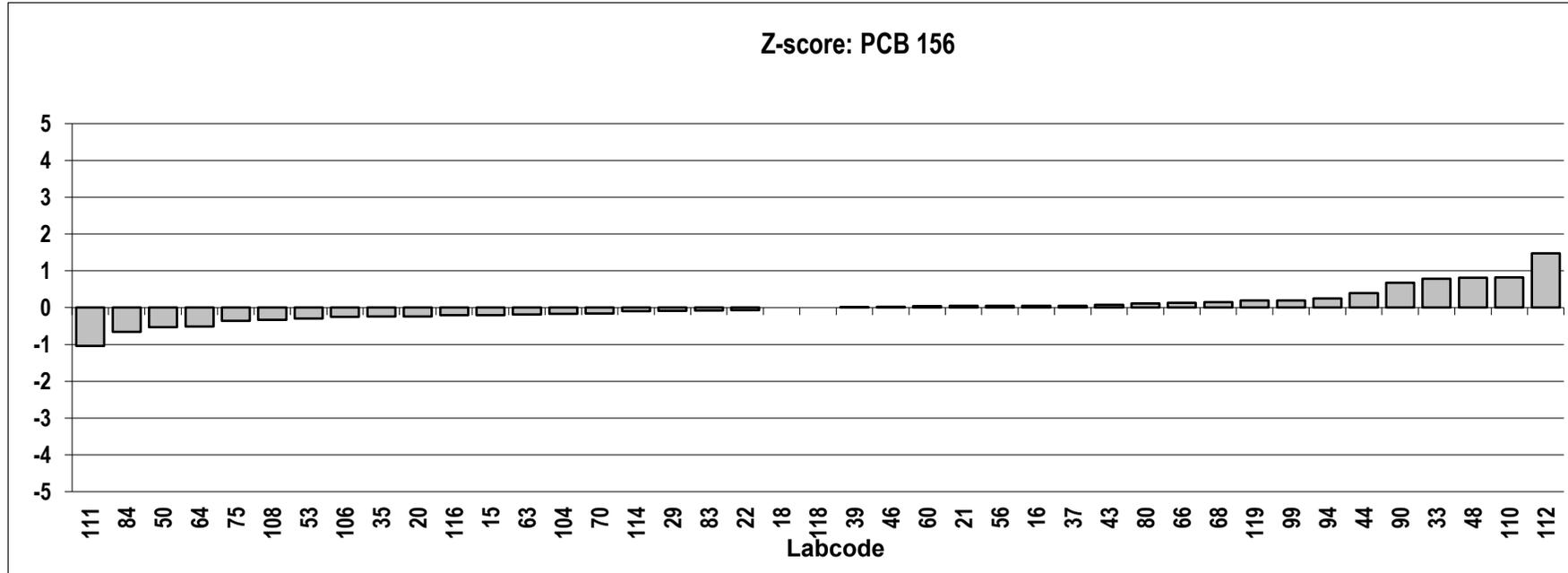
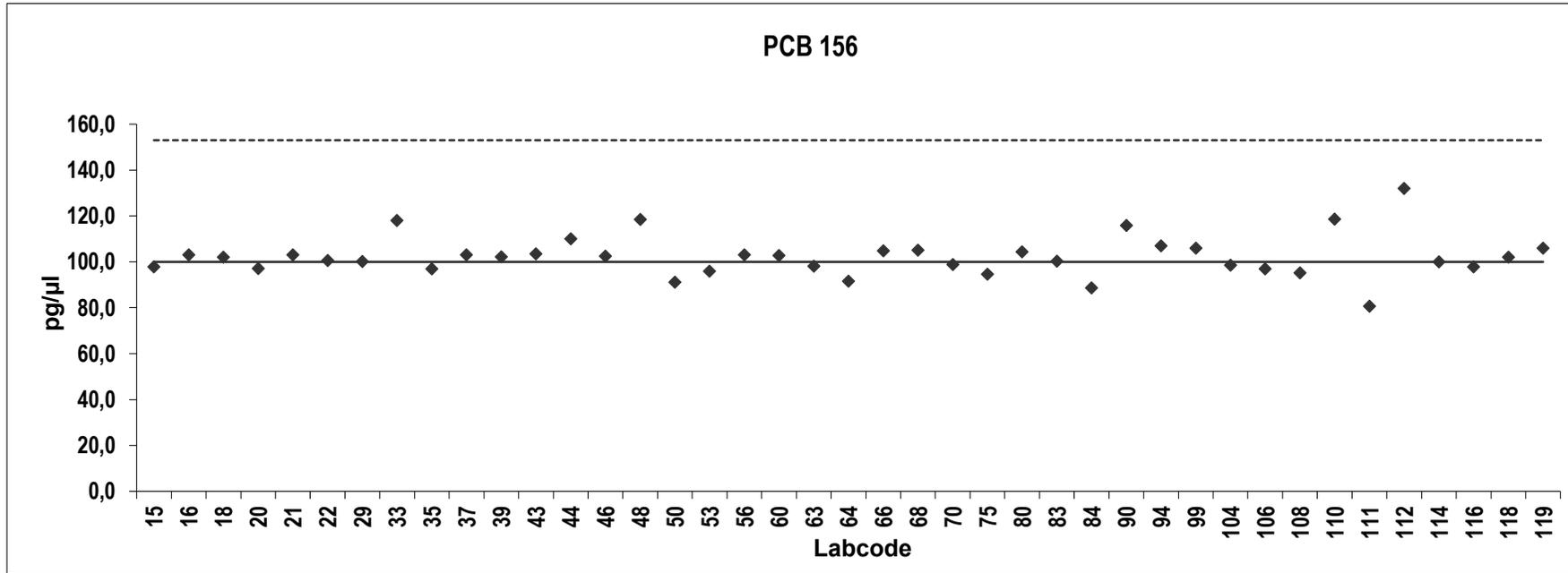
## Analyte solution

Congener: PCB 156

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	98	-0,20				
16	103	0,050				
18	102	0,00000				
20	97	-0,24				
21	103	0,049				
22	101	-0,066				
29	100	-0,089				
33	118	0,78				
35	97	-0,25				
37	103	0,052				
39	102	0,0061				
43	104	0,074				
44	110	0,39				
46	103	0,026				
48	119	0,81				
50	91	-0,53				
53	96	-0,29				
56	103	0,049				
60	103	0,036				
63	98	-0,19				
64	92	-0,51				
66	105	0,14				
68	105	0,15				
70	99	-0,16				
75	95	-0,36				
80	104	0,11				
83	100	-0,081				
84	89	-0,65				
90	116	0,68				
94	107	0,25				
99	106	0,20				
104	99	-0,17				
106	97	-0,25				
108	95	-0,33				
110	119	0,82				
111	81	-1,0				
112	132	1,5				
114	100	-0,10				
116	98	-0,21				
118	102	0,00000				
119	106	0,20				

### Consensus statistics

Consensus median, pg/μl	102
Median all values pg/μl	102
Consensus mean, pg/μl	102
Standard deviation, pg/μl	8,9
Relative standard deviation, %	8,7
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



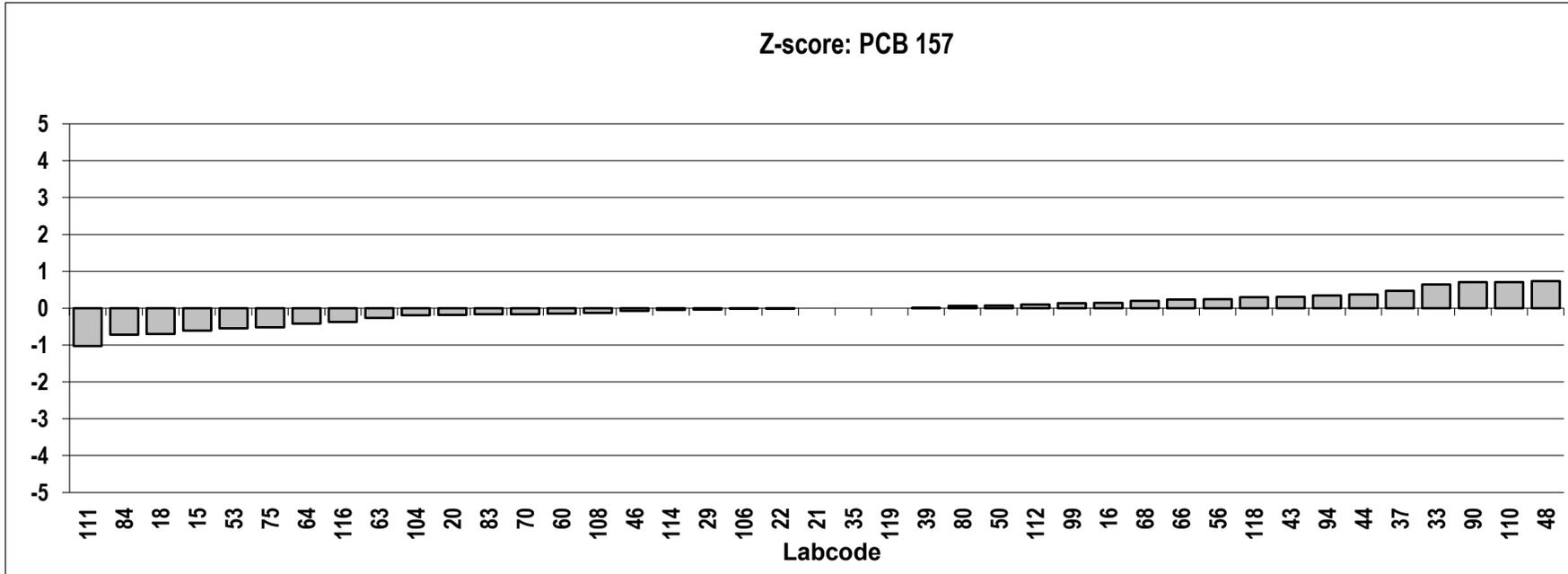
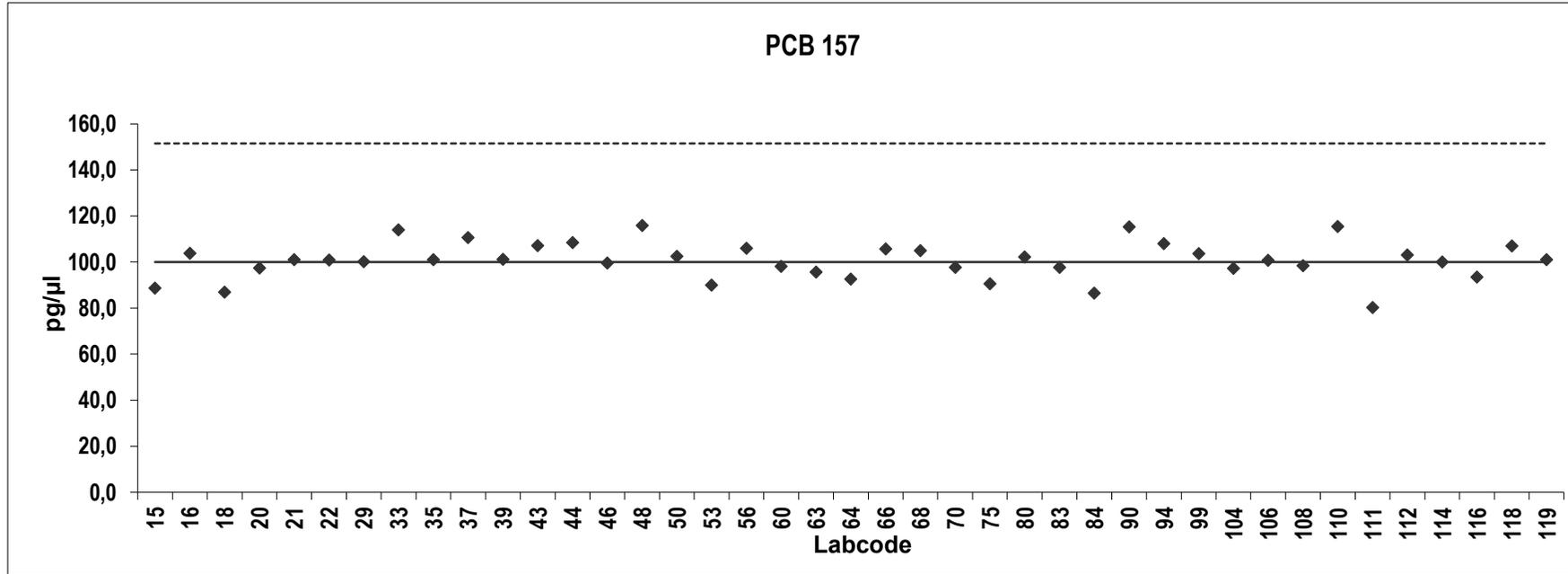
## Analyte solution

Congener: PCB 157

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	89	-0,61				
16	104	0,14				
18	87	-0,70				
20	97	-0,18				
21	101	0,00000				
22	101	-0,0092				
29	100	-0,042				
33	114	0,64				
35	101	0,00000				
37	111	0,47				
39	101	0,010				
43	107	0,30				
44	108	0,37				
46	100	-0,073				
48	116	0,74				
50	103	0,075				
53	90	-0,54				
56	106	0,25				
60	98	-0,14				
63	96	-0,26				
64	93	-0,42				
66	106	0,23				
68	105	0,20				
70	98	-0,16				
75	90	-0,52				
80	102	0,062				
83	98	-0,17				
84	87	-0,72				
90	115	0,70				
94	108	0,35				
99	104	0,13				
104	97	-0,19				
106	101	-0,012				
108	98	-0,13				
110	115	0,71				
111	80	-1,0				
112	103	0,10				
114	100	-0,050				
116	93	-0,38				
118	107	0,30				
119	101	0,00000				

### Consensus statistics

Consensus median, pg/μl	101
Median all values pg/μl	101
Consensus mean, pg/μl	101
Standard deviation, pg/μl	8,1
Relative standard deviation, %	8,0
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



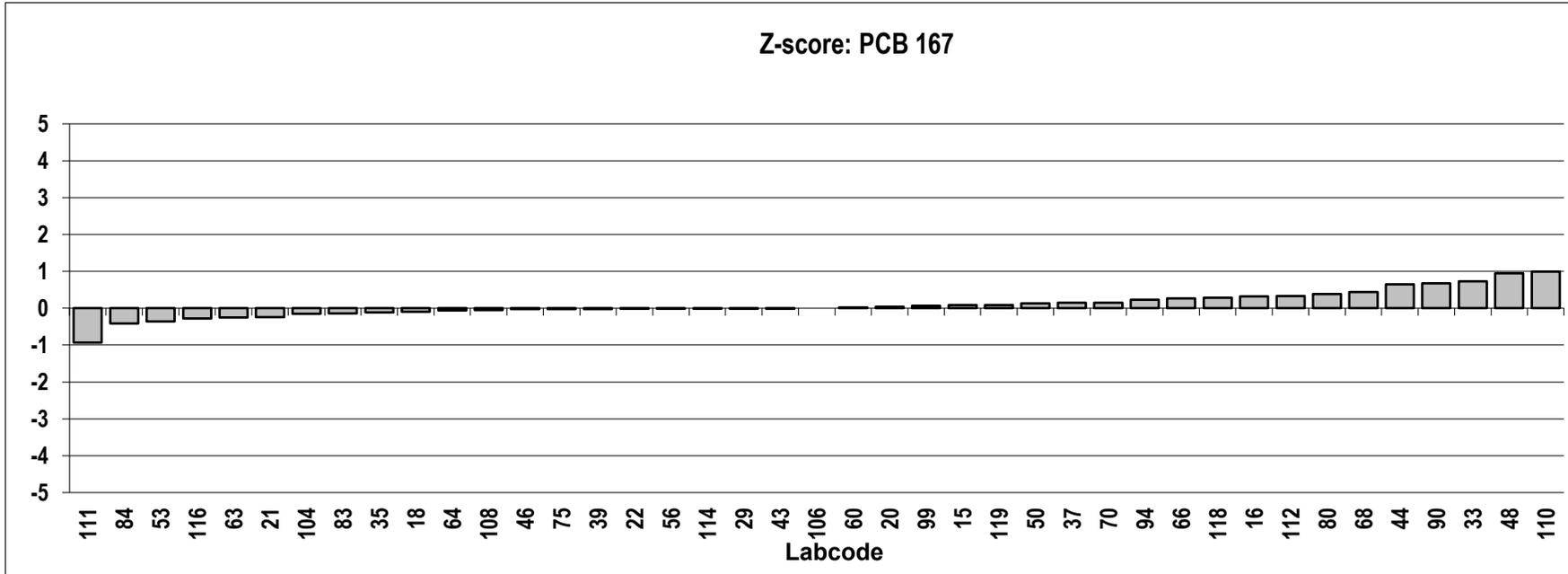
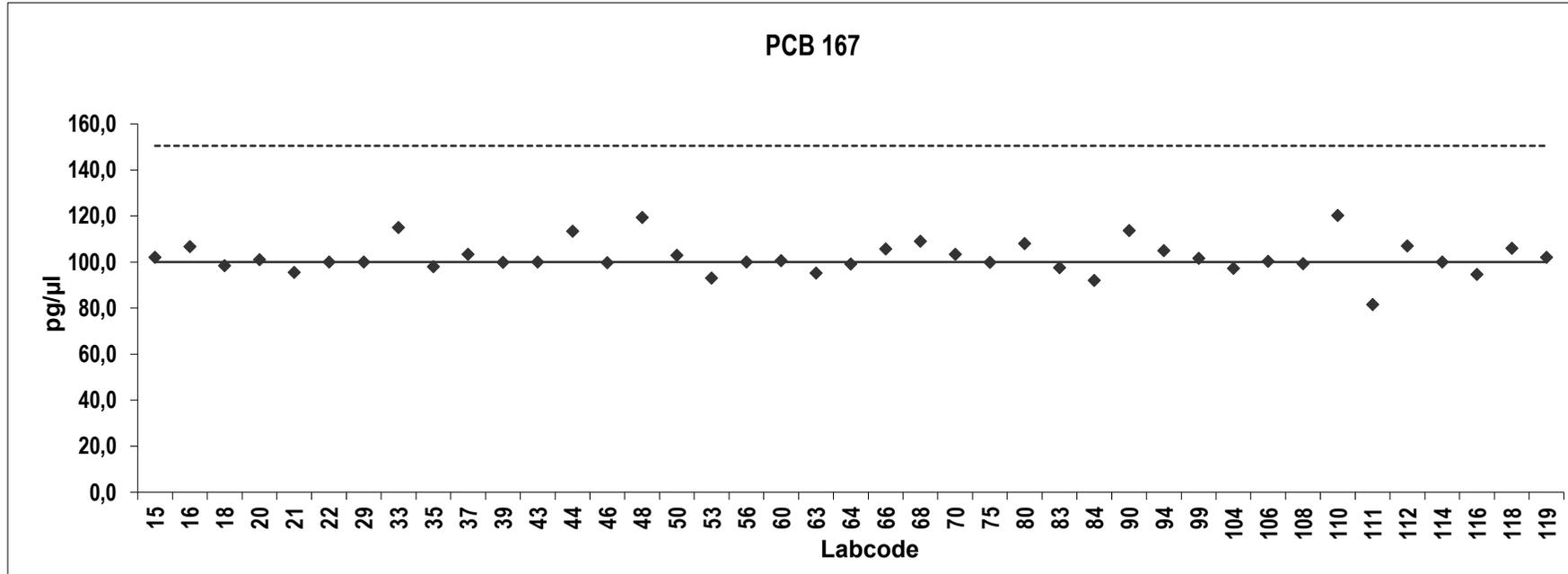
## Analyte solution

Congener: PCB 167

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	102	0,084				
16	107	0,32				
18	98	-0,10				
20	101	0,039				
21	96	-0,24				
22	100	-0,017				
29	100	-0,016				
33	115	0,73				
35	98	-0,12				
37	103	0,15				
39	100	-0,023				
43	100	-0,013				
44	113	0,65				
46	100	-0,028				
48	119	0,95				
50	103	0,13				
53	93	-0,36				
56	100	-0,016				
60	101	0,016				
63	95	-0,25				
64	99	-0,059				
66	106	0,27				
68	109	0,44				
70	103	0,15				
75	100	-0,023				
80	108	0,38				
83	97	-0,14				
84	92	-0,41				
90	114	0,67				
94	105	0,23				
99	102	0,064				
104	97	-0,15				
106	100	0,00000				
108	99	-0,053				
110	120	0,99				
111	82	-0,94				
112	107	0,33				
114	100	-0,016				
116	95	-0,28				
118	106	0,28				
119	102	0,084				

### Consensus statistics

Consensus median, pg/μl	100
Median all values pg/μl	100
Consensus mean, pg/μl	102
Standard deviation, pg/μl	7,3
Relative standard deviation, %	7,1
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



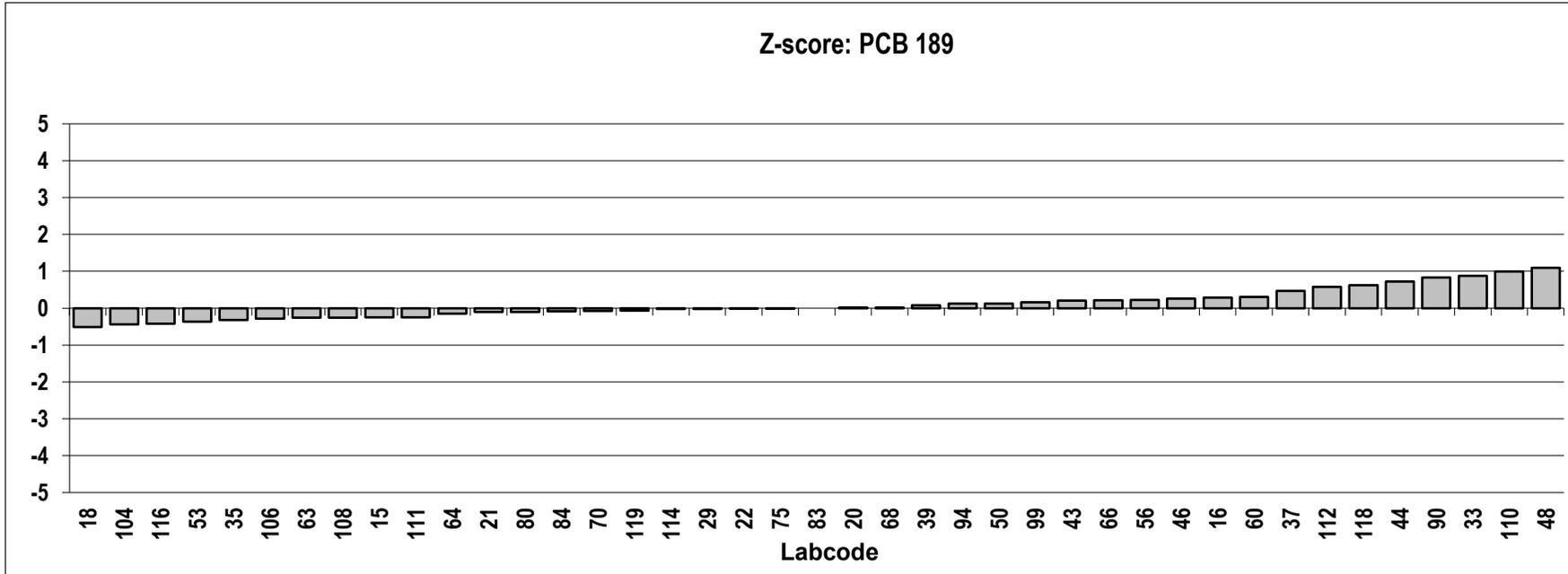
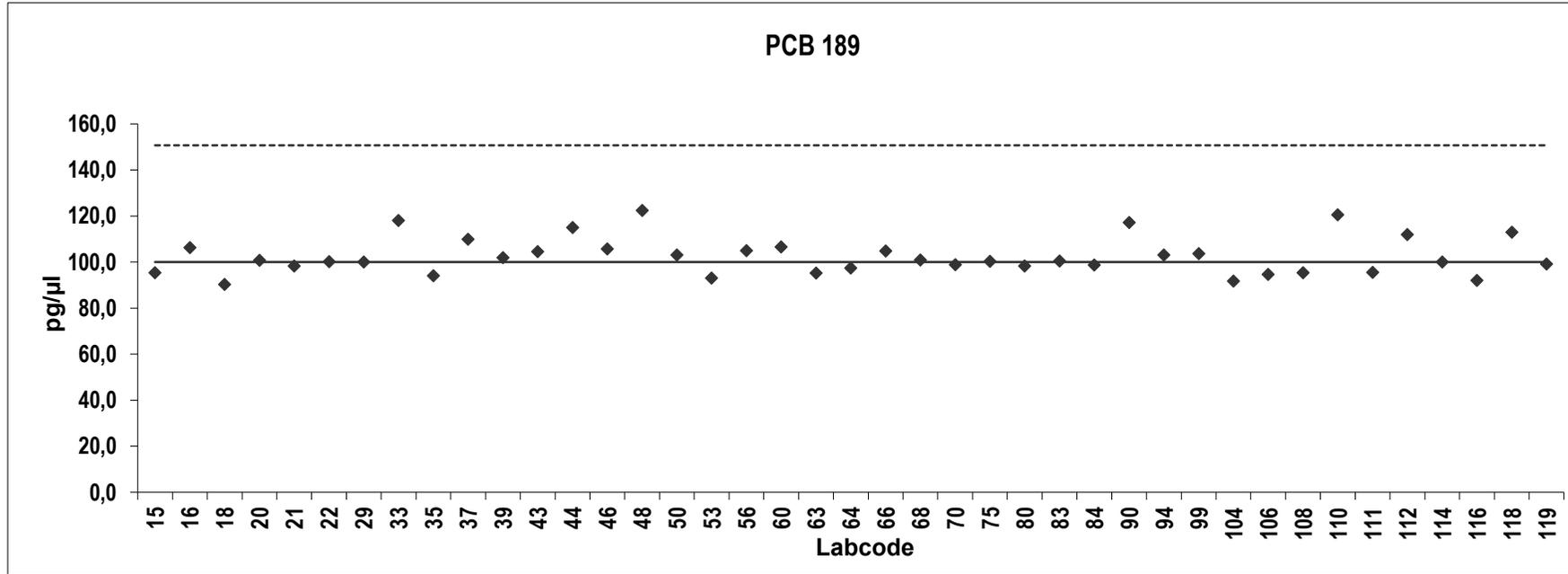
## Analyte solution

Congener: PCB 189

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	95	-0,25				
16	106	0,29				
18	90	-0,51				
20	101	0,014				
21	98	-0,11				
22	100	-0,013				
29	100	-0,022				
33	118	0,87				
35	94	-0,32				
37	110	0,47				
39	102	0,074				
43	105	0,20				
44	115	0,72				
46	106	0,26				
48	122	1,1				
50	103	0,13				
53	93	-0,37				
56	105	0,23				
60	107	0,30				
63	95	-0,26				
64	97	-0,15				
66	105	0,21				
68	101	0,019				
70	99	-0,076				
75	100	-0,010				
80	98	-0,11				
83	100	0,00000				
84	99	-0,087				
90	117	0,83				
94	103	0,13				
99	104	0,16				
104	92	-0,44				
106	95	-0,29				
108	95	-0,26				
110	120	1,0				
111	96	-0,24				
112	112	0,57				
114	100	-0,023				
116	92	-0,42				
118	113	0,62				
119	99	-0,067				

### Consensus statistics

Consensus median, pg/μl	100
Median all values pg/μl	100
Consensus mean, pg/μl	103
Standard deviation, pg/μl	8,0
Relative standard deviation, %	7,8
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



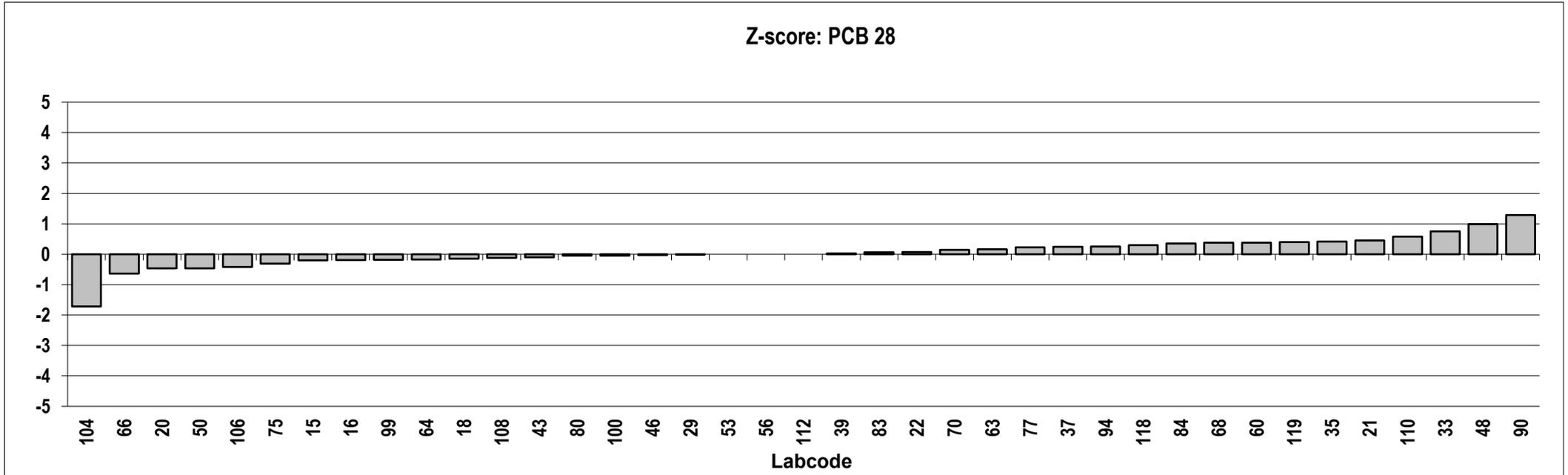
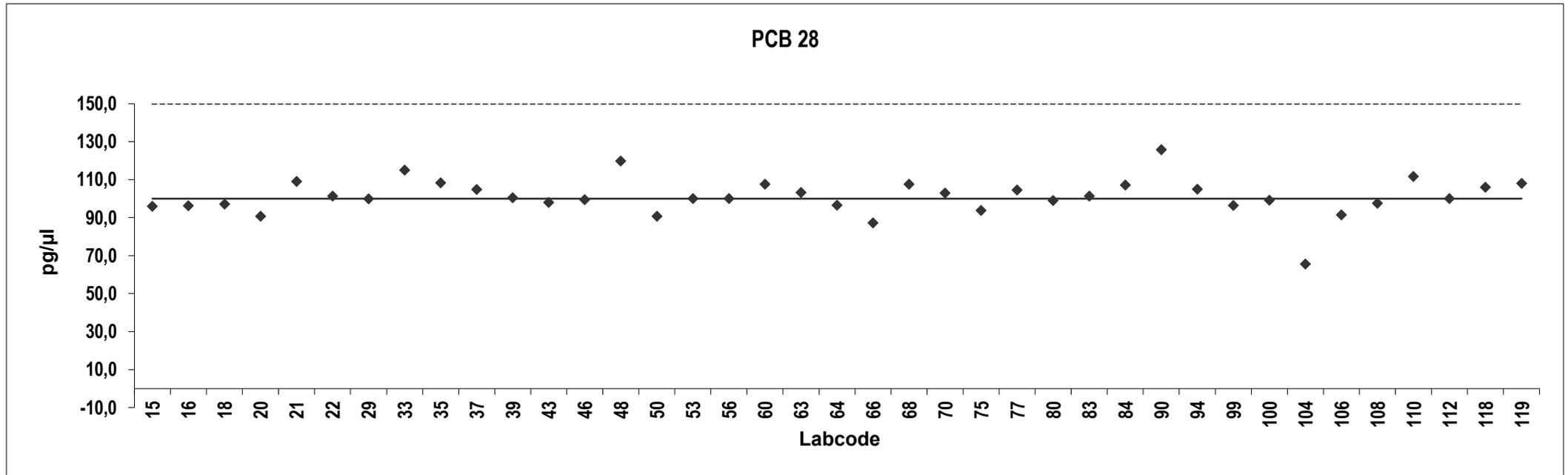
## Analyte solution

Congener: PCB 28

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	96	-0,20				
16	96	-0,19				
18	97	-0,15				
20	91	-0,47				
21	109	0,45				
22	101	0,071				
29	100	-0,0030				
33	115	0,75				
35	108	0,42				
37	105	0,24				
39	101	0,025				
43	98	-0,10				
46	99	-0,029				
48	120	0,99				
50	91	-0,46				
53	100	0,00000				
56	100	0,00000				
60	108	0,38				
63	103	0,16				
64	97	-0,17				
66	87	-0,64				
68	108	0,38				
70	103	0,15				
75	94	-0,31				
77	105	0,23				
80	99	-0,049				
83	101	0,065				
84	107	0,36				
90	126	1,3				
94	105	0,25				
99	96	-0,18				
100	99	-0,045				
104	66	-1,7				
106	92	-0,42				
108	98	-0,12				
110	112	0,58				
112	100	0,00000				
118	106	0,30				
119	108	0,40				

### Consensus statistics

Consensus median, pg/μl	100
Median all values pg/μl	100
Consensus mean, pg/μl	101
Standard deviation, pg/μl	10
Relative standard deviation, %	10
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0



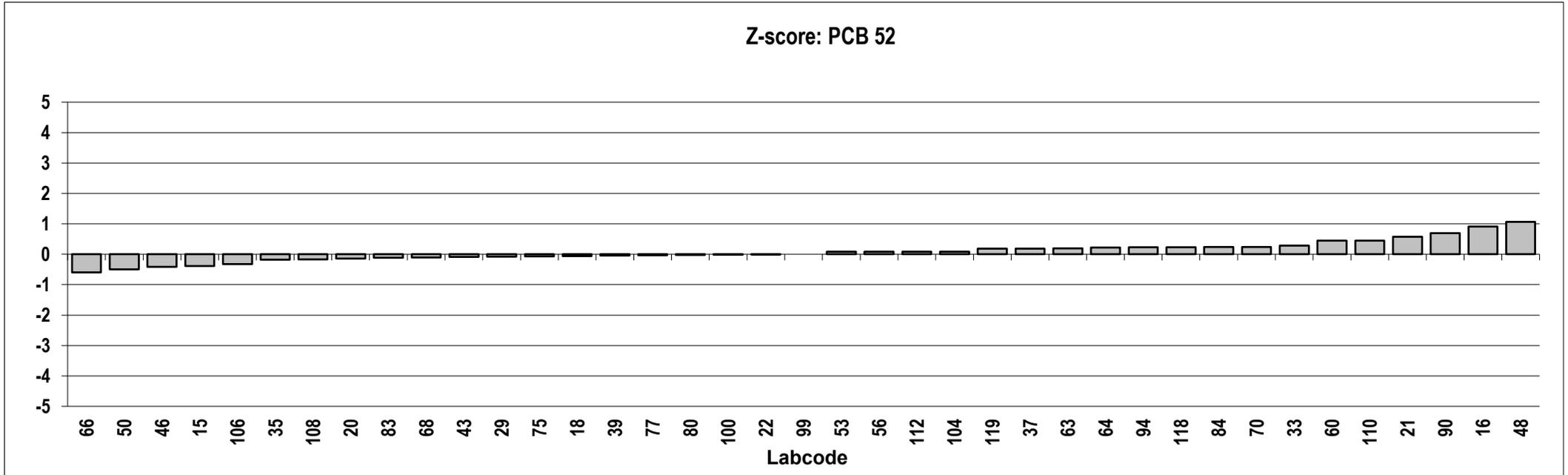
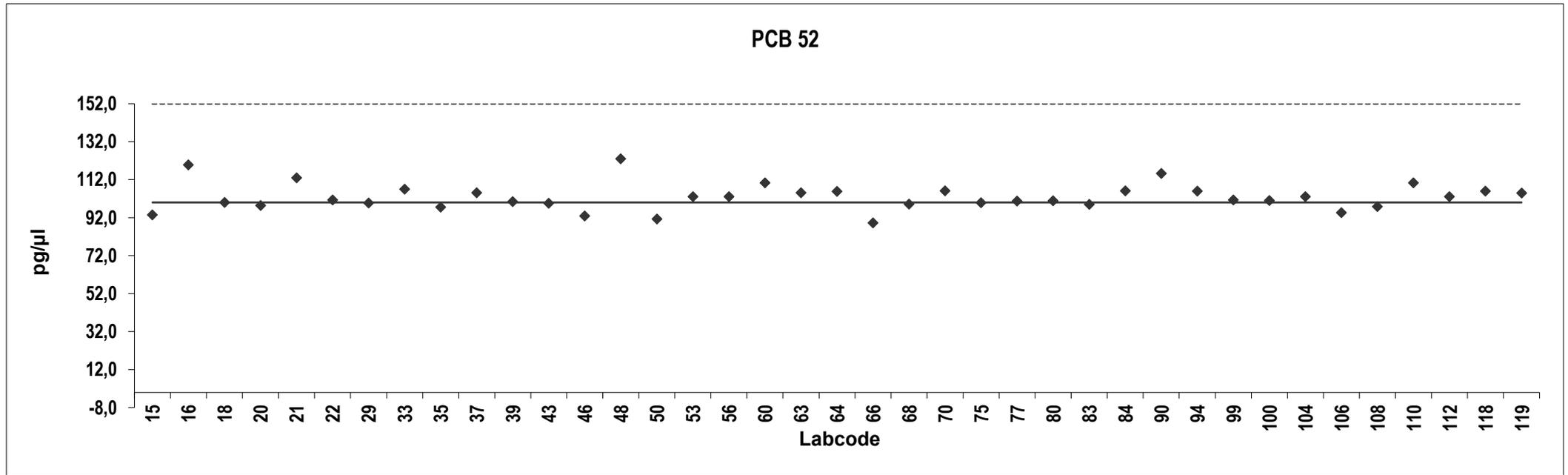
## Analyte solution

Congener: PCB 52

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	93	-0,39				
16	120	0,91				
18	100	-0,066				
20	98	-0,14				
21	113	0,58				
22	101	-0,00061				
29	100	-0,082				
33	107	0,28				
35	98	-0,18				
37	105	0,18				
39	100	-0,044				
43	100	-0,090				
46	93	-0,41				
48	123	1,1				
50	91	-0,49				
53	103	0,082				
56	103	0,082				
60	110	0,44				
63	105	0,19				
64	106	0,22				
66	89	-0,60				
68	99	-0,11				
70	106	0,24				
75	100	-0,074				
77	101	-0,031				
80	101	-0,021				
83	99	-0,11				
84	106	0,23				
90	115	0,69				
94	106	0,23				
99	101	0,00000				
100	101	-0,016				
104	103	0,087				
106	95	-0,33				
108	98	-0,17				
110	110	0,44				
112	103	0,082				
118	106	0,23				
119	105	0,18				

### Consensus statistics

Consensus median, pg/μl	101
Median all values pg/μl	101
Consensus mean, pg/μl	103
Standard deviation, pg/μl	7,0
Relative standard deviation, %	6,8
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0



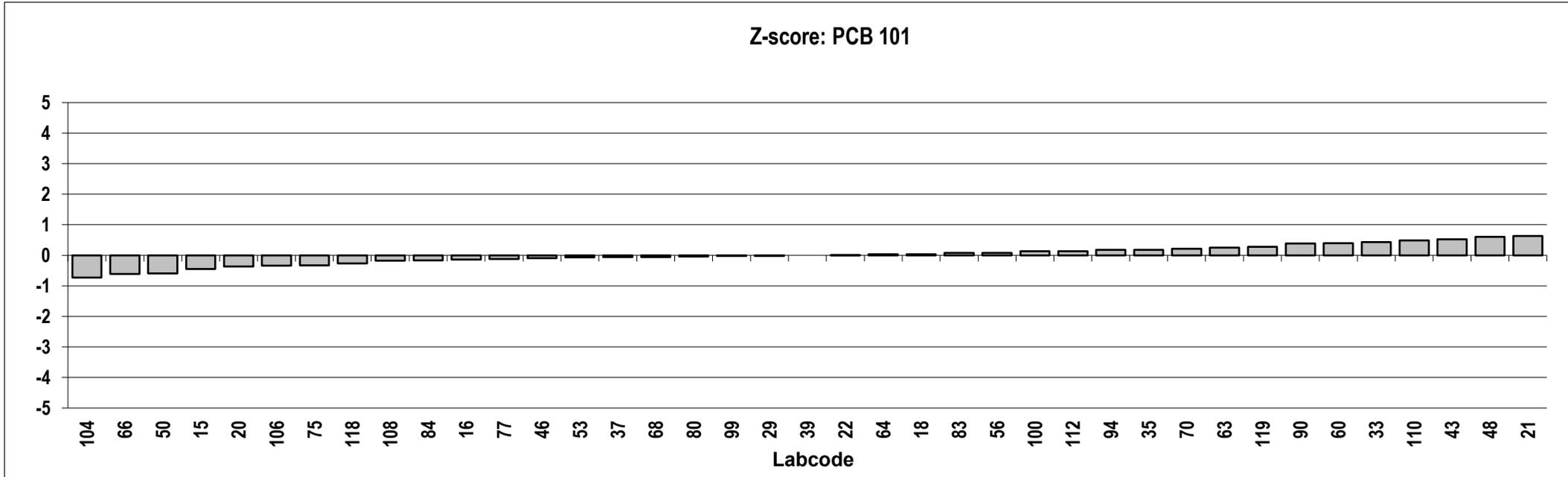
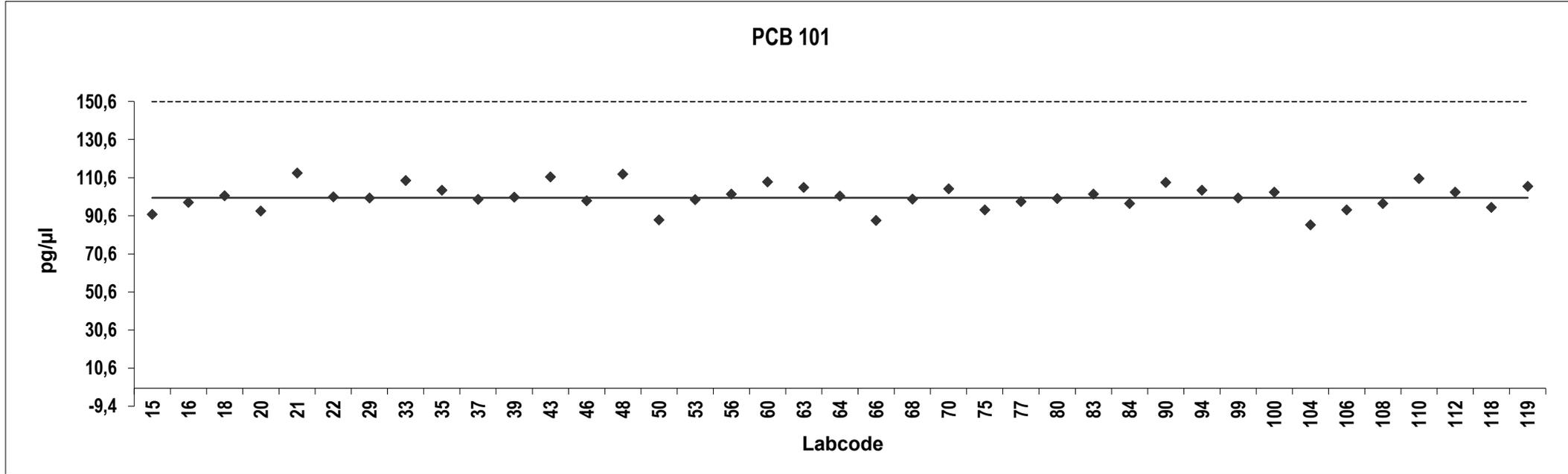
## Analyte solution

Congener: PCB 101

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	91	-0,45				
16	98	-0,14				
18	101	0,031				
20	93	-0,37				
21	113	0,63				
22	100	0,0019				
29	100	-0,021				
33	109	0,43				
35	104	0,18				
37	99	-0,059				
39	100	0,00000				
43	111	0,53				
46	98	-0,10				
48	112	0,60				
50	88	-0,60				
53	99	-0,068				
56	102	0,081				
60	108	0,39				
63	105	0,25				
64	101	0,029				
66	88	-0,61				
68	99	-0,055				
70	105	0,21				
75	94	-0,33				
77	98	-0,12				
80	100	-0,036				
83	102	0,076				
84	97	-0,17				
90	108	0,39				
94	104	0,18				
99	100	-0,023				
100	103	0,13				
104	86	-0,73				
106	94	-0,34				
108	97	-0,17				
110	110	0,49				
112	103	0,13				
118	95	-0,27				
119	106	0,28				

### Consensus statistics

Consensus median, pg/μl	100
Median all values pg/μl	100
Consensus mean, pg/μl	101
Standard deviation, pg/μl	6,6
Relative standard deviation, %	6,5
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0



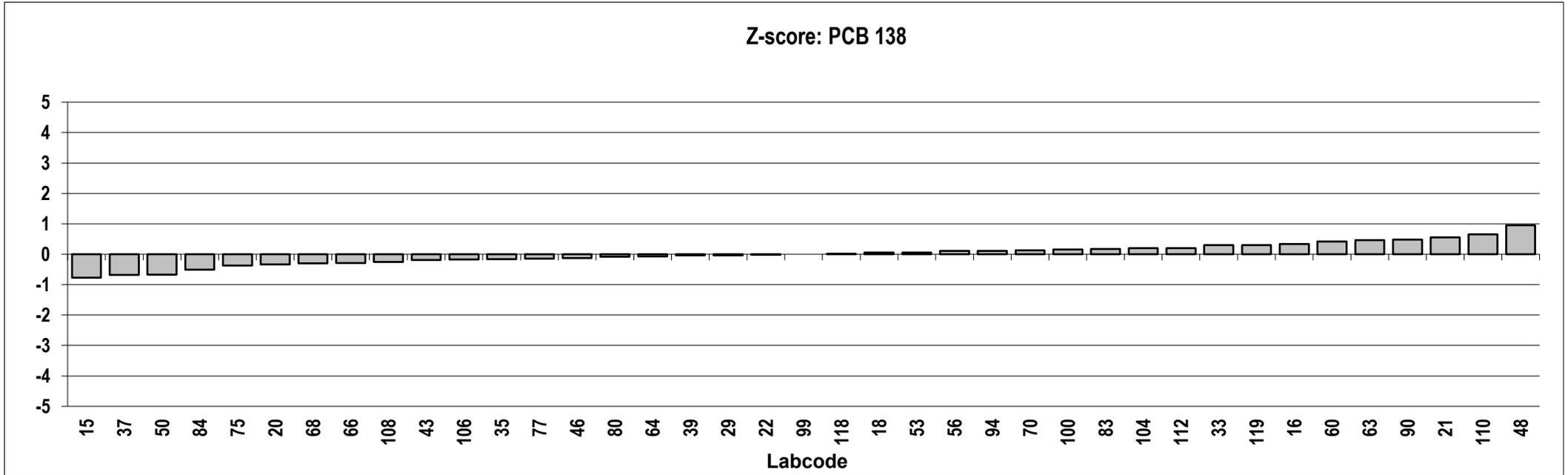
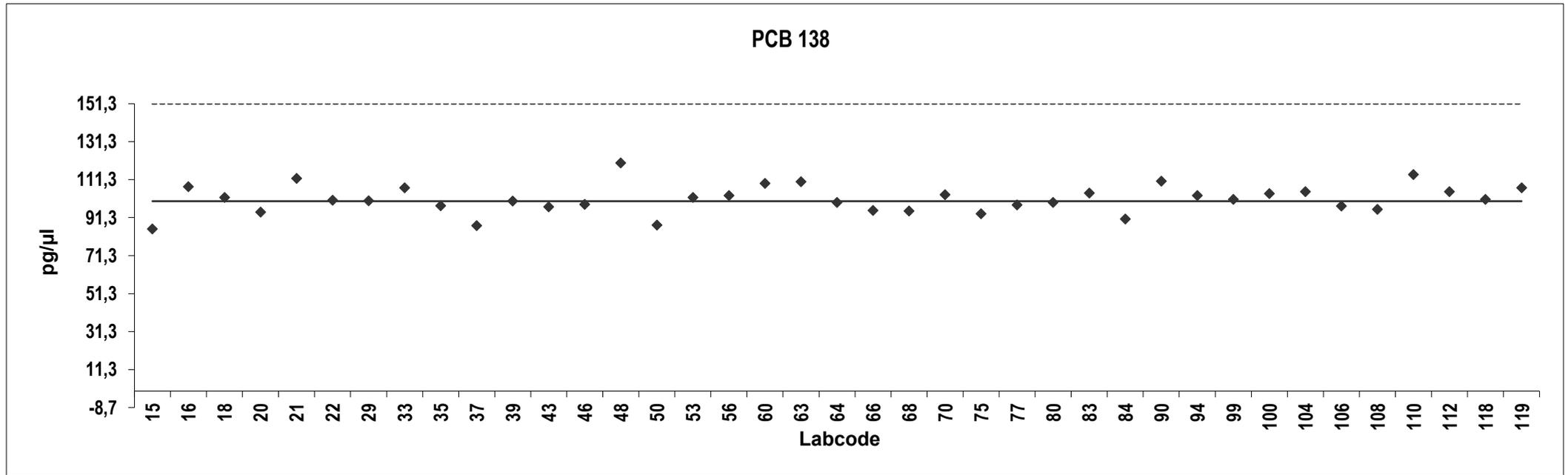
## Analyte solution

Congener: PCB 138

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	85	-0,77				
16	108	0,33				
18	102	0,055				
20	94	-0,33				
21	112	0,55				
22	101	-0,018				
29	100	-0,037				
33	107	0,30				
35	98	-0,16				
37	87	-0,68				
39	100	-0,039				
43	97	-0,19				
46	98	-0,13				
48	120	0,95				
50	87	-0,67				
53	102	0,055				
56	103	0,10				
60	109	0,42				
63	110	0,47				
64	99	-0,075				
66	95	-0,29				
68	95	-0,30				
70	103	0,13				
75	93	-0,38				
77	98	-0,14				
80	99	-0,080				
83	104	0,17				
84	91	-0,51				
90	111	0,48				
94	103	0,10				
99	101	0,00000				
100	104	0,15				
104	105	0,20				
106	98	-0,17				
108	96	-0,25				
110	114	0,65				
112	105	0,20				
118	101	0,0053				
119	107	0,30				

### Consensus statistics

Consensus median, pg/μl	101
Median all values pg/μl	101
Consensus mean, pg/μl	101
Standard deviation, pg/μl	7,4
Relative standard deviation, %	7,3
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0



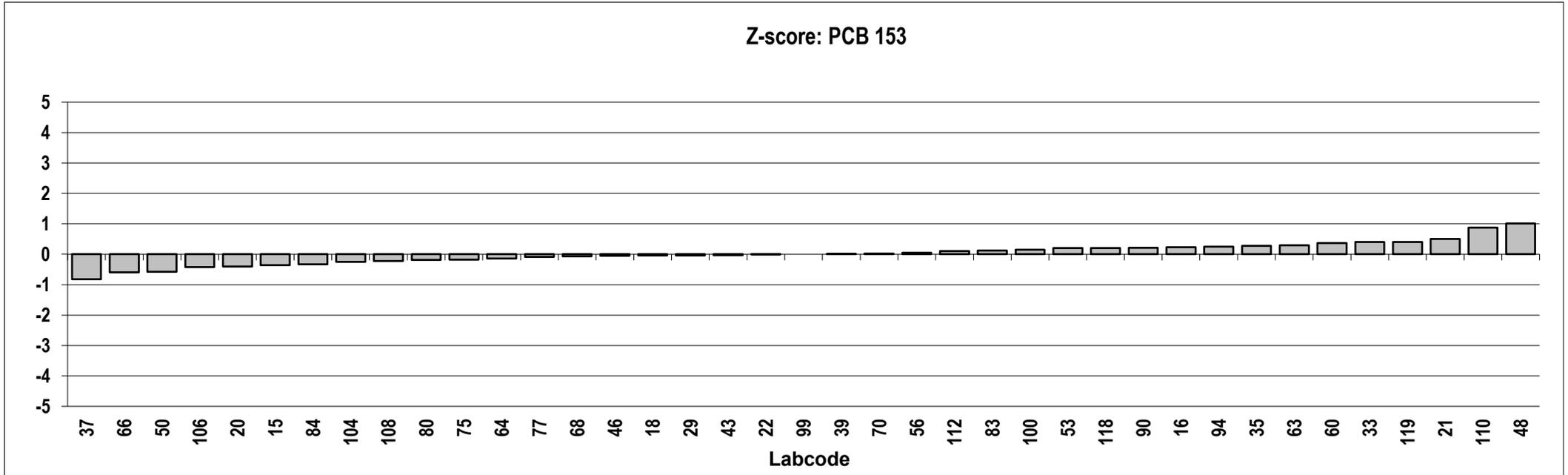
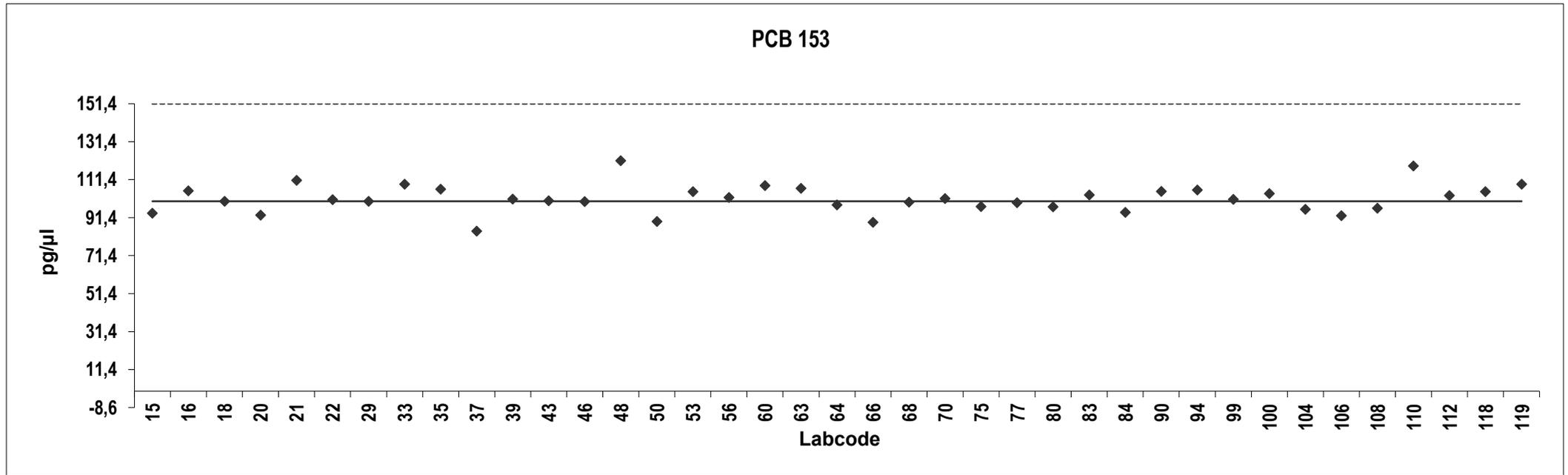
## Analyte solution

Congener: PCB 153

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	94	-0,36				
16	106	0,23				
18	100	-0,046				
20	93	-0,41				
21	111	0,50				
22	101	-0,0019				
29	100	-0,045				
33	109	0,40				
35	106	0,27				
37	84	-0,83				
39	101	0,0081				
43	100	-0,030				
46	100	-0,055				
48	121	1,0				
50	89	-0,58				
53	105	0,20				
56	102	0,053				
60	108	0,37				
63	107	0,29				
64	98	-0,14				
66	89	-0,60				
68	100	-0,068				
70	101	0,023				
75	97	-0,18				
77	99	-0,086				
80	97	-0,19				
83	103	0,12				
84	94	-0,33				
90	105	0,21				
94	106	0,25				
99	101	0,00000				
100	104	0,15				
104	96	-0,25				
106	92	-0,42				
108	96	-0,23				
110	119	0,87				
112	103	0,10				
118	105	0,20				
119	109	0,40				

### Consensus statistics

Consensus median, pg/μl	101
Median all values pg/μl	101
Consensus mean, pg/μl	101
Standard deviation, pg/μl	7,4
Relative standard deviation, %	7,3
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0



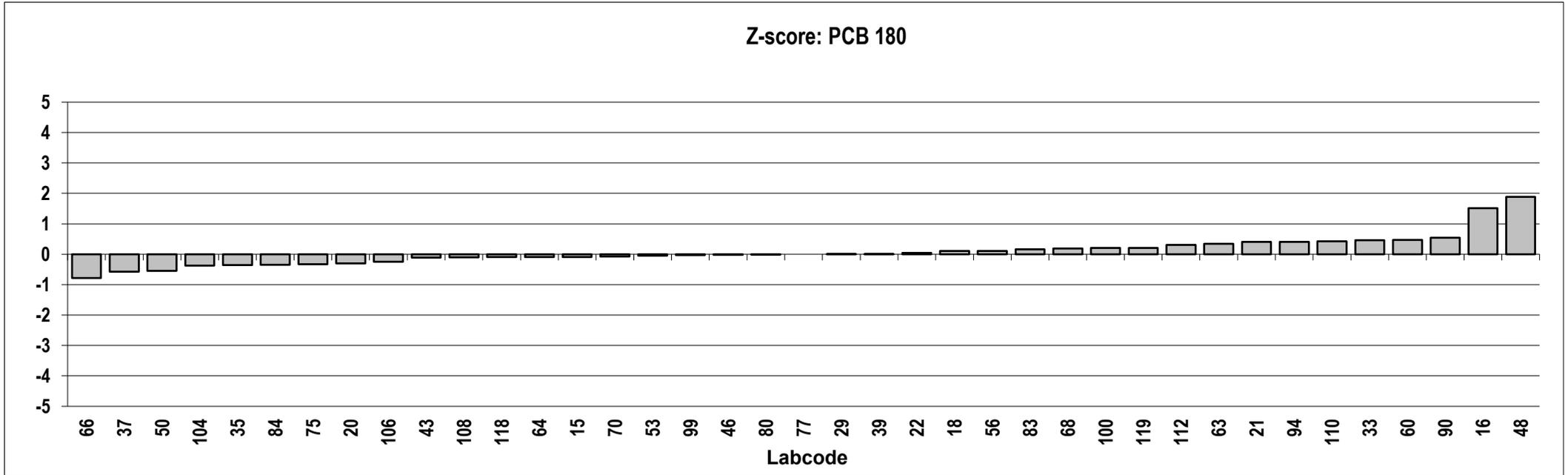
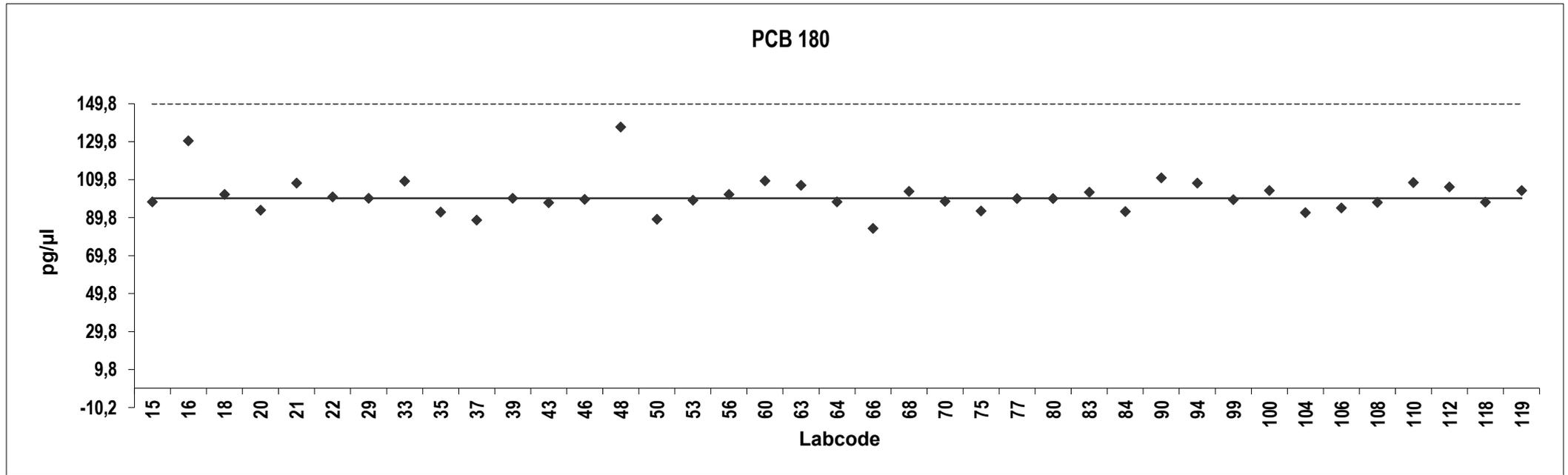
## Analyte solution

Congener: PCB 180

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	98	-0,089				
16	130	1,5				
18	102	0,11				
20	94	-0,30				
21	108	0,41				
22	101	0,046				
29	100	0,0054				
33	109	0,46				
35	93	-0,36				
37	88	-0,57				
39	100	0,0085				
43	98	-0,11				
46	99	-0,021				
48	138	1,9				
50	89	-0,55				
53	99	-0,043				
56	102	0,11				
60	109	0,47				
63	107	0,35				
64	98	-0,089				
66	84	-0,78				
68	104	0,19				
70	98	-0,075				
75	93	-0,33				
77	100	0,00000				
80	100	-0,0029				
83	103	0,16				
84	93	-0,35				
90	111	0,54				
94	108	0,41				
99	99	-0,027				
100	104	0,21				
104	92	-0,37				
106	95	-0,25				
108	98	-0,10				
110	108	0,42				
112	106	0,31				
118	98	-0,094				
119	104	0,21				

### Consensus statistics

Consensus median, pg/μl	100
Median all values pg/μl	100
Consensus mean, pg/μl	102
Standard deviation, pg/μl	10
Relative standard deviation, %	10
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0



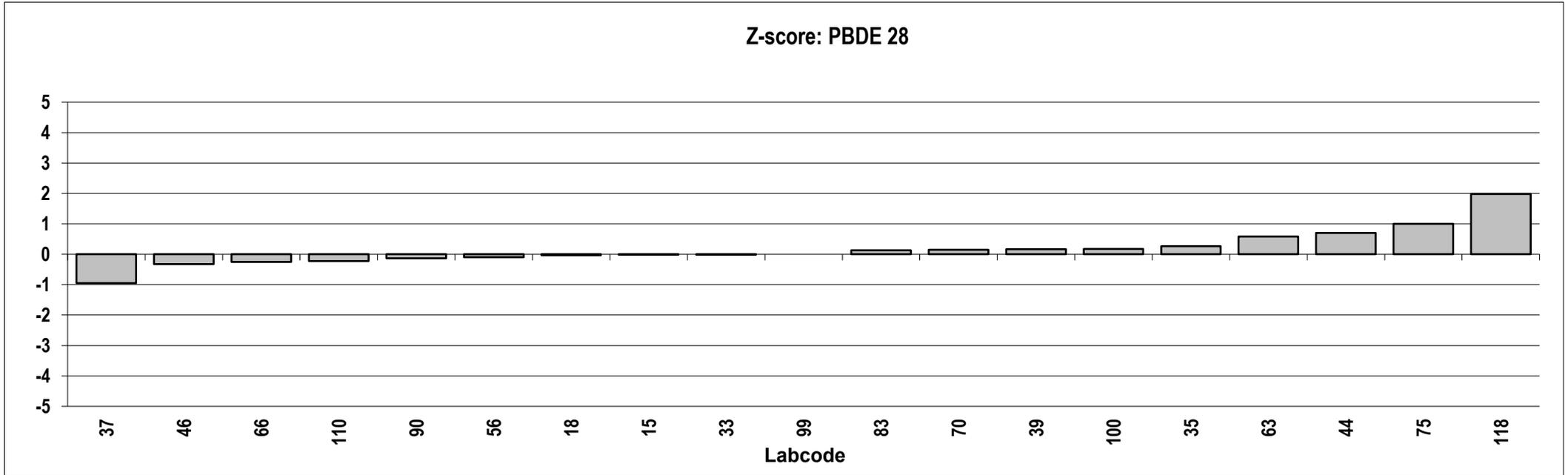
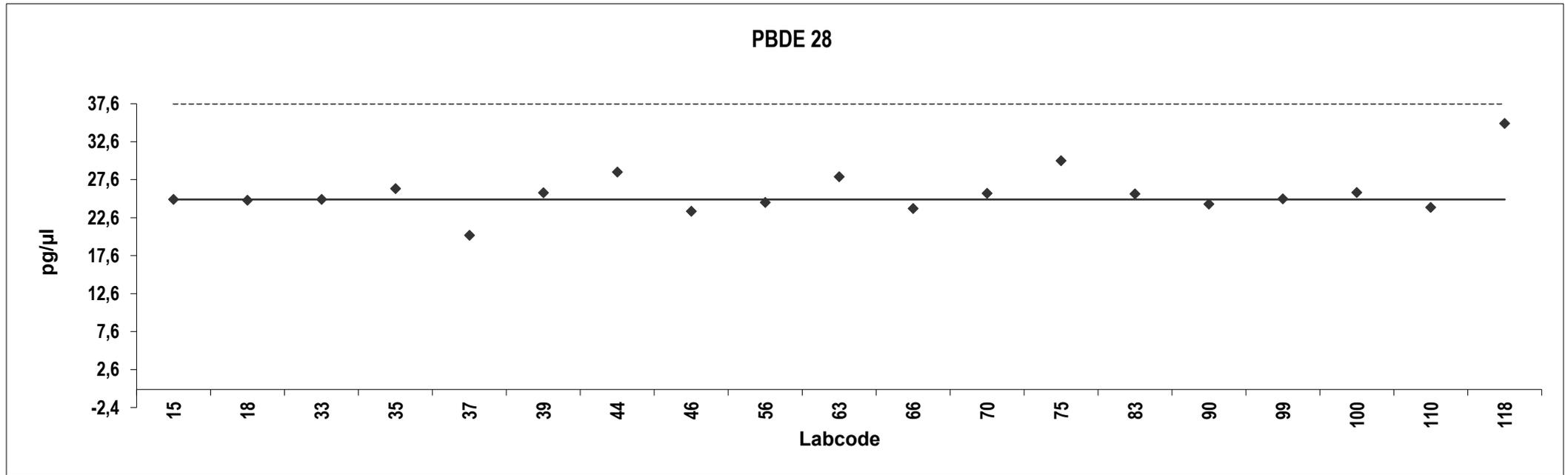
## Analyte solution

Congener: PBDE 28

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	25	-0,014				
18	25	-0,034				
33	25	-0,014				
35	26	0,27				
37	20	-0,95				
39	26	0,16				
44	29	0,70				
46	23	-0,32				
56	25	-0,094				
63	28	0,58				
66	24	-0,25				
70	26	0,15				
75	30	1,0				
83	26	0,13				
90	24	-0,14				
99	25	0,00000				
100	26	0,17				
110	24	-0,23				
118	35	2,0				

### Consensus statistics

Consensus median, pg/μl	25
Median all values pg/μl	25
Consensus mean, pg/μl	26
Standard deviation, pg/μl	3,0
Relative standard deviation, %	12
No. of values reported	19
No. of values removed	0
No. of reported non-detects	0



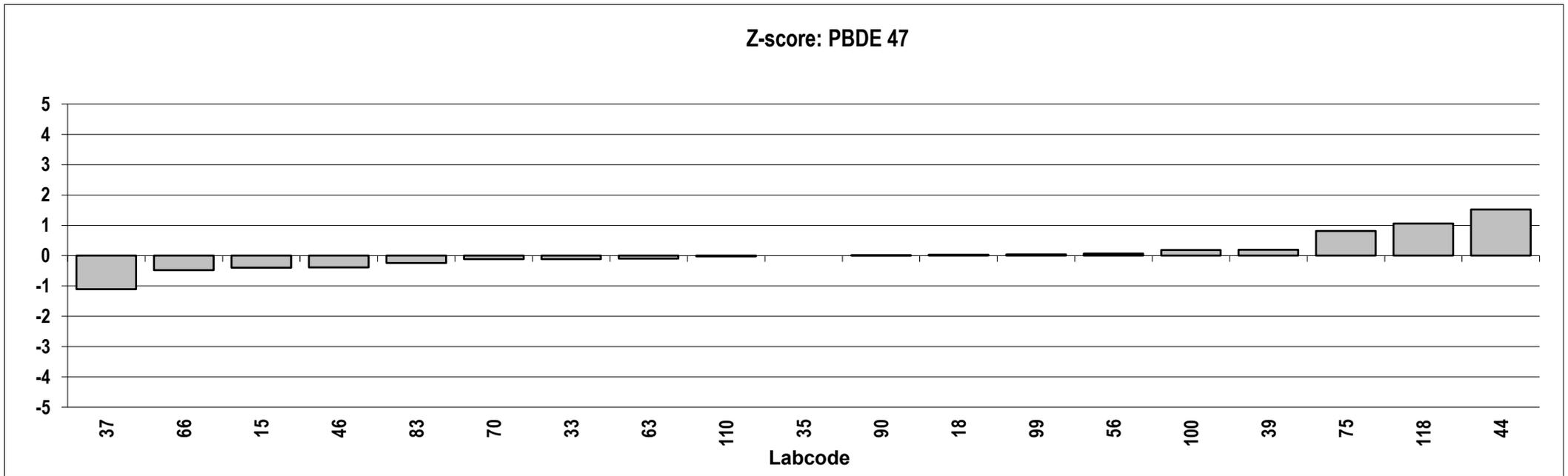
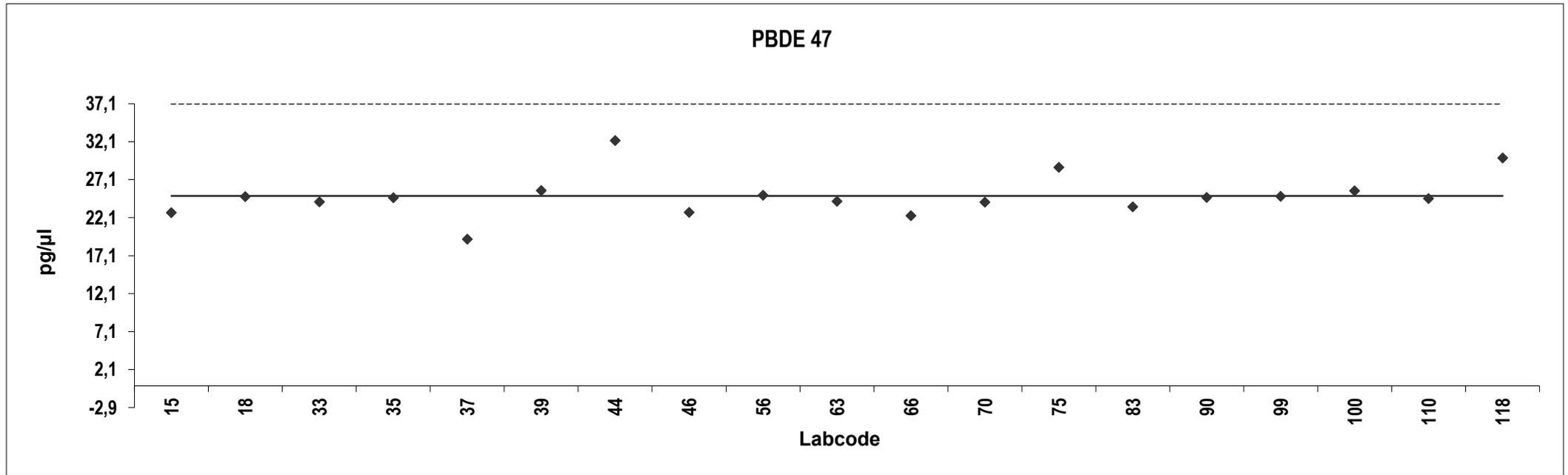
## Analyte solution

Congener: PBDE 47

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	23	-0,40				
18	25	0,028				
33	24	-0,11				
35	25	0,00000				
37	19	-1,1				
39	26	0,19				
44	32	1,5				
46	23	-0,39				
56	25	0,069				
63	24	-0,10				
66	22	-0,48				
70	24	-0,12				
75	29	0,81				
83	24	-0,24				
90	25	0,0069				
99	25	0,039				
100	26	0,18				
110	25	-0,022				
118	30	1,1				

### Consensus statistics

Consensus median, pg/μl	25
Median all values pg/μl	25
Consensus mean, pg/μl	25
Standard deviation, pg/μl	2,9
Relative standard deviation, %	11
No. of values reported	19
No. of values removed	0
No. of reported non-detects	0



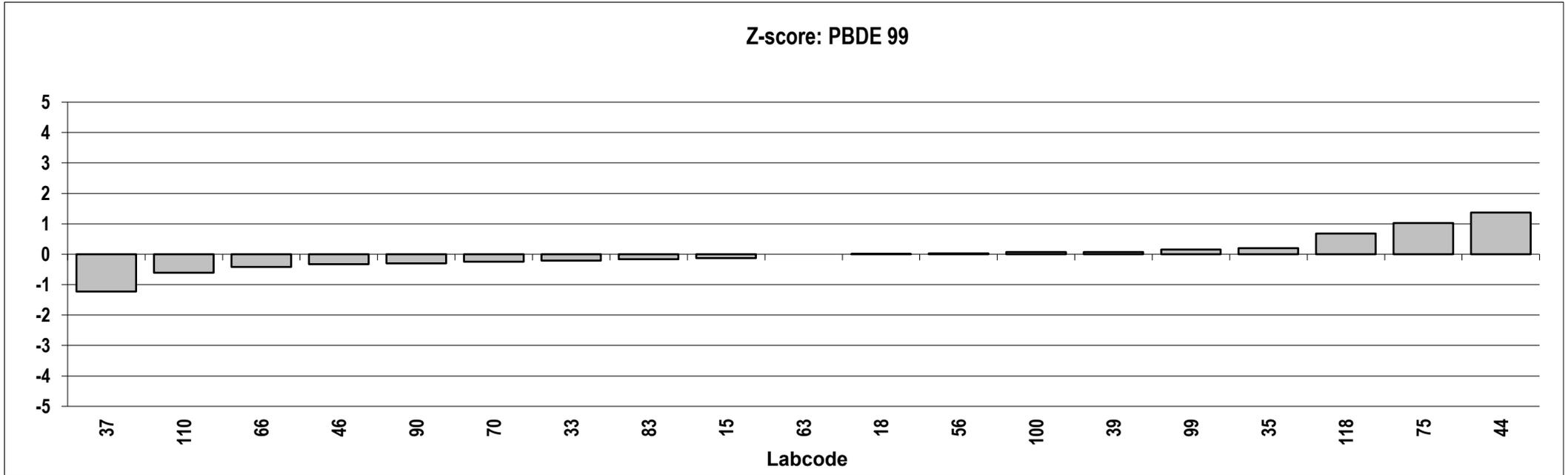
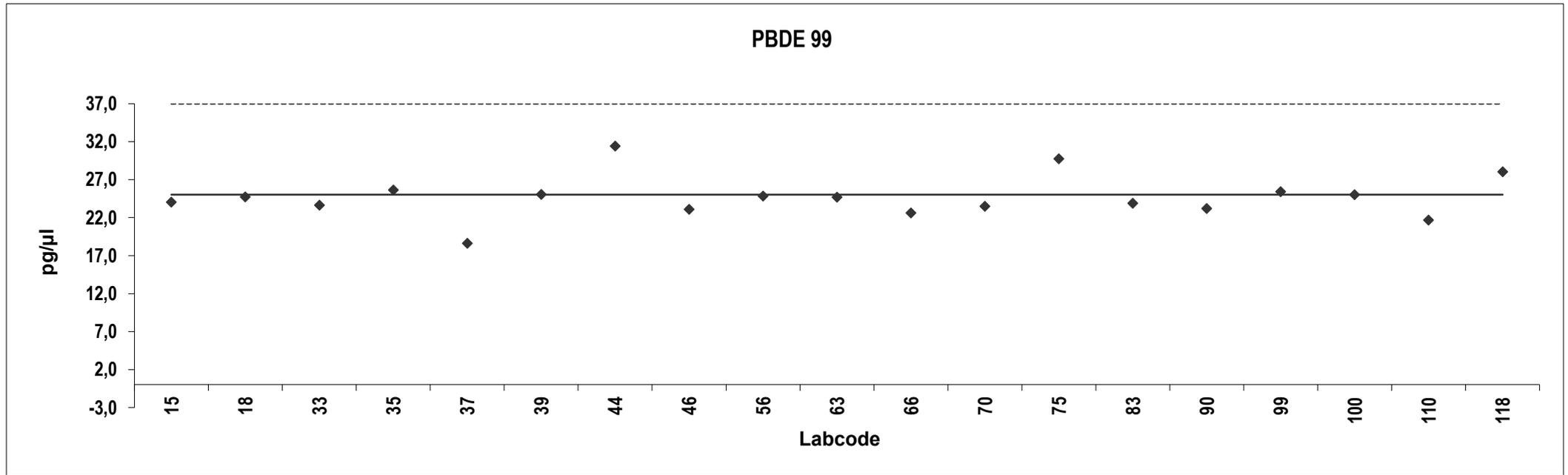
## Analyte solution

Congener: PBDE 99

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	24	-0,13				
18	25	0,010				
33	24	-0,21				
35	26	0,19				
37	19	-1,23				
39	25	0,074				
44	31	1,4				
46	23	-0,32				
56	25	0,030				
63	25	0,00000				
66	23	-0,42				
70	23	-0,24				
75	30	1,0				
83	24	-0,16				
90	23	-0,30				
99	25	0,15				
100	25	0,071				
110	22	-0,61				
118	28	0,68				

### Consensus statistics

Consensus median, pg/μl	25
Median all values pg/μl	25
Consensus mean, pg/μl	25
Standard deviation, pg/μl	2,8
Relative standard deviation, %	11
No. of values reported	19
No. of values removed	0
No. of reported non-detects	0



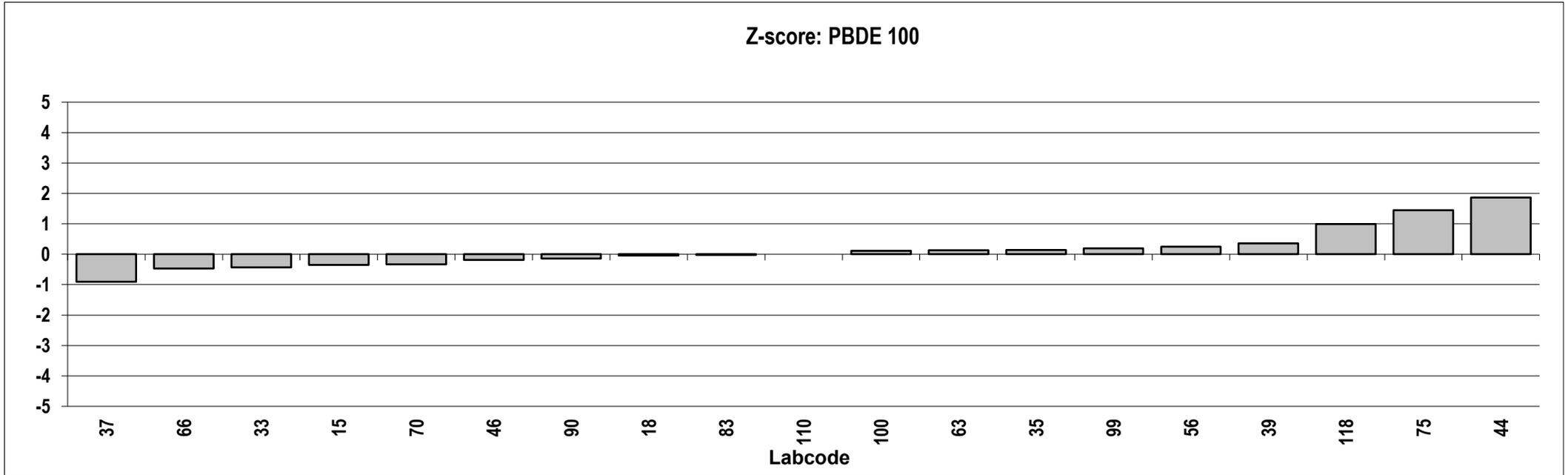
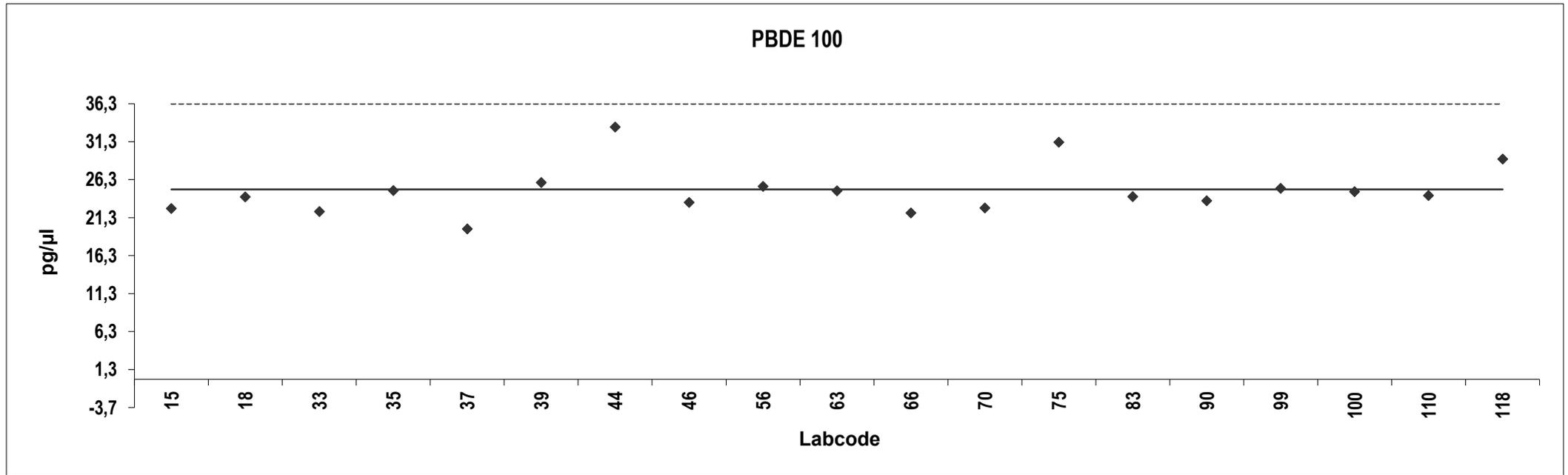
## Analyte solution

Congener: PBDE 100

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	23	-0,35				
18	24	-0,039				
33	22	-0,43				
35	25	0,13				
37	20	-0,91				
39	26	0,35				
44	33	1,9				
46	23	-0,18				
56	25	0,25				
63	25	0,13				
66	22	-0,47				
70	23	-0,34				
75	31	1,4				
83	24	-0,026				
90	24	-0,14				
99	25	0,20				
100	25	0,11				
110	24	0,00000				
118	29	0,99				

### Consensus statistics

Consensus median, pg/μl	24
Median all values pg/μl	24
Consensus mean, pg/μl	25
Standard deviation, pg/μl	3,2
Relative standard deviation, %	13
No. of values reported	19
No. of values removed	0
No. of reported non-detects	0



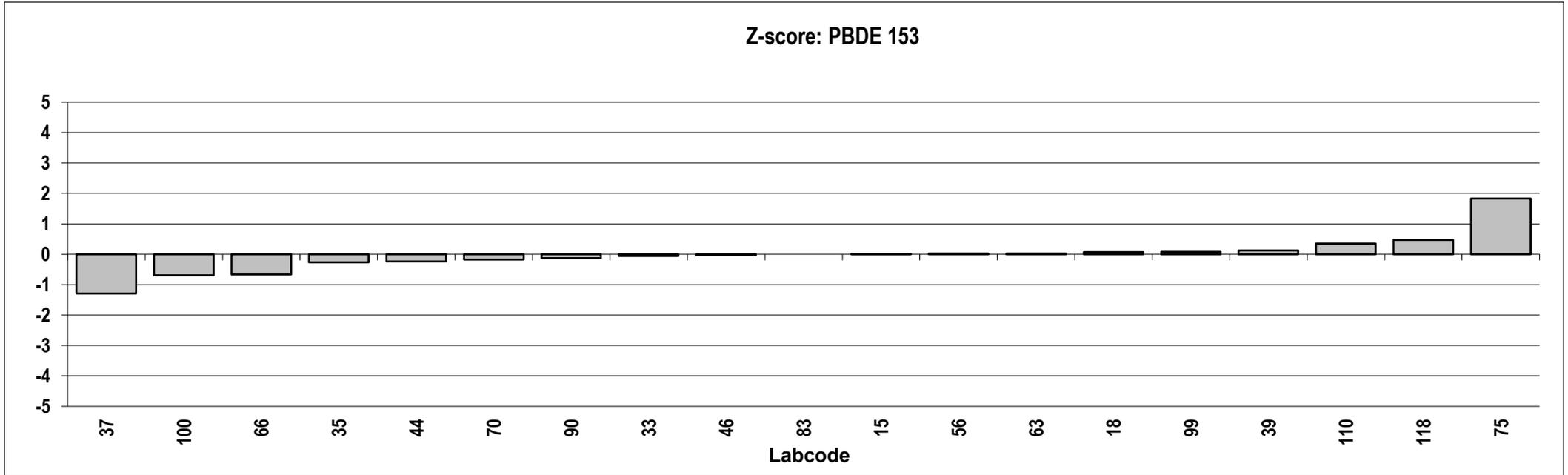
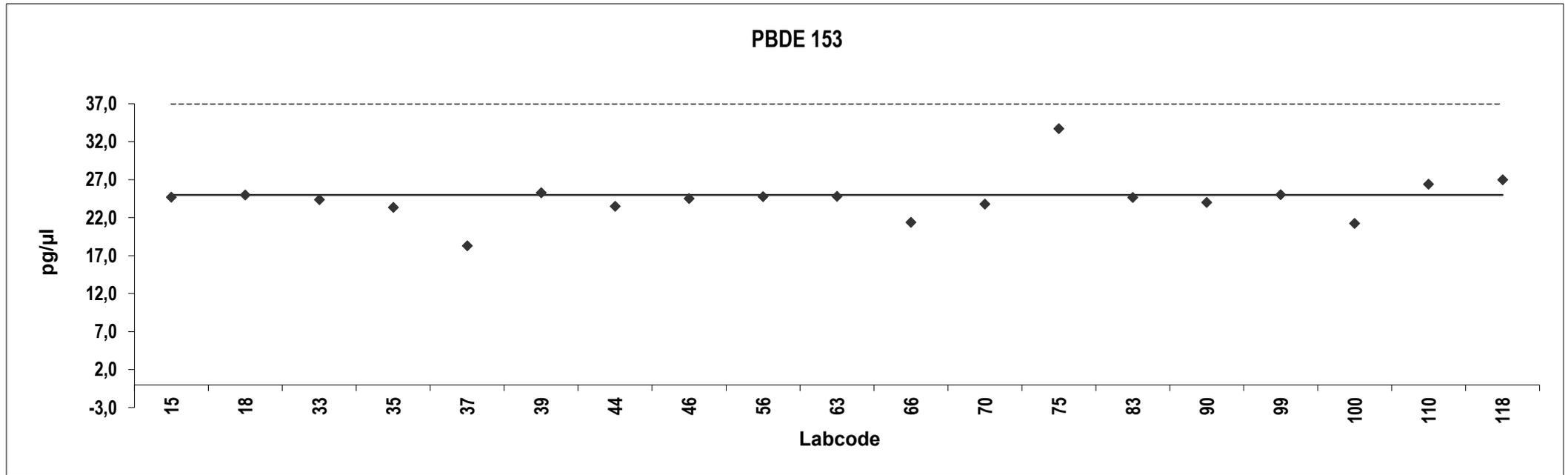
## Analyte solution

Congener: PBDE 153

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	25	0,0046				
18	25	0,065				
33	24	-0,056				
35	23	-0,27				
37	18	-1,3				
39	25	0,13				
44	24	-0,24				
46	25	-0,029				
56	25	0,025				
63	25	0,029				
66	21	-0,66				
70	24	-0,18				
75	34	1,8				
83	25	0,00000				
90	24	-0,13				
99	25	0,075				
100	21	-0,69				
110	26	0,35				
118	27	0,47				

### Consensus statistics

Consensus median, pg/μl	25
Median all values pg/μl	25
Consensus mean, pg/μl	25
Standard deviation, pg/μl	3,0
Relative standard deviation, %	12
No. of values reported	19
No. of values removed	0
No. of reported non-detects	0



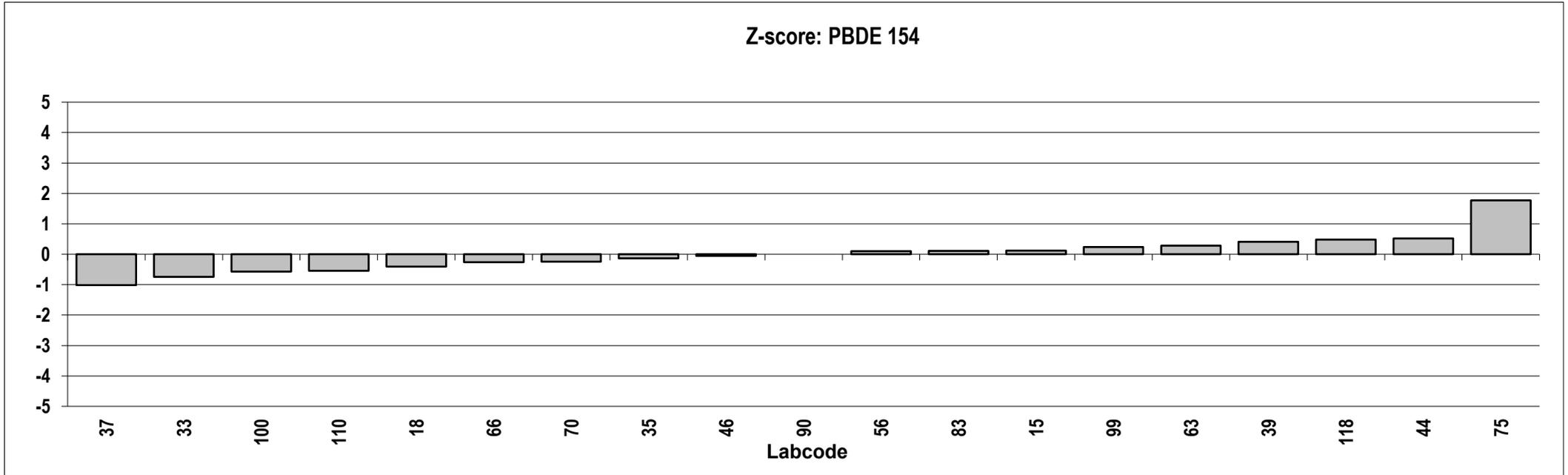
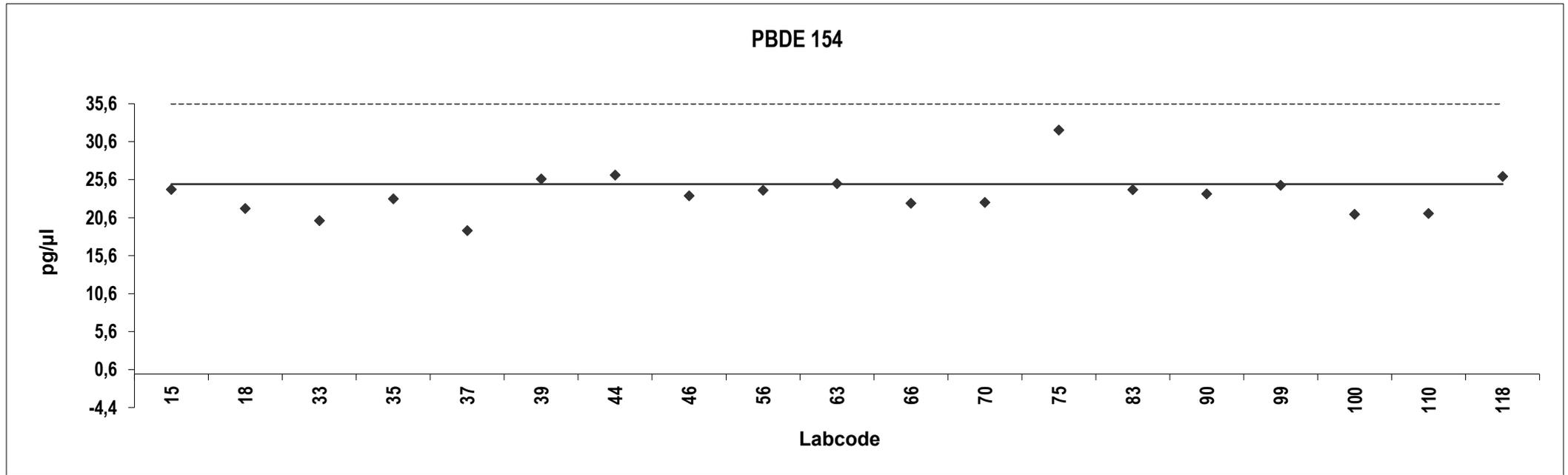
## Analyte solution

Congener: PBDE 154

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	24	0,12				
18	22	-0,41				
33	20	-0,74				
35	23	-0,14				
37	19	-1,0				
39	26	0,41				
44	26	0,52				
46	23	-0,054				
56	24	0,10				
63	25	0,28				
66	23	-0,26				
70	23	-0,24				
75	32	1,8				
83	24	0,11				
90	24	0,00000				
99	25	0,23				
100	21	-0,57				
110	21	-0,54				
118	26	0,48				

### Consensus statistics

Consensus median, pg/μl	24
Median all values pg/μl	24
Consensus mean, pg/μl	24
Standard deviation, pg/μl	2,8
Relative standard deviation, %	12
No. of values reported	19
No. of values removed	0
No. of reported non-detects	0



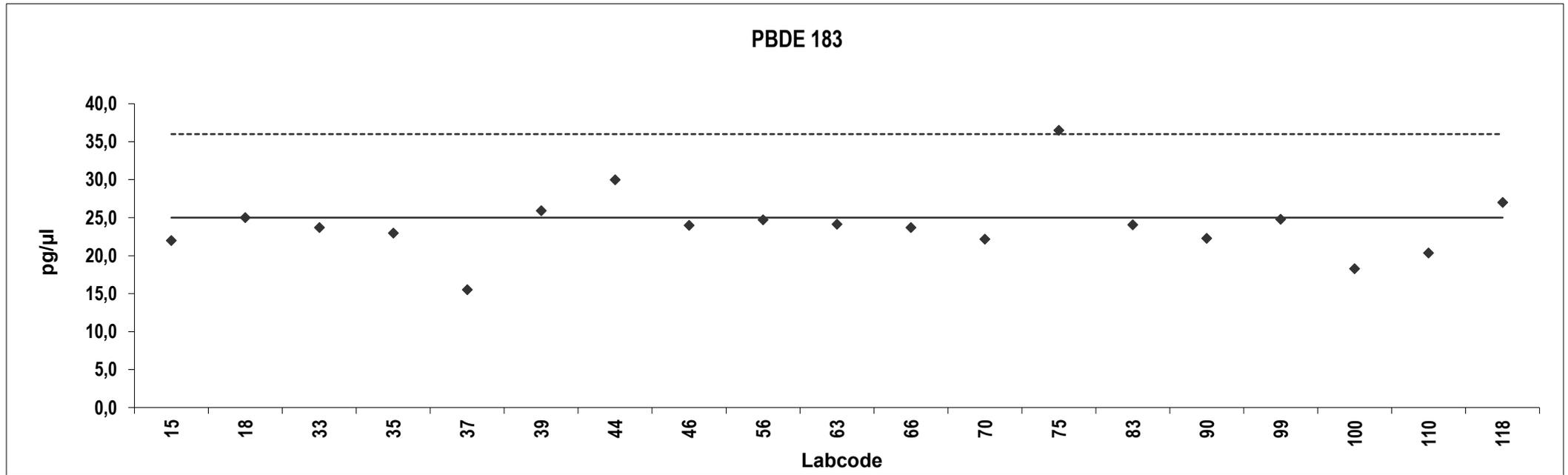
## Analyte solution

Congener: PBDE 183

Lab code	Conc. pg/μl	Z-score	Notes	Lab code	Conc. pg/μl	Notes
15	22	-0,39				
18	25	0,24				
33	24	-0,031				
35	23	-0,19				
37	16	-1,8				
39	26	0,43				
44	30	1,3				
46	24	0,031				
56	25	0,18				
63	24	0,057				
66	24	-0,031				
70	22	-0,35				
75	36	2,6	Outlier			
83	24	0,044				
90	22	-0,33				
99	25	0,19				
100	18	-1,2				
110	20	-0,73				
118	27	0,66				

### Consensus statistics

Consensus median, pg/μl	24
Median all values pg/μl	24
Consensus mean, pg/μl	23
Standard deviation, pg/μl	3,2
Relative standard deviation, %	14
No. of values reported	19
No. of values removed	1
No. of reported non-detects	0



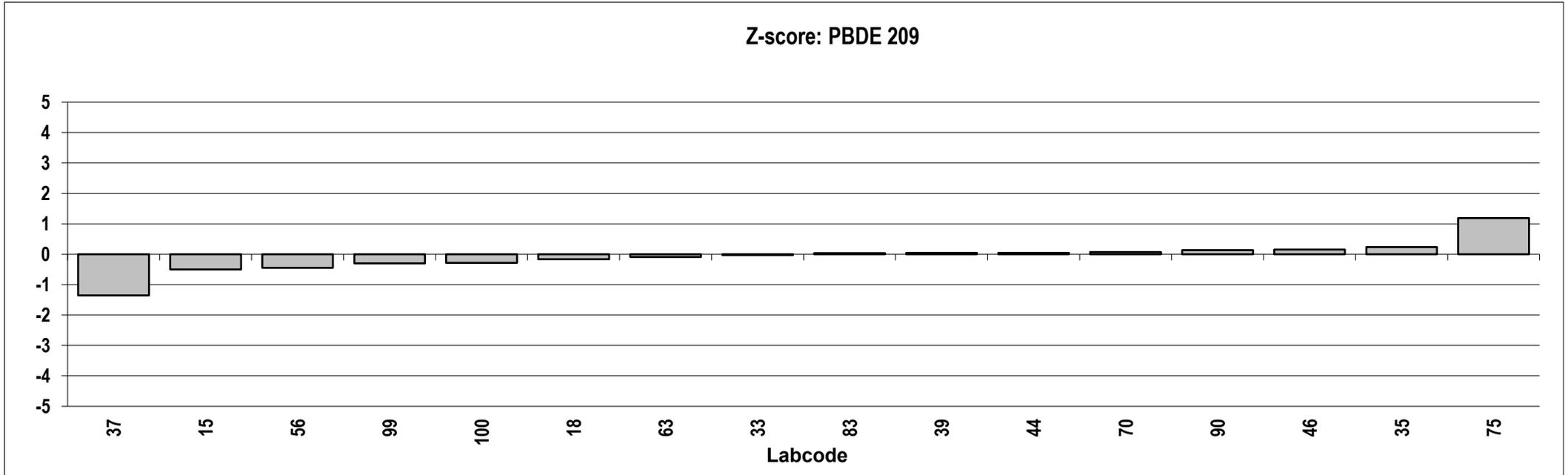
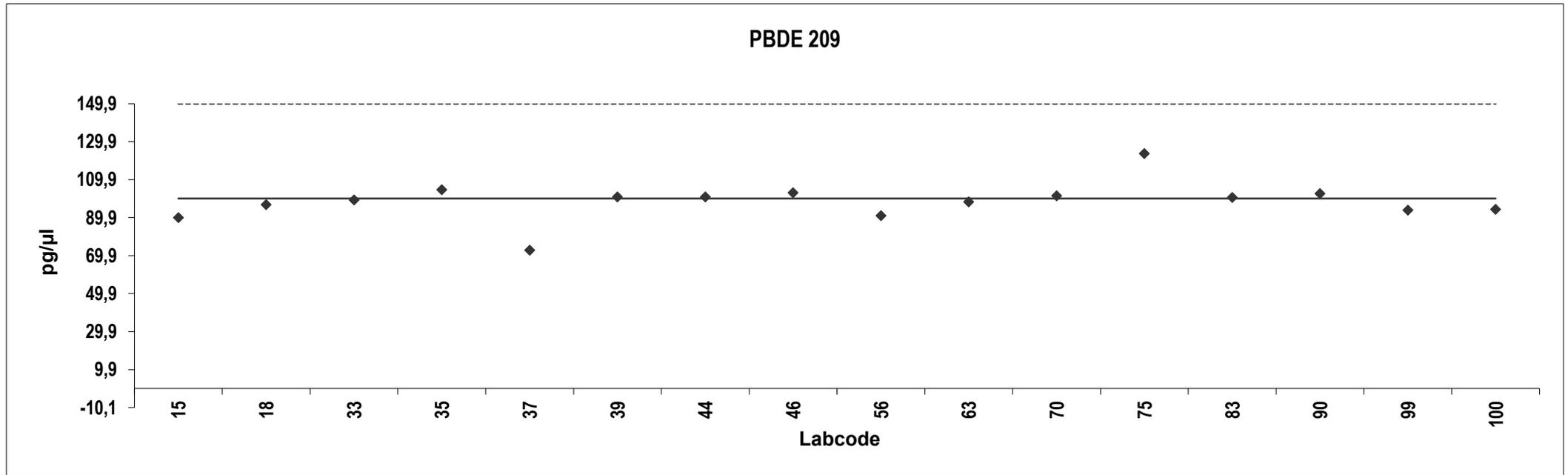
## Analyte solution

Congener: PBDE 209

Lab code	Conc. pg/ $\mu$ l	Z-score	Notes	Lab code	Conc. pg/ $\mu$ l	Notes
15	90	-0,50				
18	97	-0,16				
33	99	-0,032				
35	105	0,23				
37	73	-1,4				
39	101	0,044				
44	101	0,048				
46	103	0,15				
56	91	-0,45				
63	98	-0,089				
70	101	0,071				
75	124	1,2				
83	101	0,032				
90	103	0,13				
99	94	-0,30				
100	94	-0,28				

### Consensus statistics

Consensus median, pg/ $\mu$ l	100
Median all values pg/ $\mu$ l	100
Consensus mean, pg/ $\mu$ l	98
Standard deviation, pg/ $\mu$ l	10
Relative standard deviation, %	10
No. of values reported	16
No. of values removed	0
No. of reported non-detects	0



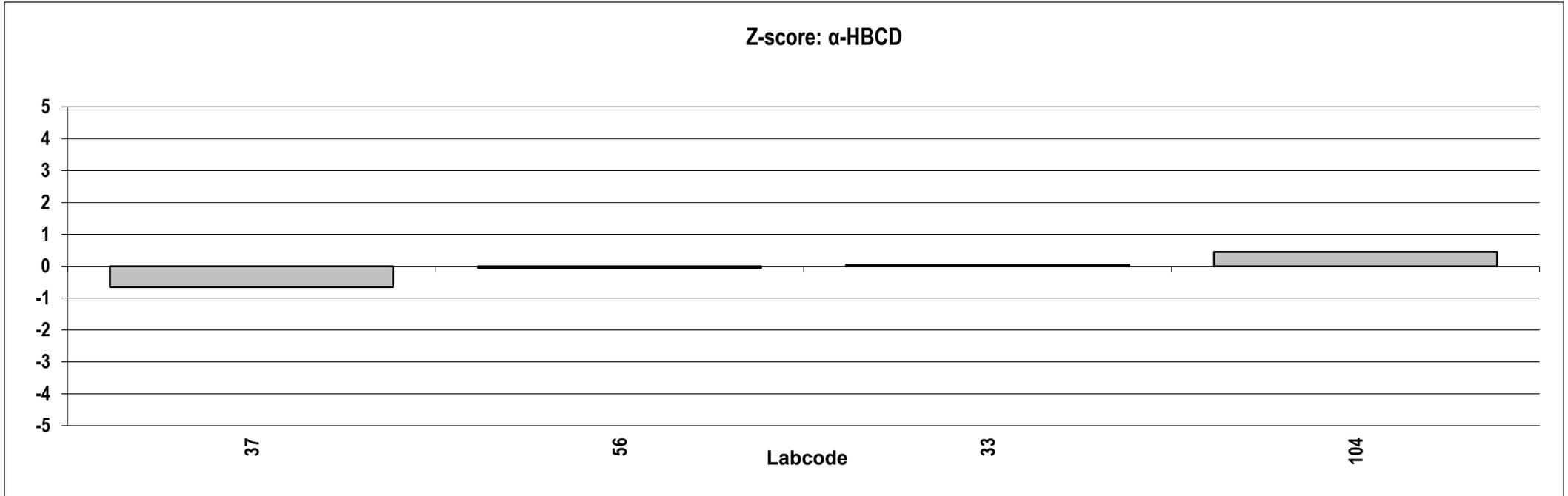
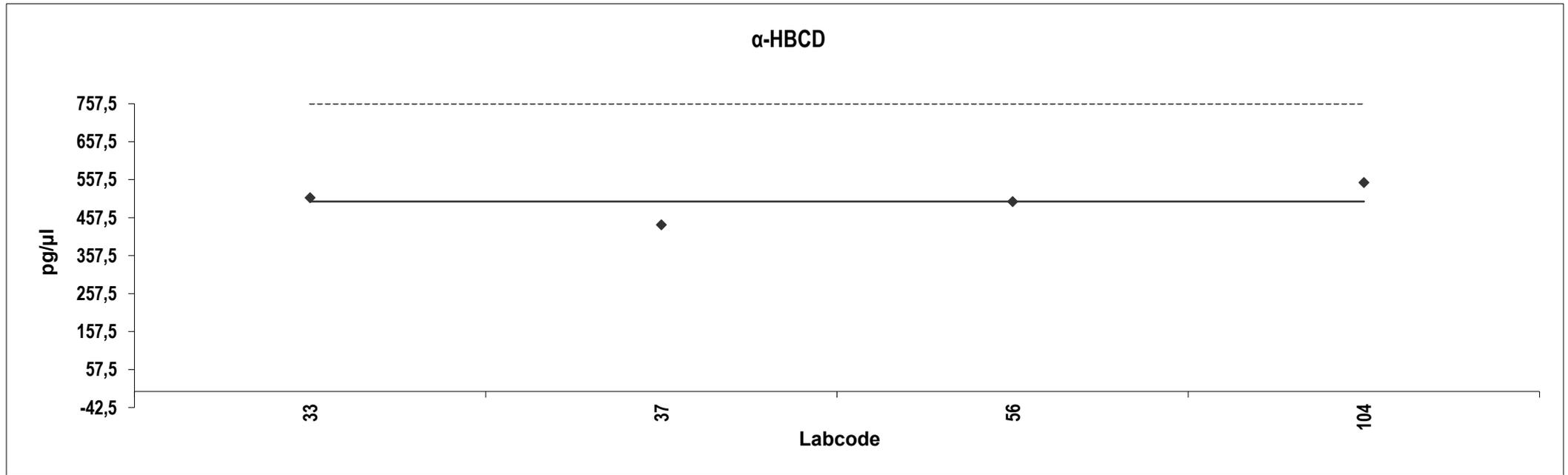
## Analyte solution

Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/ $\mu$ l	Z-score	Notes	Lab code	Conc. pg/ $\mu$ l	Notes
33	510	0,050				
37	439	-0,65				
56	500	-0,050				
104	550	0,45				

### Consensus statistics

Consensus median, pg/ $\mu$ l	505
Median all values pg/ $\mu$ l	505
Consensus mean, pg/ $\mu$ l	500
Standard deviation, pg/ $\mu$ l	46
Relative standard deviation, %	9,2
No. of values reported	4
No. of values removed	0
No. of reported non-detects	0





## **Appendix 2:**



Presentation of results for  
Mackerel 2024



## Appendix 2: Presentation of results: Mackerel 2024

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

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

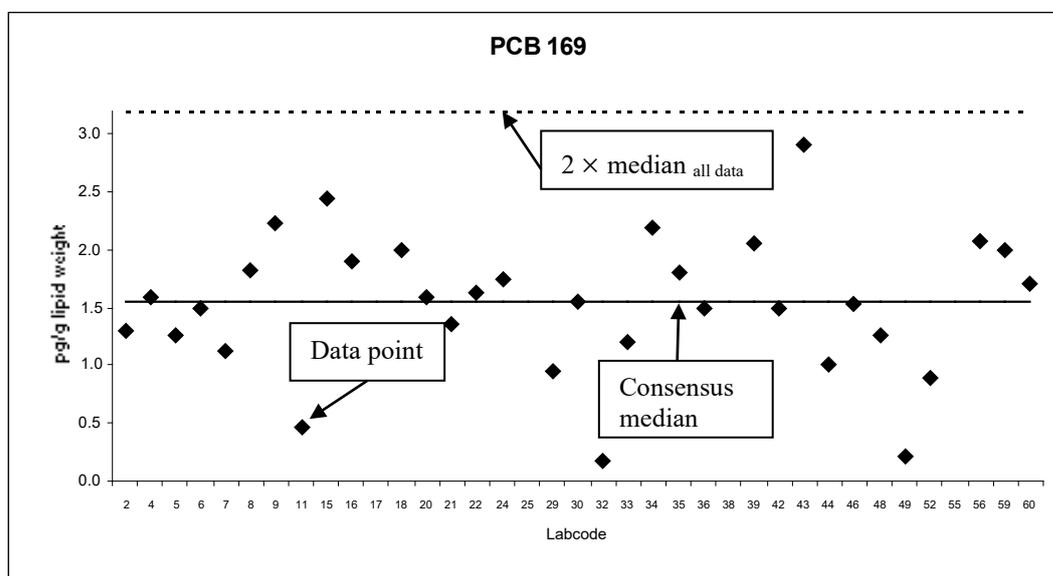
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding  $2 \times$  this median were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

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

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

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

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



### Z-Scores of individual congeners

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

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

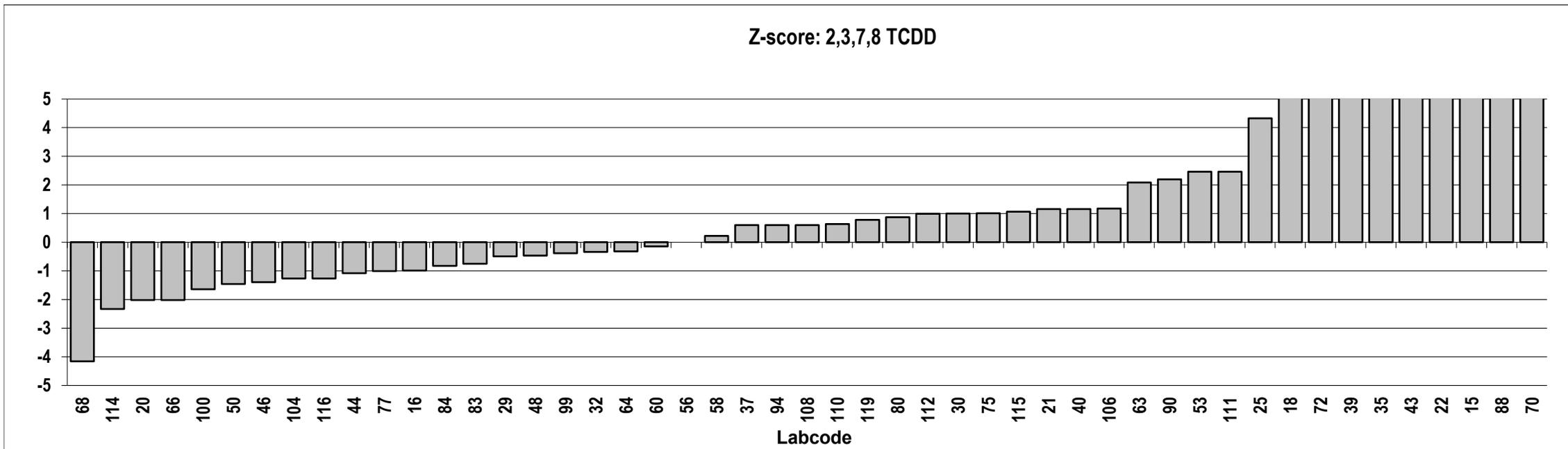
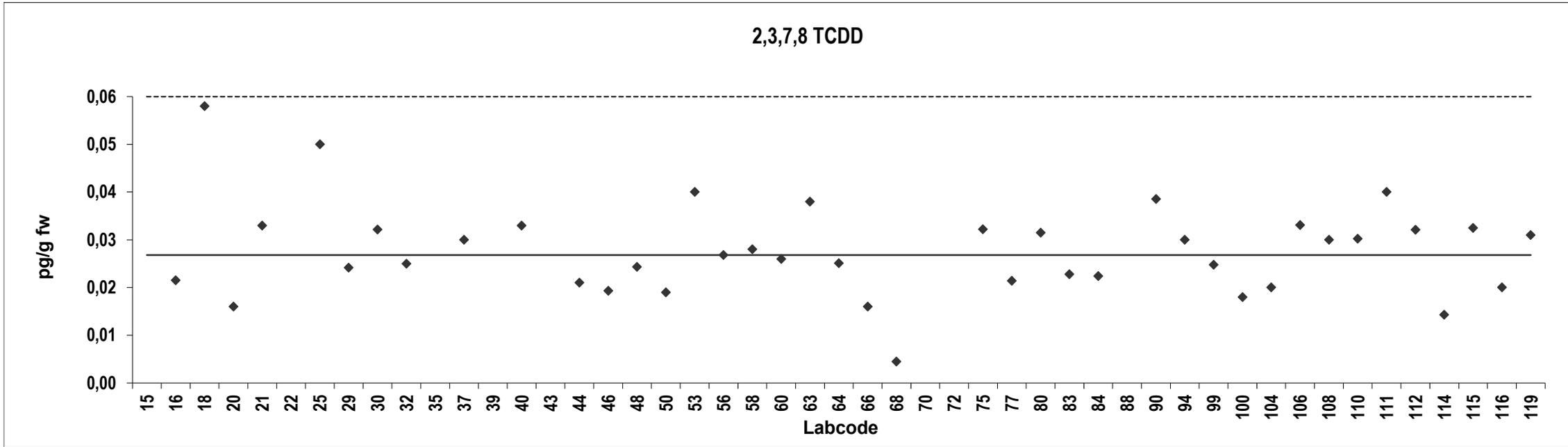
where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,091	12	Outlier	114	0,014	-2,3	
16	0,021	-0,99		115	0,033	1,1	ND
18	0,058	5,8		116	0,020	-1,3	ND
20	0,016	-2,0		119	0,031	0,78	
21	0,033	1,2					
22	0,078	9,5	Outlier				
25	0,050	4,3	ND				
29	0,024	-0,49					
30	0,032	1,0					
32	0,025	-0,34					
35	0,070	8,1	Outlier,ND				
37	0,030	0,60					
39	0,065	7,2	Outlier				
40	0,033	1,2					
43	0,075	9,0	Outlier,ND				
44	0,021	-1,1					
46	0,019	-1,4					
48	0,024	-0,47					
50	0,019	-1,5					
53	0,040	2,5	ND				
56	0,027	0,00000					
58	0,028	0,22					
60	0,026	-0,15					
63	0,038	2,1					
64	0,025	-0,32					
66	0,016	-2,0					
68	0,0045	-4,2	ND				
70	0,85	153	Outlier				
72	0,063	6,8	Outlier,ND				
75	0,032	1,0					
77	0,021	-1,0					
80	0,032	0,88					
83	0,023	-0,75					
84	0,022	-0,82					
88	0,14	20	Outlier,ND				
90	0,039	2,2					
94	0,030	0,60					
99	0,025	-0,38					
100	0,018	-1,6	ND				
104	0,020	-1,3					
106	0,033	1,2					
108	0,030	0,60					
110	0,030	0,64					
111	0,040	2,5	ND				
112	0,032	0,99					

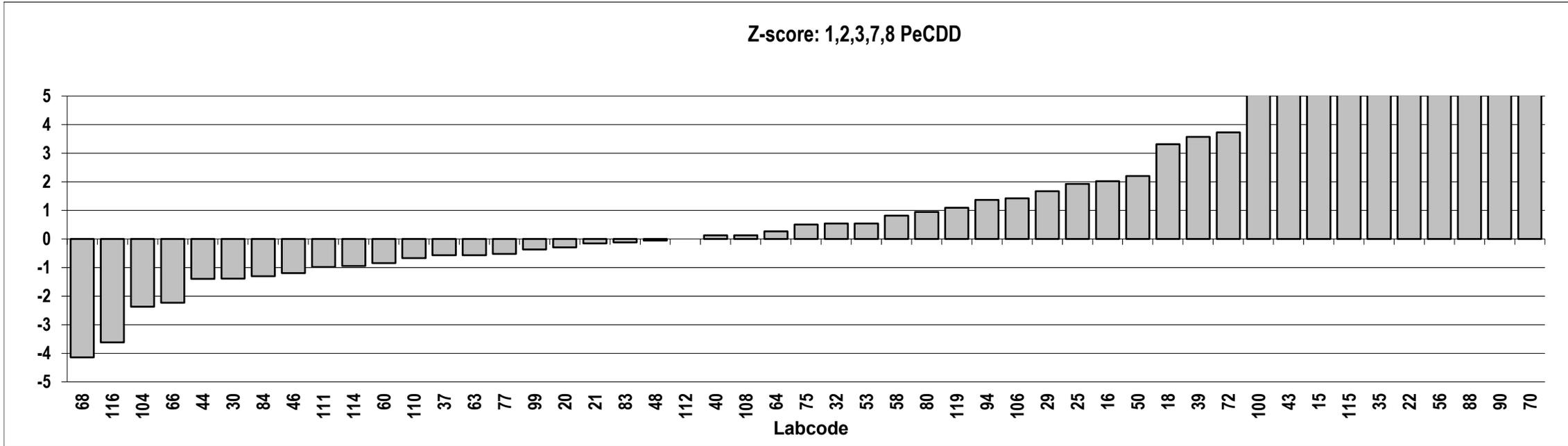
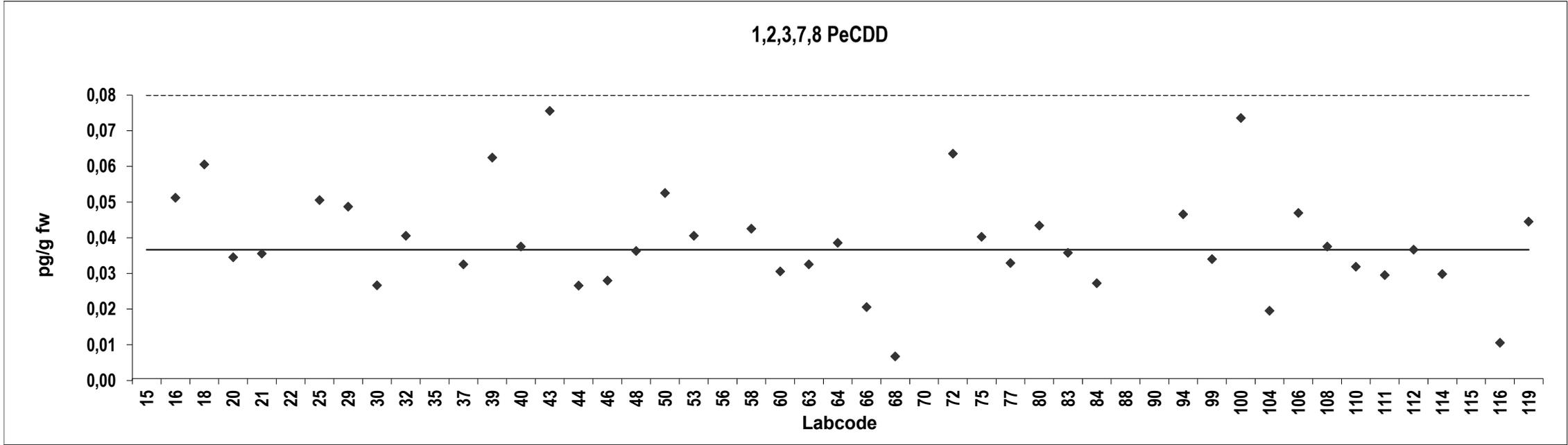
Consensus statistics	
Consensus median, pg/g	0,027
Median all values pg/g	0,030
Consensus mean, pg/g	0,028
Standard deviation, pg/g	0,0097
Relative standard deviation, %	35
No. of values reported	49
No. of values removed	8
No. of reported non-detects	11



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,080	6,1	Outlier	114	0,029	-0,95	
16	0,051	2,0		115	0,083	6,4	Outlier,ND
18	0,060	3,3		116	0,010	-3,6	ND
20	0,034	-0,29		119	0,044	1,1	
21	0,035	-0,15					
22	0,13	13	Outlier				
25	0,050	1,9	ND				
29	0,048	1,7					
30	0,026	-1,4					
32	0,040	0,54	ND				
35	0,12	12	Outlier,ND				
37	0,032	-0,57					
39	0,062	3,6					
40	0,037	0,12					
43	0,075	5,4	ND				
44	0,026	-1,4					
46	0,027	-1,2					
48	0,036	-0,055					
50	0,052	2,2					
53	0,040	0,54	ND				
56	0,13	13	Outlier				
58	0,042	0,82					
60	0,030	-0,84					
63	0,032	-0,57					
64	0,038	0,26					
66	0,020	-2,2					
68	0,0062	-4,1	ND				
70	0,53	69	Outlier				
72	0,063	3,7	ND				
75	0,040	0,50					
77	0,032	-0,52					
80	0,043	0,94					
83	0,035	-0,12					
84	0,027	-1,3					
88	0,15	15	Outlier,ND				
90	0,17	19	Outlier				
94	0,046	1,4					
99	0,033	-0,36					
100	0,073	5,1	ND				
104	0,019	-2,4					
106	0,046	1,4					
108	0,037	0,12					
110	0,031	-0,67					
111	0,029	-0,98					
112	0,036	0,00000					

Consensus statistics	
Consensus median, pg/g	0,036
Median all values pg/g	0,040
Consensus mean, pg/g	0,038
Standard deviation, pg/g	0,015
Relative standard deviation, %	38
No. of values reported	49
No. of values removed	8
No. of reported non-detects	11

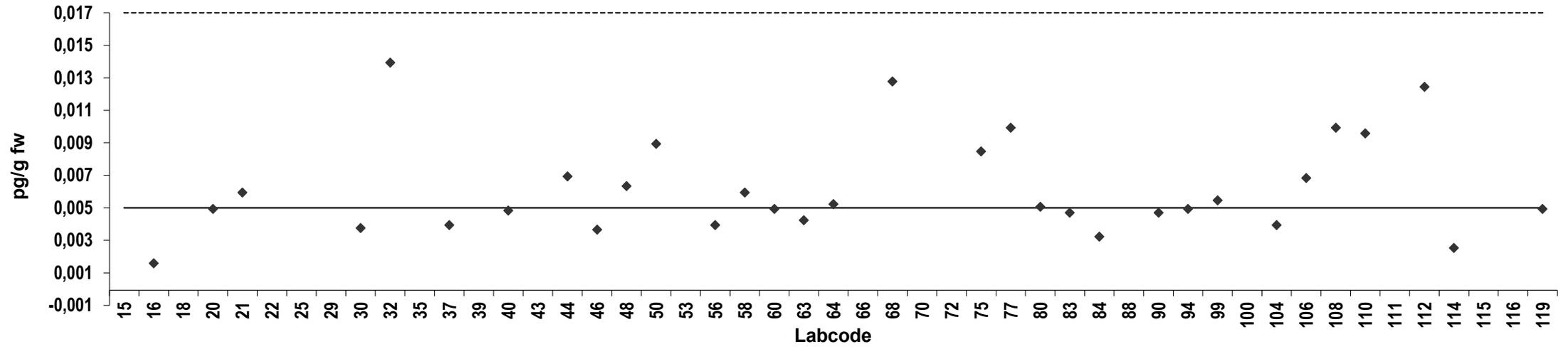


**Mackerel**  
**Congener: 1,2,3,4,7,8 HxCDD**

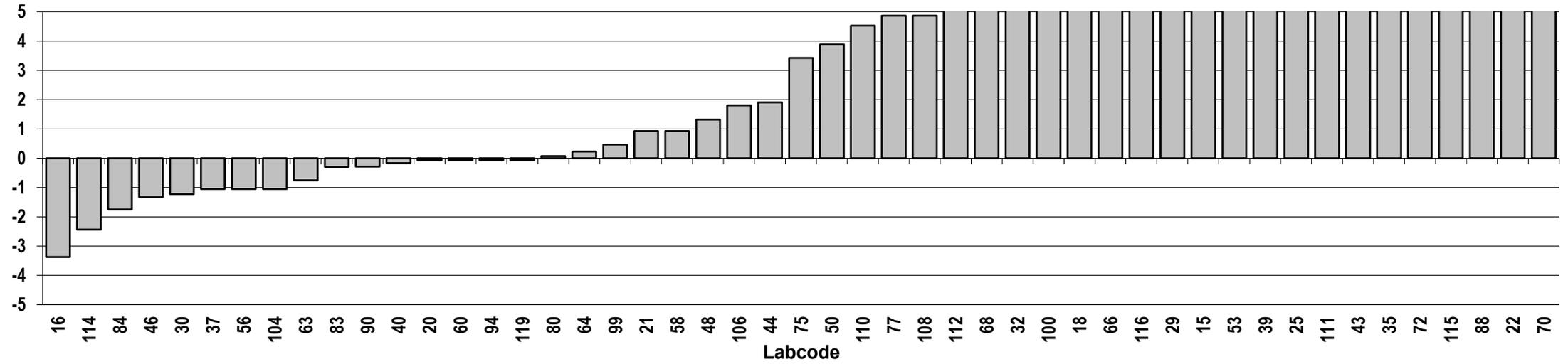
Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,034	29	Outlier,ND	114	0,0026	-2,4	
16	0,0017	-3,4	ND	115	0,14	136	Outlier,ND
18	0,019	14	Outlier,ND	116	0,020	15	Outlier
20	0,0050	-0,066	ND	119	0,0050	-0,066	ND
21	0,0060	0,92	ND				
22	0,21	207	Outlier				
25	0,050	44	Outlier,ND				
29	0,028	22	Outlier,ND				
30	0,0038	-1,2					
32	0,014	8,8					
35	0,10	94	Outlier,ND				
37	0,0040	-1,1					
39	0,044	39	Outlier				
40	0,0049	-0,16					
43	0,099	93	Outlier,ND				
44	0,0070	1,9	ND				
46	0,0037	-1,3					
48	0,0064	1,3	ND				
50	0,0090	3,9	ND				
53	0,040	34	Outlier,ND				
56	0,0040	-1,1					
58	0,0060	0,92					
60	0,0050	-0,066	ND				
63	0,0043	-0,76					
64	0,0053	0,23					
66	0,019	14	Outlier				
68	0,013	7,7	ND				
70	0,42	409	Outlier				
72	0,13	123	Outlier,ND				
75	0,0085	3,4	ND				
77	0,010	4,9	ND				
80	0,0051	0,066					
83	0,0048	-0,30					
84	0,0033	-1,7					
88	0,19	187	Outlier,ND				
90	0,0048	-0,29					
94	0,0050	-0,066	ND				
99	0,0055	0,46	ND				
100	0,018	13	Outlier,ND				
104	0,0040	-1,1	ND				
106	0,0069	1,8					
108	0,010	4,9	ND				
110	0,0097	4,5					
111	0,050	44	Outlier,ND				
112	0,013	7,3					

Consensus statistics	
Consensus median, pg/g	0,0051
Median all values pg/g	0,0085
Consensus mean, pg/g	0,0063
Standard deviation, pg/g	0,0030
Relative standard deviation, %	48
No. of values reported	49
No. of values removed	17
No. of reported non-detects	27

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



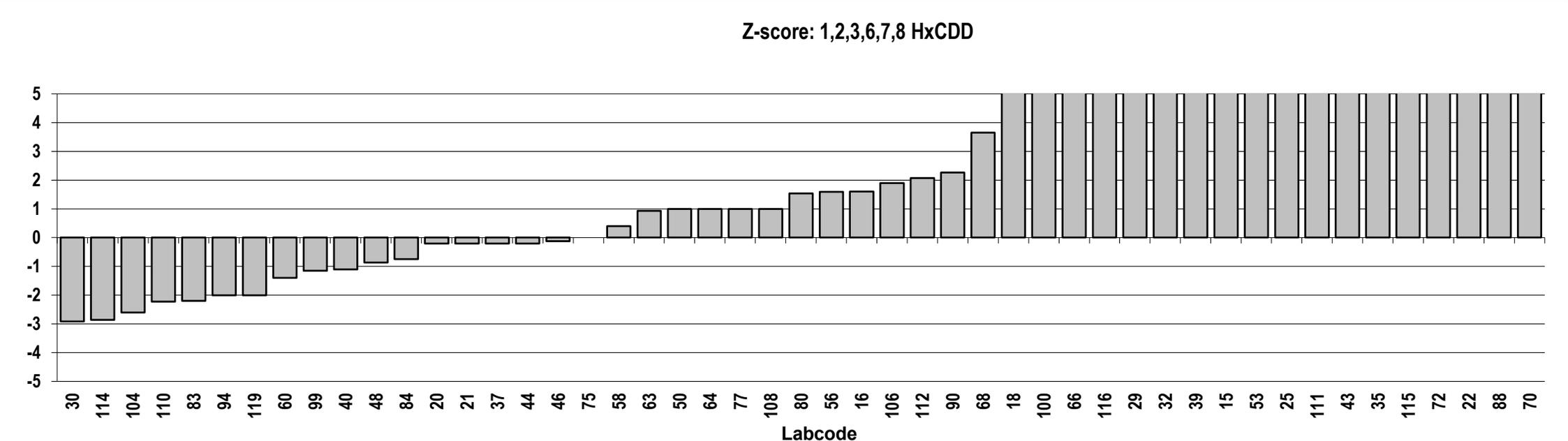
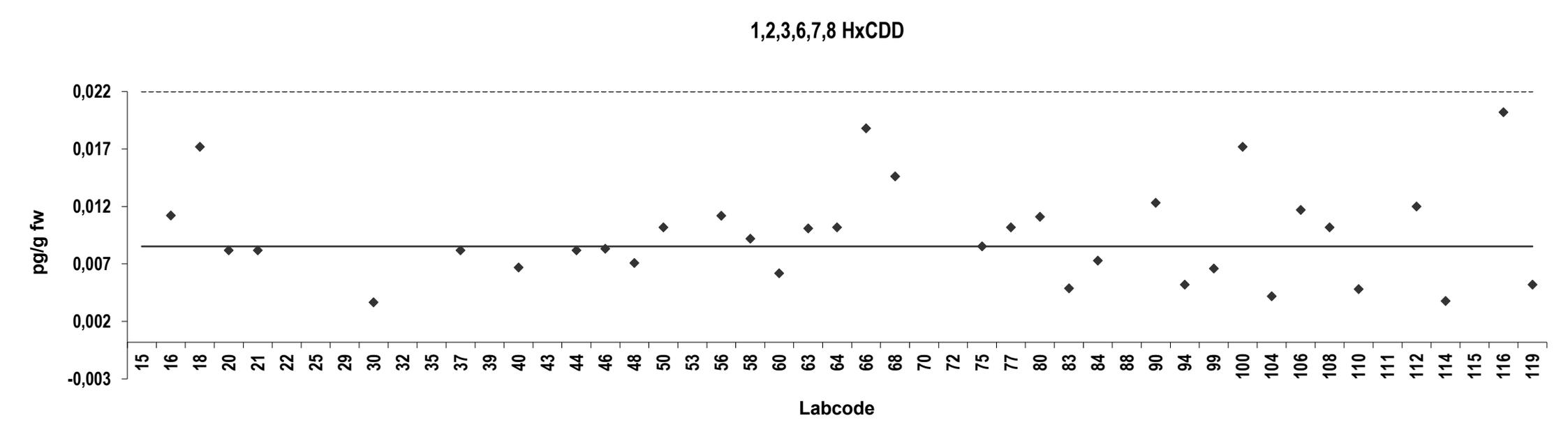
Z-score: 1,2,3,4,7,8 HxCDD



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,038	17	Outlier,ND	114	0,0036	-2,9	
16	0,011	1,6		115	0,13	70	Outlier,ND
18	0,017	5,2	ND	116	0,020	7,0	
20	0,0080	-0,20		119	0,0050	-2,0	ND
21	0,0080	-0,20					
22	0,19	108	Outlier				
25	0,050	25	Outlier,ND				
29	0,028	11	Outlier,ND				
30	0,0035	-2,9					
32	0,028	12	Outlier				
35	0,10	55	Outlier,ND				
37	0,0080	-0,20					
39	0,035	16	Outlier				
40	0,0065	-1,1					
43	0,099	54	Outlier,ND				
44	0,0080	-0,20					
46	0,0081	-0,12					
48	0,0069	-0,86					
50	0,010	0,99	ND				
53	0,040	19	Outlier,ND				
56	0,011	1,6					
58	0,0090	0,39					
60	0,0060	-1,4					
63	0,0099	0,93					
64	0,010	0,99					
66	0,019	6,1	ND				
68	0,014	3,7	ND				
70	1,2	691	Outlier				
72	0,13	73	Outlier,ND				
75	0,0083	0,00000	ND				
77	0,010	0,99	ND				
80	0,011	1,5					
83	0,0047	-2,2					
84	0,0071	-0,74					
88	0,20	114	Outlier,ND				
90	0,012	2,3					
94	0,0050	-2,0	ND				
99	0,0064	-1,2					
100	0,017	5,2	ND				
104	0,0040	-2,6	ND				
106	0,012	1,9					
108	0,010	0,99	ND				
110	0,0046	-2,2	ND				
111	0,050	25	Outlier,ND				
112	0,012	2,1					

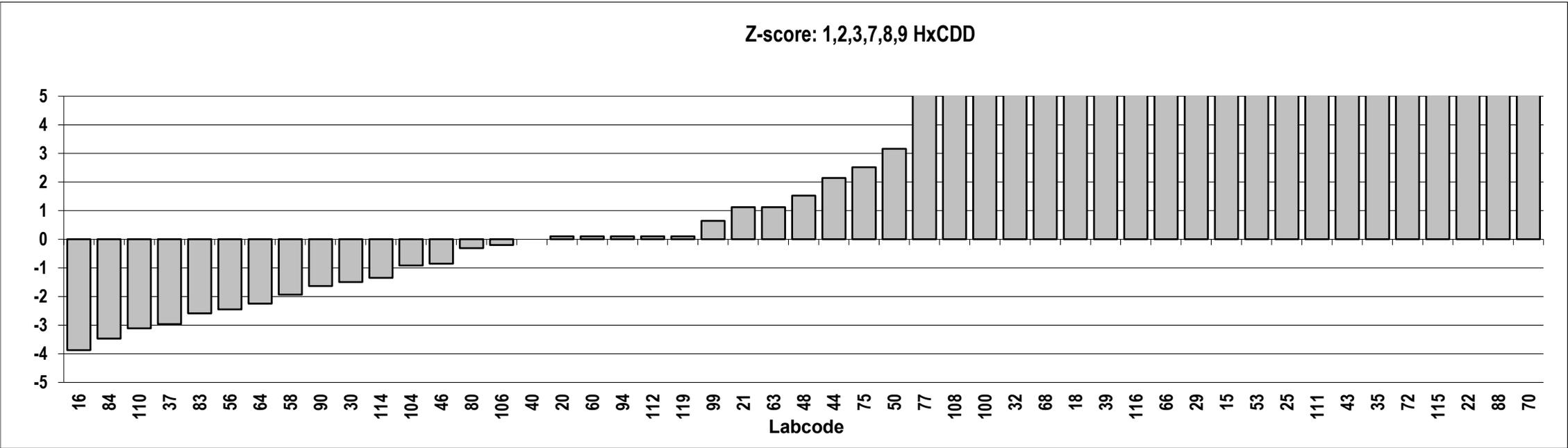
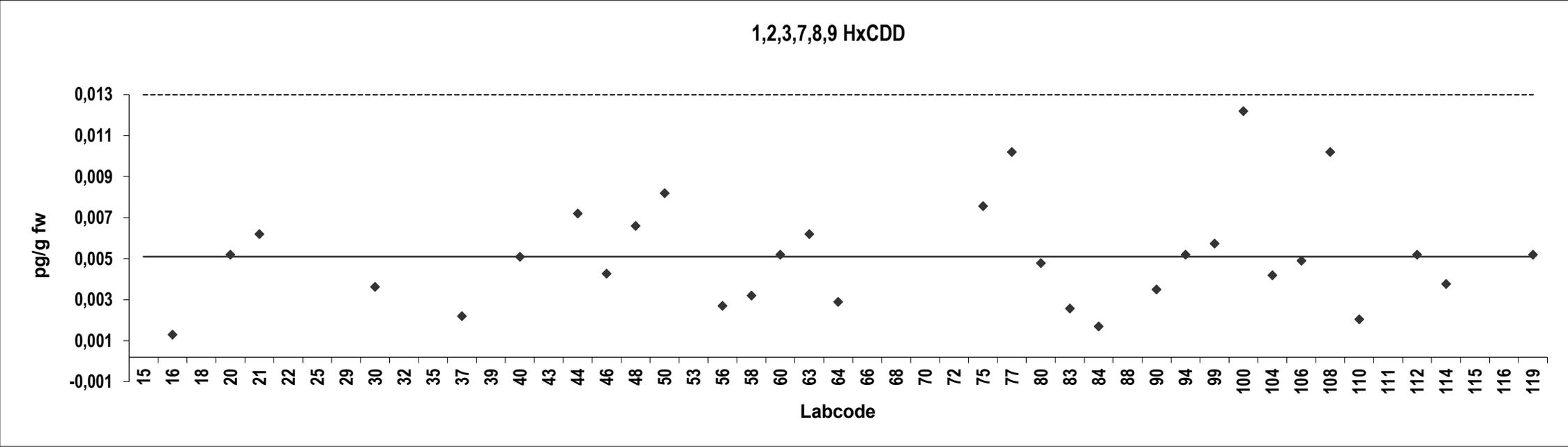
Consensus statistics	
Consensus median, pg/g	0,0083
Median all values pg/g	0,011
Consensus mean, pg/g	0,0093
Standard deviation, pg/g	0,0042
Relative standard deviation, %	45
No. of values reported	49
No. of values removed	14
No. of reported non-detects	22



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,034	29	Outlier,ND	114	0,0036	-1,4	
16	0,0011	-3,9	ND	115	0,13	129	Outlier,ND
18	0,018	13	Outlier,ND	116	0,020	15	Outlier
20	0,0050	0,10	ND	119	0,0050	0,10	ND
21	0,0060	1,1	ND				
22	0,17	166	Outlier				
25	0,050	46	Outlier,ND				
29	0,022	18	Outlier,ND				
30	0,0034	-1,5					
32	0,013	8,3	Outlier				
35	0,10	97	Outlier,ND				
37	0,0020	-3,0					
39	0,019	15	Outlier				
40	0,0049	0,00000	ND				
43	0,099	96	Outlier,ND				
44	0,0070	2,1	ND				
46	0,0041	-0,85					
48	0,0064	1,5	ND				
50	0,0080	3,2	ND				
53	0,040	36	Outlier,ND				
56	0,0025	-2,4					
58	0,0030	-1,9	ND				
60	0,0050	0,10	ND				
63	0,0060	1,1	ND				
64	0,0027	-2,2					
66	0,021	16	Outlier				
68	0,015	10	Outlier,ND				
70	0,81	826	Outlier				
72	0,13	128	Outlier,ND				
75	0,0074	2,5	ND				
77	0,010	5,2	ND				
80	0,0046	-0,31					
83	0,0024	-2,6					
84	0,0015	-3,5					
88	0,18	177	Outlier,ND				
90	0,0033	-1,6					
94	0,0050	0,10	ND				
99	0,0055	0,65	ND				
100	0,012	7,2	ND				
104	0,0040	-0,92	ND				
106	0,0047	-0,20					
108	0,010	5,2	ND				
110	0,0019	-3,1	ND				
111	0,050	46	Outlier,ND				
112	0,0050	0,10	ND				

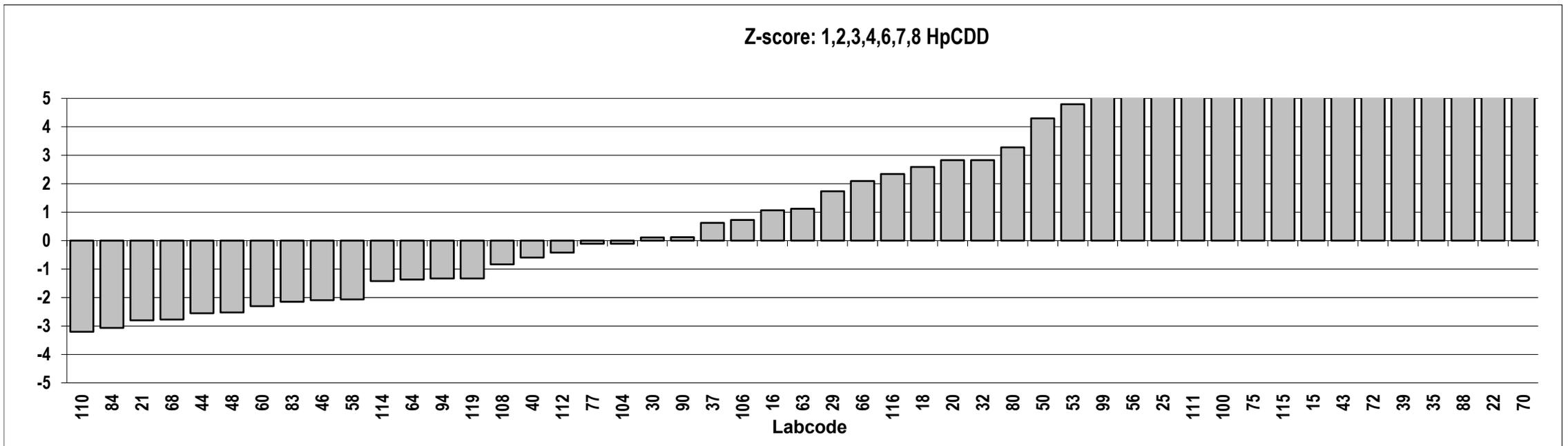
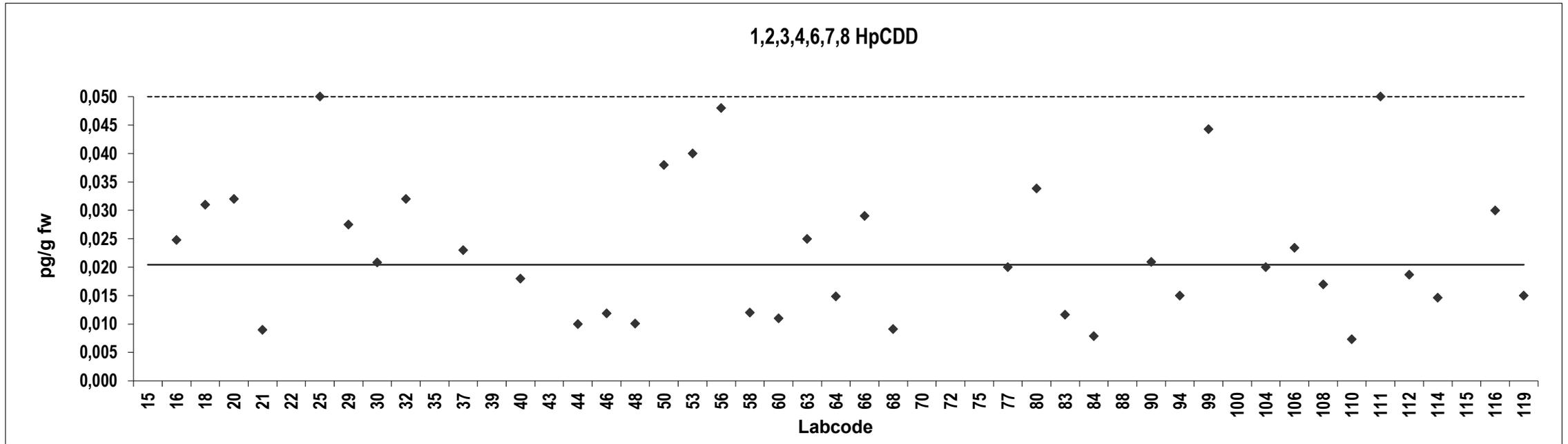
Consensus statistics	
Consensus median, pg/g	0,0049
Median all values pg/g	0,0064
Consensus mean, pg/g	0,0049
Standard deviation, pg/g	0,0026
Relative standard deviation, %	52
No. of values reported	49
No. of values removed	18
No. of reported non-detects	32



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,098	19	Outlier,ND	114	0,015	-1,4	
16	0,025	1,1		115	0,085	16	Outlier,ND
18	0,031	2,6	ND	116	0,030	2,3	
20	0,032	2,8		119	0,015	-1,3	ND
21	0,0090	-2,8					
22	5,2	1264	Outlier				
25	0,050	7,2	ND				
29	0,028	1,7	ND				
30	0,021	0,11					
32	0,032	2,8					
35	0,20	44	Outlier,ND				
37	0,023	0,63					
39	0,17	37	Outlier				
40	0,018	-0,60					
43	0,099	19	Outlier,ND				
44	0,010	-2,6					
46	0,012	-2,1					
48	0,010	-2,5					
50	0,038	4,3					
53	0,040	4,8	ND				
56	0,048	6,7					
58	0,012	-2,1					
60	0,011	-2,3					
63	0,025	1,1					
64	0,015	-1,4					
66	0,029	2,1					
68	0,0091	-2,8	ND				
70	16	3884	Outlier				
72	0,13	27	Outlier,ND				
75	0,070	12	Outlier				
77	0,020	-0,11	ND				
80	0,034	3,3					
83	0,012	-2,2					
84	0,0079	-3,1					
88	0,41	96	Outlier				
90	0,021	0,12					
94	0,015	-1,3	ND				
99	0,044	5,8	ND				
100	0,067	11	Outlier,ND				
104	0,020	-0,11	ND				
106	0,023	0,73					
108	0,017	-0,84					
110	0,0074	-3,2	ND				
111	0,050	7,2	ND				
112	0,019	-0,42					

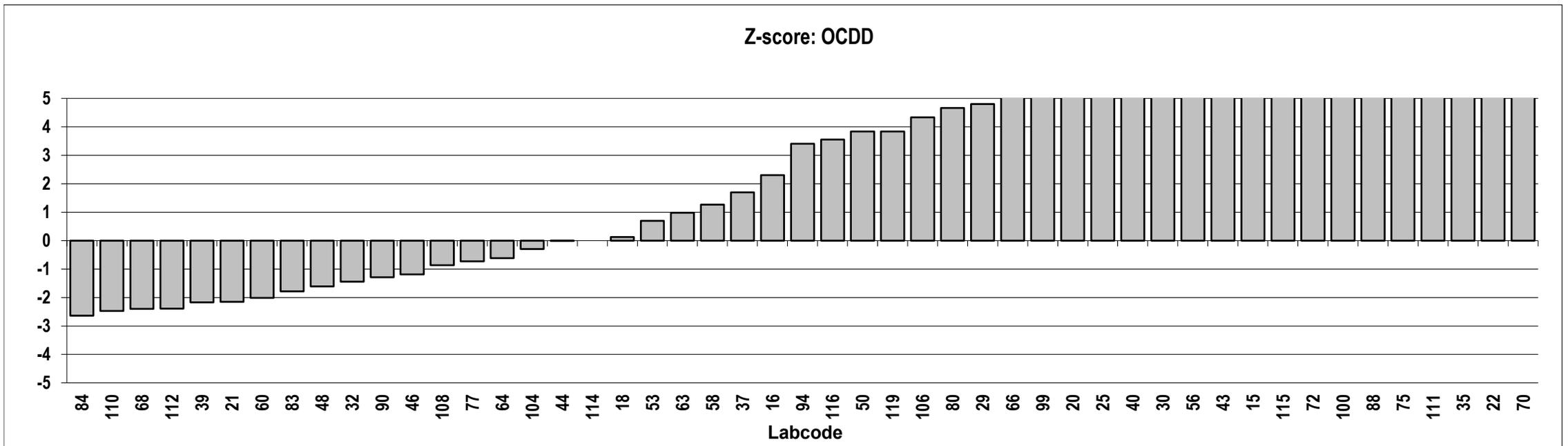
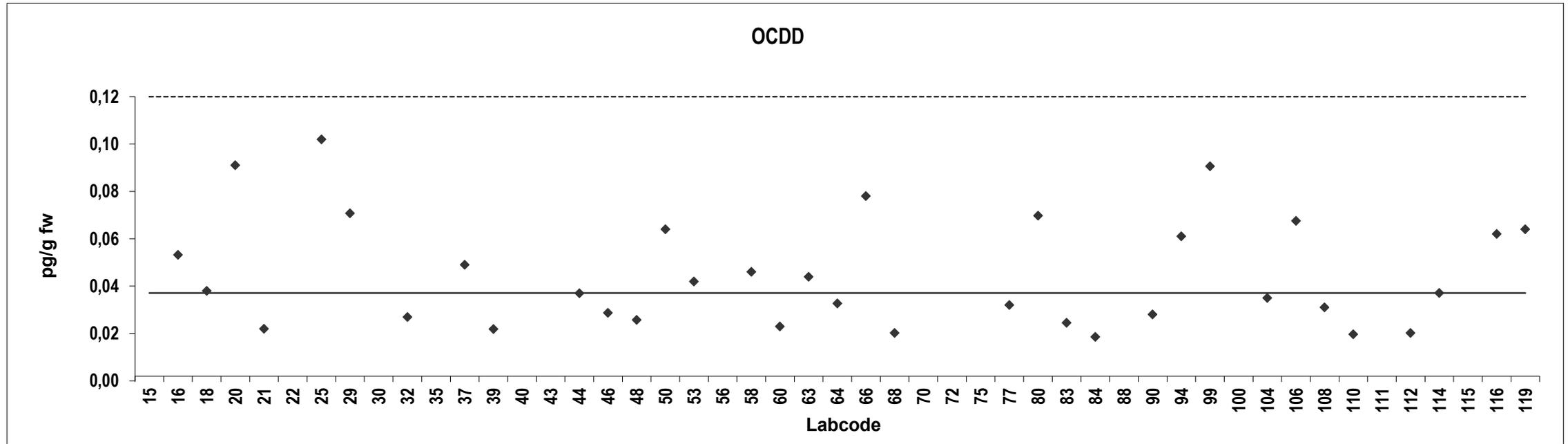
Consensus statistics	
Consensus median, pg/g	0,020
Median all values pg/g	0,025
Consensus mean, pg/g	0,023
Standard deviation, pg/g	0,012
Relative standard deviation, %	53
No. of values reported	49
No. of values removed	11
No. of reported non-detects	18



**Mackerel**  
**Congener: OCDD**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,21	25	Outlier	114	0,035	0,00000	
16	0,051	2,3		115	0,29	36	Outlier,ND
18	0,036	0,13	ND	116	0,060	3,5	
20	0,089	7,7		119	0,062	3,8	
21	0,020	-2,2					
22	3,3	466	Outlier				
25	0,10	9,2	ND				
29	0,069	4,8	ND				
30	0,18	20	Outlier				
32	0,025	-1,4					
35	1,0	137	Outlier,ND				
37	0,047	1,7					
39	0,020	-2,2					
40	0,16	18	Outlier				
43	0,20	23	Outlier,ND				
44	0,035	-0,015					
46	0,027	-1,2					
48	0,024	-1,6					
50	0,062	3,8					
53	0,040	0,70	ND				
56	0,18	21	Outlier				
58	0,044	1,3					
60	0,021	-2,0					
63	0,042	0,98					
64	0,031	-0,62					
66	0,076	5,8					
68	0,018	-2,4	ND				
70	102	14550	Outlier				
72	0,31	39	Outlier,ND				
75	0,49	65	Outlier				
77	0,030	-0,73	ND				
80	0,068	4,7					
83	0,023	-1,8					
84	0,017	-2,6					
88	0,40	53	Outlier				
90	0,026	-1,3					
94	0,059	3,4					
99	0,089	7,6	ND				
100	0,34	43	Outlier,ND				
104	0,033	-0,30					
106	0,066	4,3					
108	0,029	-0,87					
110	0,018	-2,5	ND				
111	0,50	66	Outlier,ND				
112	0,018	-2,4					

Consensus statistics	
Consensus median, pg/g	0,035
Median all values pg/g	0,059
Consensus mean, pg/g	0,043
Standard deviation, pg/g	0,023
Relative standard deviation, %	54
No. of values reported	49
No. of values removed	14
No. of reported non-detects	14

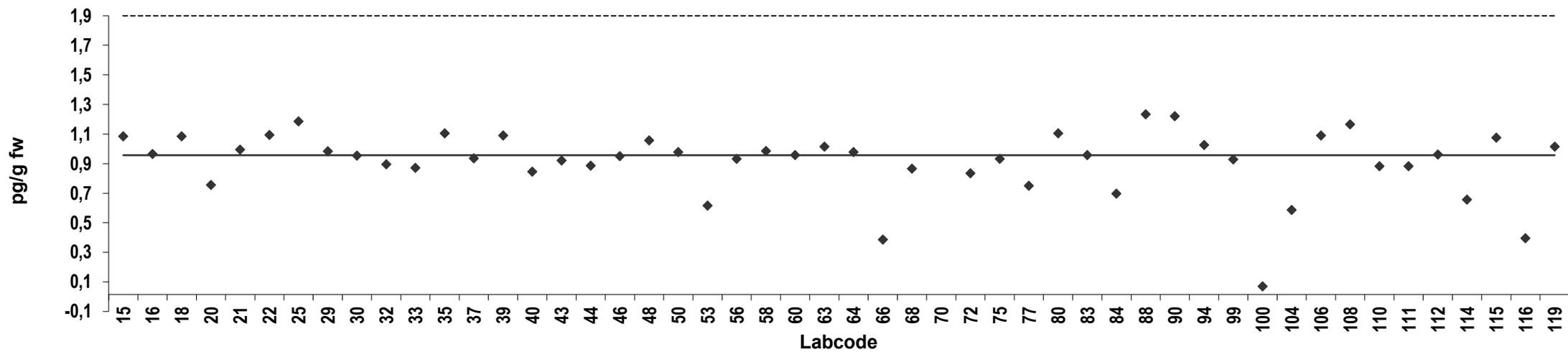


**Mackerel**  
Congener: 2,3,7,8 TCDF

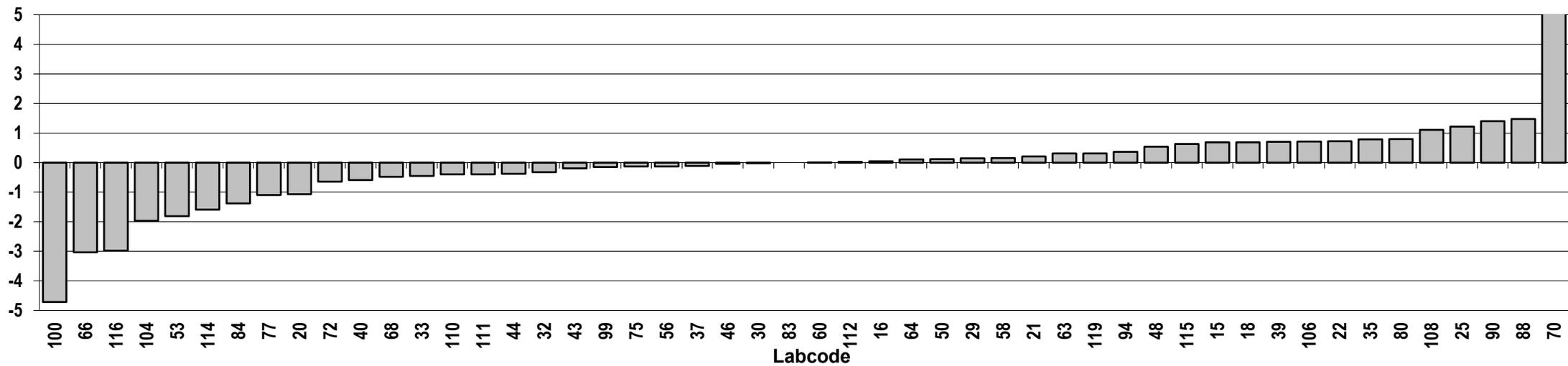
Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	1,1	0,68		112	0,95	0,024	
16	0,95	0,041		114	0,64	-1,6	
18	1,1	0,68		115	1,1	0,63	
20	0,74	-1,1		116	0,38	-3,0	
21	0,98	0,20		119	1,0	0,31	
22	1,1	0,72					
25	1,2	1,2					
29	0,97	0,15					
30	0,94	-0,018					
32	0,88	-0,33					
33	0,86	-0,45					
35	1,1	0,78					
37	0,92	-0,11					
39	1,1	0,70					
40	0,83	-0,59					
43	0,90	-0,19					
44	0,87	-0,38					
46	0,93	-0,038					
48	1,0	0,54					
50	0,96	0,11					
53	0,60	-1,8					
56	0,92	-0,13					
58	0,97	0,15					
60	0,94	0,0079					
63	1,0	0,31					
64	0,96	0,11					
66	0,37	-3,0					
68	0,85	-0,48					
70	3,2	12	Outlier				
72	0,82	-0,65					
75	0,92	-0,14					
77	0,74	-1,1					
80	1,1	0,79					
83	0,94	0,00000					
84	0,68	-1,4					
88	1,2	1,5					
90	1,2	1,4					
94	1,0	0,36					
99	0,91	-0,15					
100	0,054	-4,7					
104	0,57	-2,0					
106	1,1	0,71					
108	1,2	1,1					
110	0,87	-0,40					
111	0,87	-0,40					

Consensus statistics	
Consensus median, pg/g	0,94
Median all values pg/g	0,94
Consensus mean, pg/g	0,90
Standard deviation, pg/g	0,22
Relative standard deviation, %	24
No. of values reported	50
No. of values removed	1
No. of reported non-detects	0

2,3,7,8 TCDF



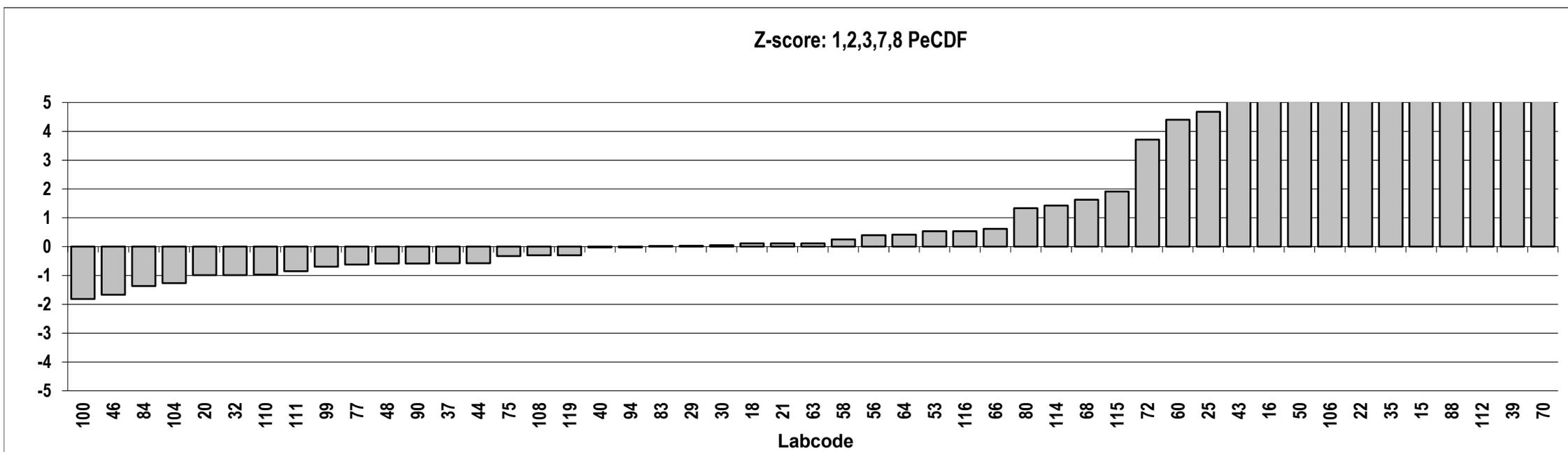
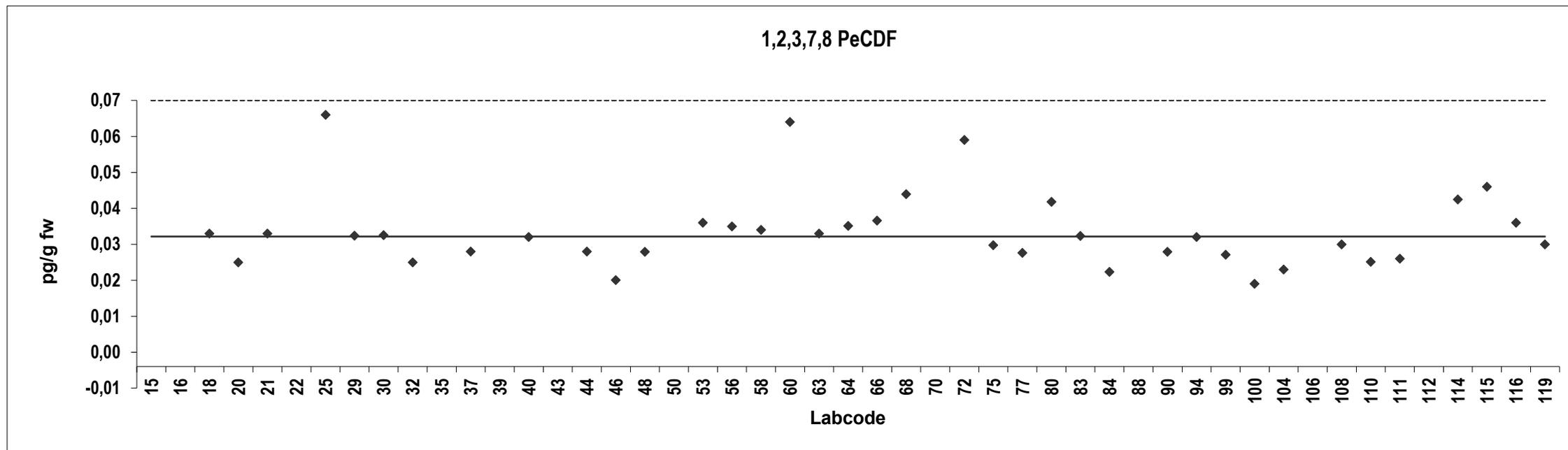
Z-score: 2,3,7,8 TCDF



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,12	11	Outlier	114	0,046	1,4	
16	0,078	5,7	Outlier	115	0,050	1,9	
18	0,037	0,12		116	0,040	0,53	
20	0,029	-0,99		119	0,034	-0,30	
21	0,037	0,12					
22	0,100	8,8	Outlier				
25	0,070	4,7					
29	0,036	0,034					
30	0,037	0,049					
32	0,029	-0,99					
35	0,10	8,8	Outlier,ND				
37	0,032	-0,58					
39	0,17	19	Outlier				
40	0,036	-0,022					
43	0,075	5,4	Outlier,ND				
44	0,032	-0,58					
46	0,024	-1,7					
48	0,032	-0,59					
50	0,085	6,8	Outlier				
53	0,040	0,53	ND				
56	0,039	0,39					
58	0,038	0,25					
60	0,068	4,4					
63	0,037	0,12					
64	0,039	0,41					
66	0,041	0,61	ND				
68	0,048	1,6					
70	0,51	66	Outlier				
72	0,063	3,7	ND				
75	0,034	-0,33					
77	0,032	-0,62					
80	0,046	1,3					
83	0,036	0,022					
84	0,026	-1,4					
88	0,14	14	Outlier,ND				
90	0,032	-0,58					
94	0,036	-0,022					
99	0,031	-0,70					
100	0,023	-1,8	ND				
104	0,027	-1,3					
106	0,095	8,1	Outlier				
108	0,034	-0,30					
110	0,029	-0,97					
111	0,030	-0,85					
112	0,15	16	Outlier				

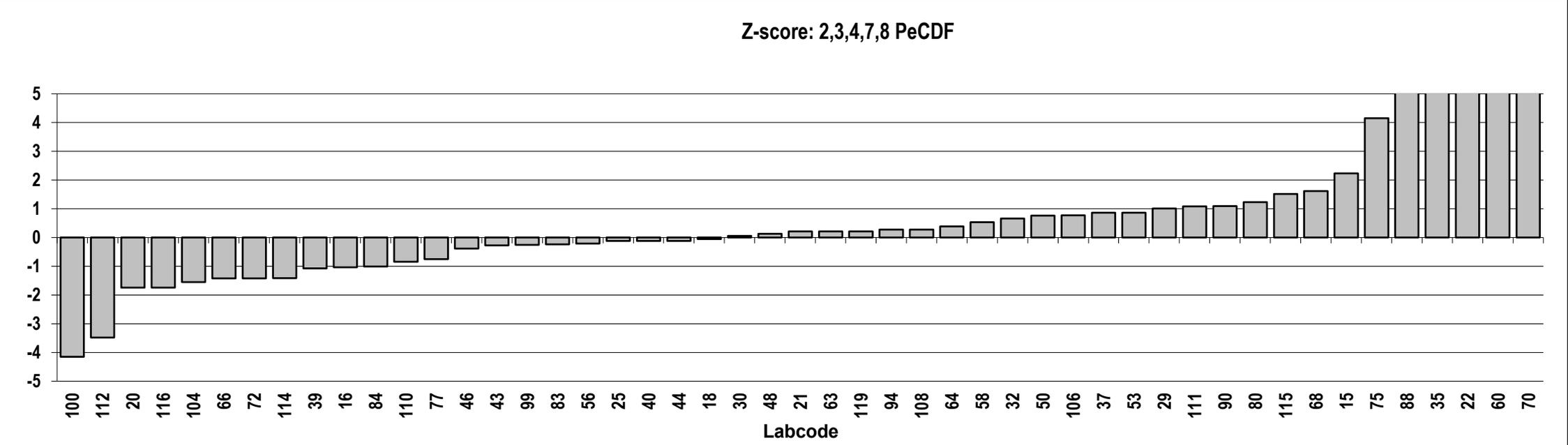
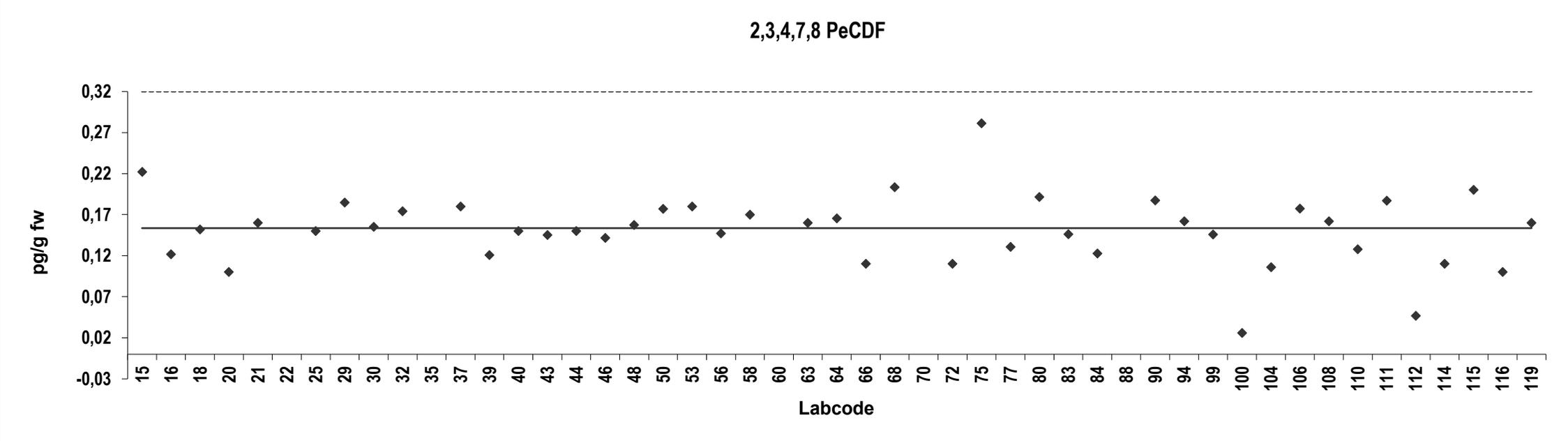
Consensus statistics	
Consensus median, pg/g	0,036
Median all values pg/g	0,037
Consensus mean, pg/g	0,038
Standard deviation, pg/g	0,011
Relative standard deviation, %	28
No. of values reported	49
No. of values removed	11
No. of reported non-detects	7



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,22	2,2		114	0,11	-1,4	
16	0,12	-1,0		115	0,20	1,5	
18	0,15	-0,052		116	0,10	-1,7	
20	0,10	-1,7		119	0,16	0,21	
21	0,16	0,21					
22	0,40	8,1	Outlier				
25	0,15	-0,12					
29	0,18	1,0					
30	0,16	0,052					
32	0,17	0,66					
35	0,35	6,5	Outlier				
37	0,18	0,86					
39	0,12	-1,1					
40	0,15	-0,12					
43	0,15	-0,27					
44	0,15	-0,12					
46	0,14	-0,39					
48	0,16	0,13					
50	0,18	0,76					
53	0,18	0,86					
56	0,15	-0,21					
58	0,17	0,53					
60	0,44	9,3	Outlier				
63	0,16	0,21					
64	0,17	0,38					
66	0,11	-1,4					
68	0,20	1,6					
70	1,2	35	Outlier				
72	0,11	-1,4					
75	0,28	4,2					
77	0,13	-0,75					
80	0,19	1,2					
83	0,15	-0,24					
84	0,12	-1,0					
88	0,34	6,0	Outlier,ND				
90	0,19	1,1					
94	0,16	0,27					
99	0,15	-0,25					
100	0,026	-4,2					
104	0,11	-1,5					
106	0,18	0,78					
108	0,16	0,27					
110	0,13	-0,84					
111	0,19	1,1					
112	0,047	-3,5					

Consensus statistics	
Consensus median, pg/g	0,15
Median all values pg/g	0,16
Consensus mean, pg/g	0,15
Standard deviation, pg/g	0,043
Relative standard deviation, %	28
No. of values reported	49
No. of values removed	5
No. of reported non-detects	1

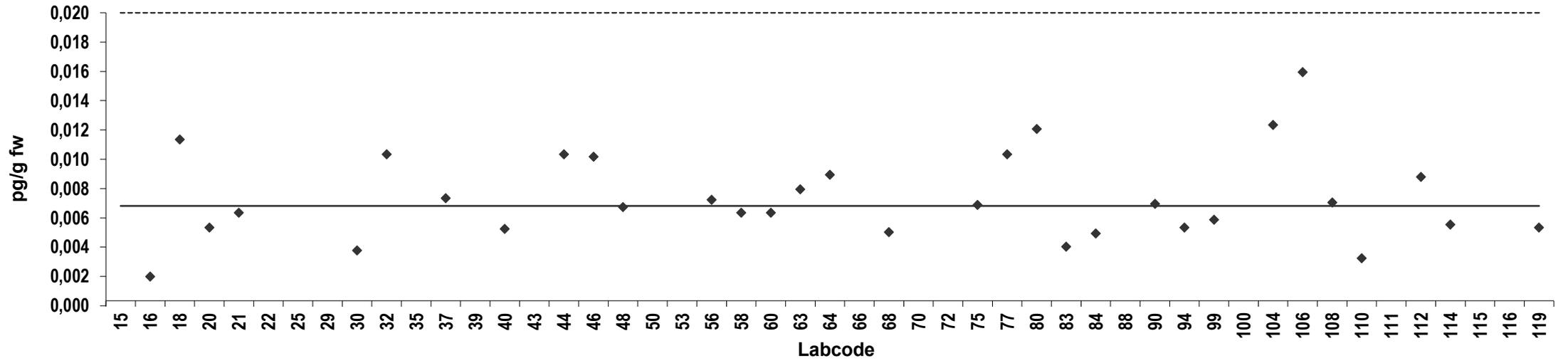


**Mackerel**  
Congener: 1,2,3,4,7,8 HxCDF

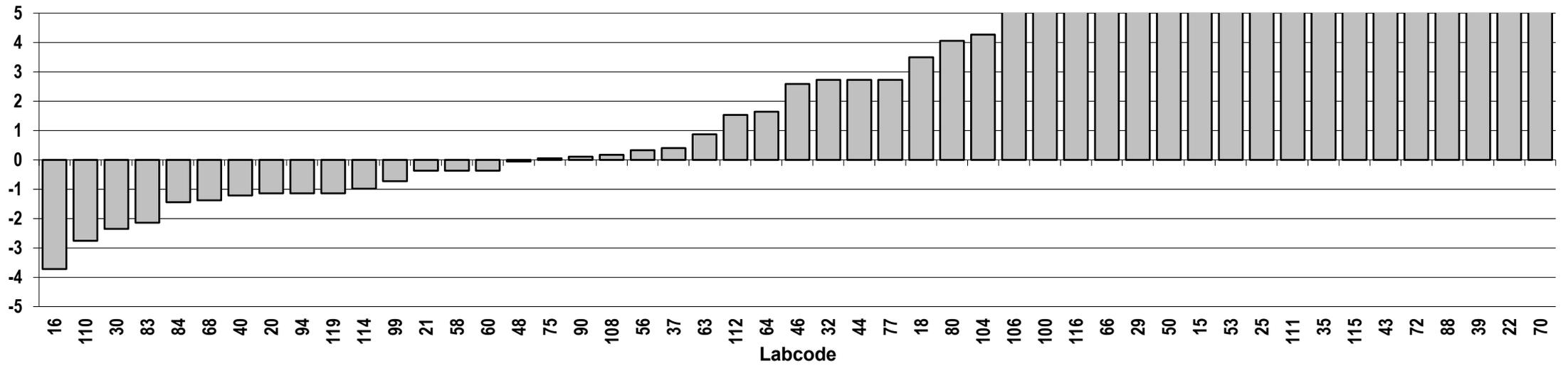
Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,039	25	Outlier,ND	114	0,0052	-0,98	
16	0,0017	-3,7	ND	115	0,091	65	Outlier,ND
18	0,011	3,5	ND	116	0,020	10	Outlier
20	0,0050	-1,1	ND	119	0,0050	-1,1	ND
21	0,0060	-0,37					
22	0,17	129	Outlier				
25	0,050	34	Outlier,ND				
29	0,028	16	Outlier,ND				
30	0,0034	-2,3					
32	0,010	2,7	ND				
35	0,080	57	Outlier,ND				
37	0,0070	0,41					
39	0,15	114	Outlier				
40	0,0049	-1,2	ND				
43	0,099	71	Outlier,ND				
44	0,010	2,7	ND				
46	0,0098	2,6					
48	0,0064	-0,057	ND				
50	0,034	21	Outlier,ND				
53	0,040	26	Outlier,ND				
56	0,0069	0,33					
58	0,0060	-0,37					
60	0,0060	-0,37					
63	0,0076	0,87					
64	0,0086	1,6					
66	0,020	11	Outlier,ND				
68	0,0047	-1,4	ND				
70	2,9	2249	Outlier				
72	0,13	95	Outlier,ND				
75	0,0065	0,057					
77	0,010	2,7	ND				
80	0,012	4,1					
83	0,0037	-2,1					
84	0,0046	-1,4					
88	0,15	113	Outlier,ND				
90	0,0066	0,11					
94	0,0050	-1,1	ND				
99	0,0055	-0,72	ND				
100	0,020	10	Outlier				
104	0,012	4,3	ND				
106	0,016	7,0					
108	0,0067	0,17					
110	0,0029	-2,8	ND				
111	0,050	34	Outlier,ND				
112	0,0085	1,5					

Consensus statistics	
Consensus median, pg/g	0,0065
Median all values pg/g	0,010
Consensus mean, pg/g	0,0070
Standard deviation, pg/g	0,0030
Relative standard deviation, %	43
No. of values reported	49
No. of values removed	17
No. of reported non-detects	26

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



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

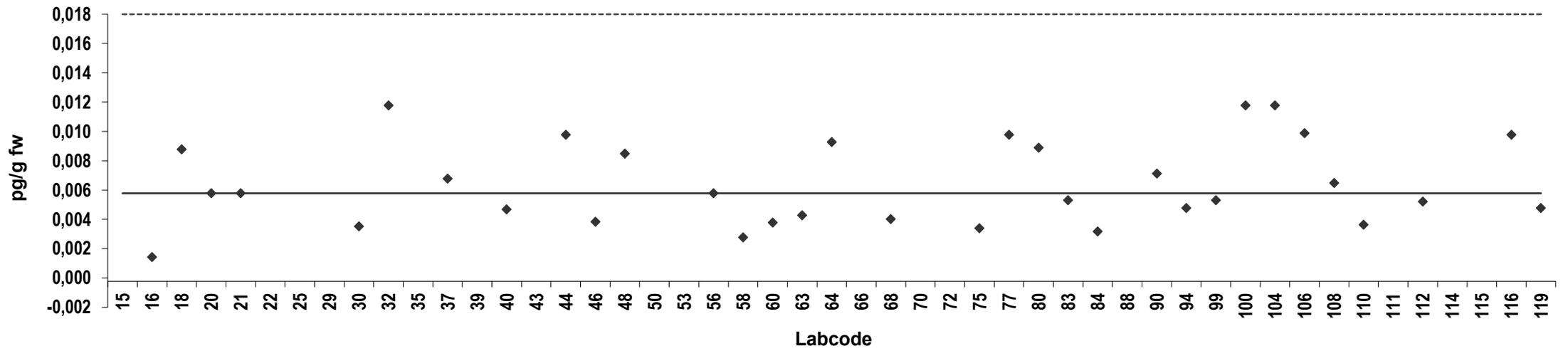


**Mackerel**  
Congener: 1,2,3,6,7,8 HxCDF

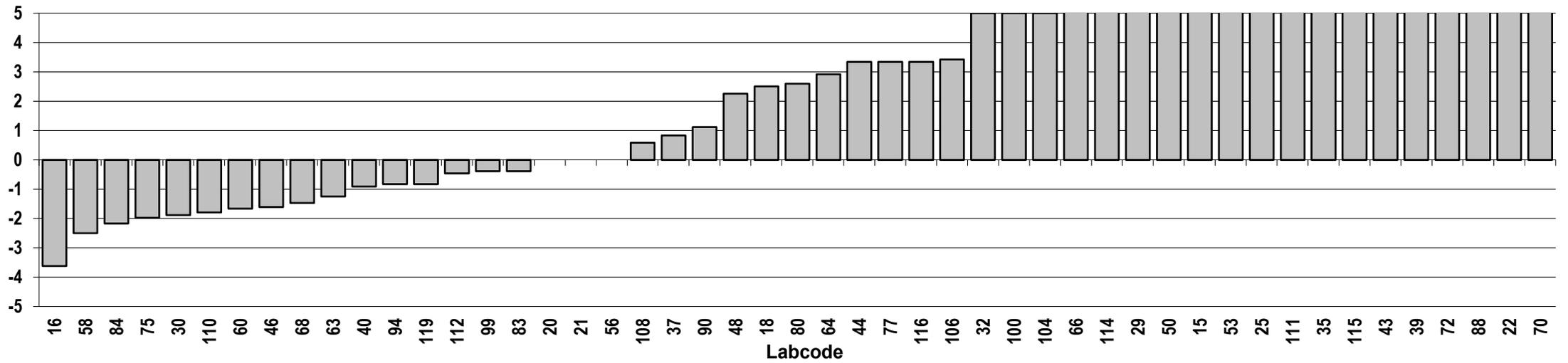
Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,038	26	Outlier,ND	114	0,026	17	Outlier
16	0,0017	-3,6	ND	115	0,091	71	Outlier,ND
18	0,0090	2,5	ND	116	0,010	3,3	
20	0,0060	0,00000		119	0,0050	-0,83	ND
21	0,0060	0,00000	ND				
22	0,16	129	Outlier				
25	0,050	37	Outlier,ND				
29	0,028	18	Outlier,ND				
30	0,0037	-1,9					
32	0,012	5,0					
35	0,080	62	Outlier,ND				
37	0,0070	0,83					
39	0,11	84	Outlier				
40	0,0049	-0,92					
43	0,099	78	Outlier,ND				
44	0,010	3,3	ND				
46	0,0041	-1,6					
48	0,0087	2,3					
50	0,031	21	Outlier,ND				
53	0,040	28	Outlier,ND				
56	0,0060	0,00000					
58	0,0030	-2,5					
60	0,0040	-1,7					
63	0,0045	-1,3					
64	0,0095	2,9					
66	0,019	11	Outlier,ND				
68	0,0042	-1,5	ND				
70	1,0	866	Outlier				
72	0,13	103	Outlier,ND				
75	0,0036	-2,0	ND				
77	0,010	3,3	ND				
80	0,0091	2,6					
83	0,0055	-0,39					
84	0,0034	-2,2					
88	0,14	113	Outlier,ND				
90	0,0073	1,1					
94	0,0050	-0,83	ND				
99	0,0055	-0,39	ND				
100	0,012	5,0					
104	0,012	5,0	ND				
106	0,010	3,4					
108	0,0067	0,58					
110	0,0039	-1,8	ND				
111	0,050	37	Outlier,ND				
112	0,0054	-0,47					

Consensus statistics	
Consensus median, pg/g	0,0060
Median all values pg/g	0,0091
Consensus mean, pg/g	0,0066
Standard deviation, pg/g	0,0029
Relative standard deviation, %	44
No. of values reported	49
No. of values removed	16
No. of reported non-detects	24

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



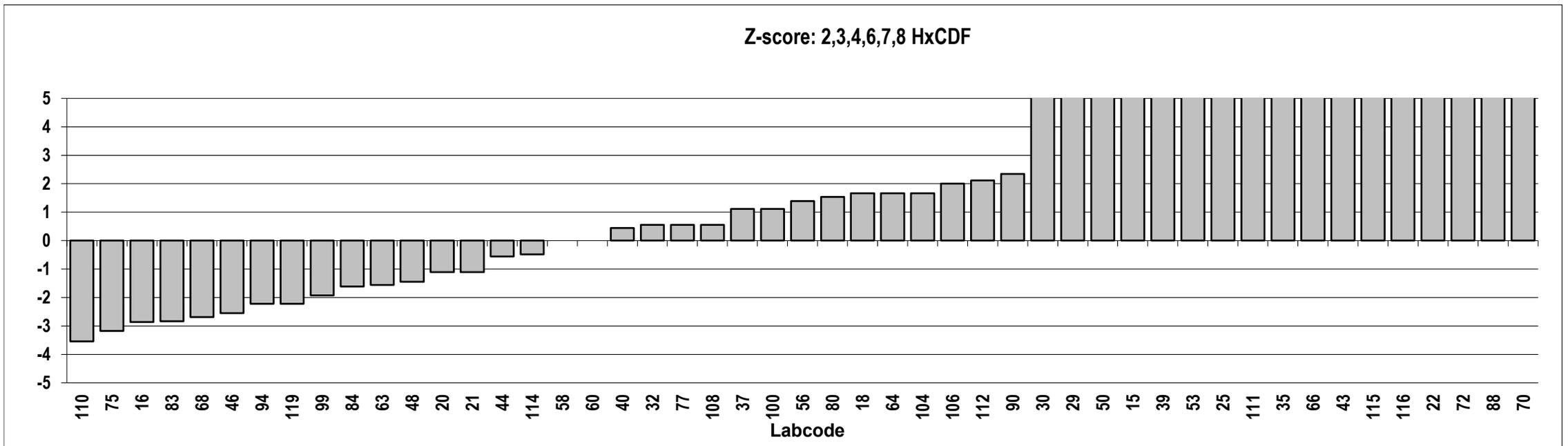
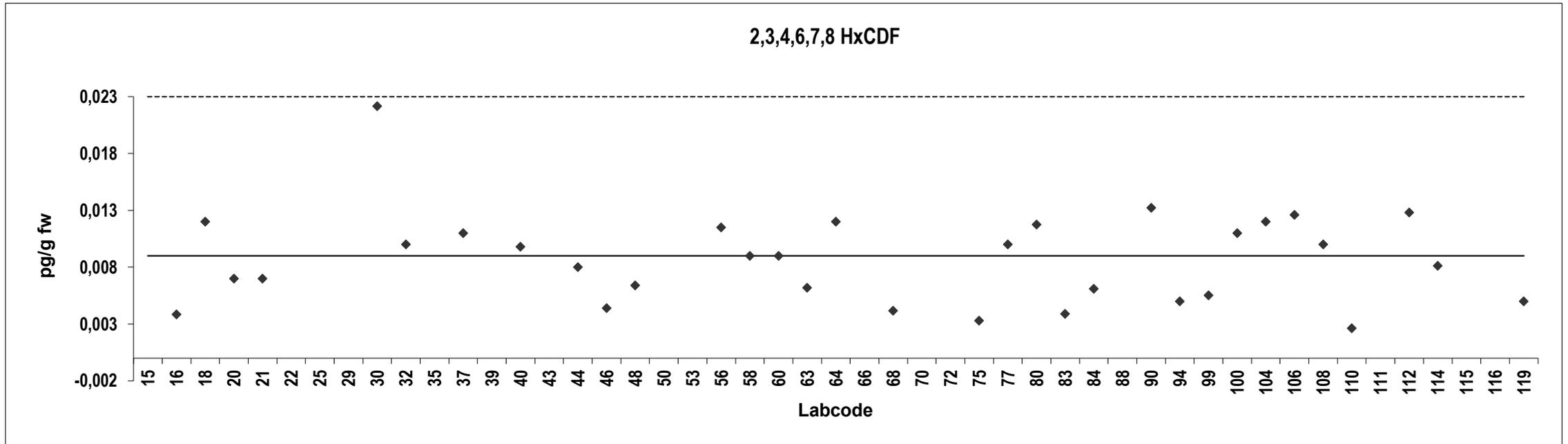
Z-score: 1,2,3,6,7,8 HxCDF



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,036	15	Outlier,ND	114	0,0081	-0,49	
16	0,0039	-2,9		115	0,10	53	Outlier,ND
18	0,012	1,7	ND	116	0,11	56	Outlier
20	0,0070	-1,1		119	0,0050	-2,2	ND
21	0,0070	-1,1					
22	0,12	60	Outlier				
25	0,050	23	Outlier,ND				
29	0,028	10	Outlier,ND				
30	0,022	7,3					
32	0,010	0,56					
35	0,080	39	Outlier,ND				
37	0,011	1,1					
39	0,039	17	Outlier				
40	0,0098	0,44					
43	0,099	50	Outlier,ND				
44	0,0080	-0,56	ND				
46	0,0044	-2,6					
48	0,0064	-1,4					
50	0,029	11	Outlier				
53	0,040	17	Outlier,ND				
56	0,012	1,4					
58	0,0090	0,00000					
60	0,0090	0,00000					
63	0,0062	-1,6					
64	0,012	1,7					
66	0,095	48	Outlier				
68	0,0042	-2,7	ND				
70	0,93	513	Outlier				
72	0,13	67	Outlier,ND				
75	0,0033	-3,2	ND				
77	0,010	0,56	ND				
80	0,012	1,5					
83	0,0039	-2,8					
84	0,0061	-1,6					
88	0,15	81	Outlier,ND				
90	0,013	2,3					
94	0,0050	-2,2	ND				
99	0,0055	-1,9	ND				
100	0,011	1,1					
104	0,012	1,7	ND				
106	0,013	2,0					
108	0,010	0,56					
110	0,0026	-3,5	ND				
111	0,050	23	Outlier,ND				
112	0,013	2,1					

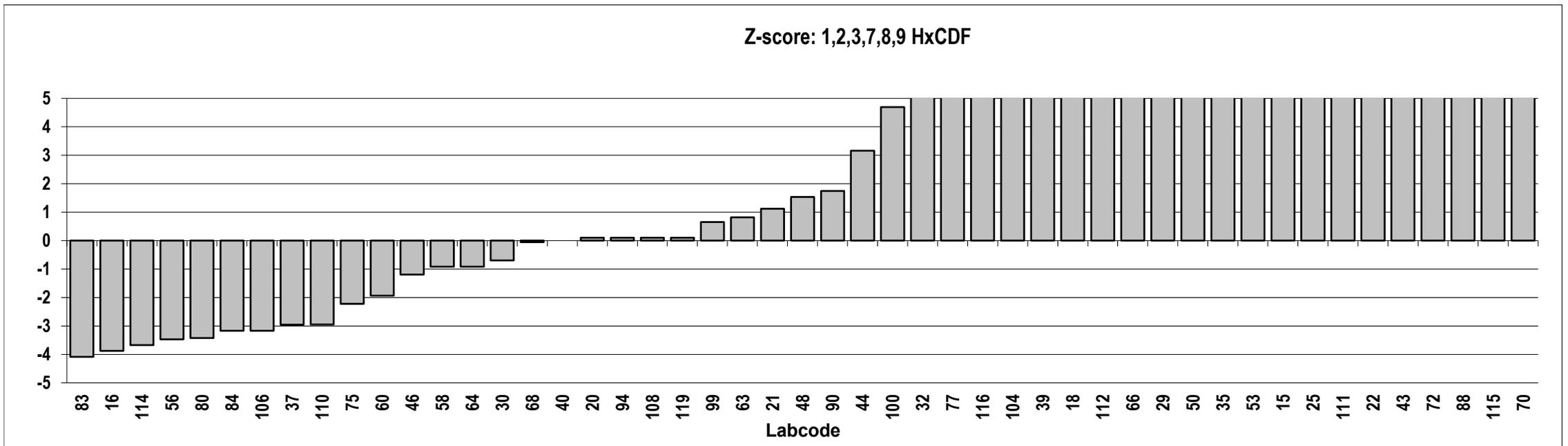
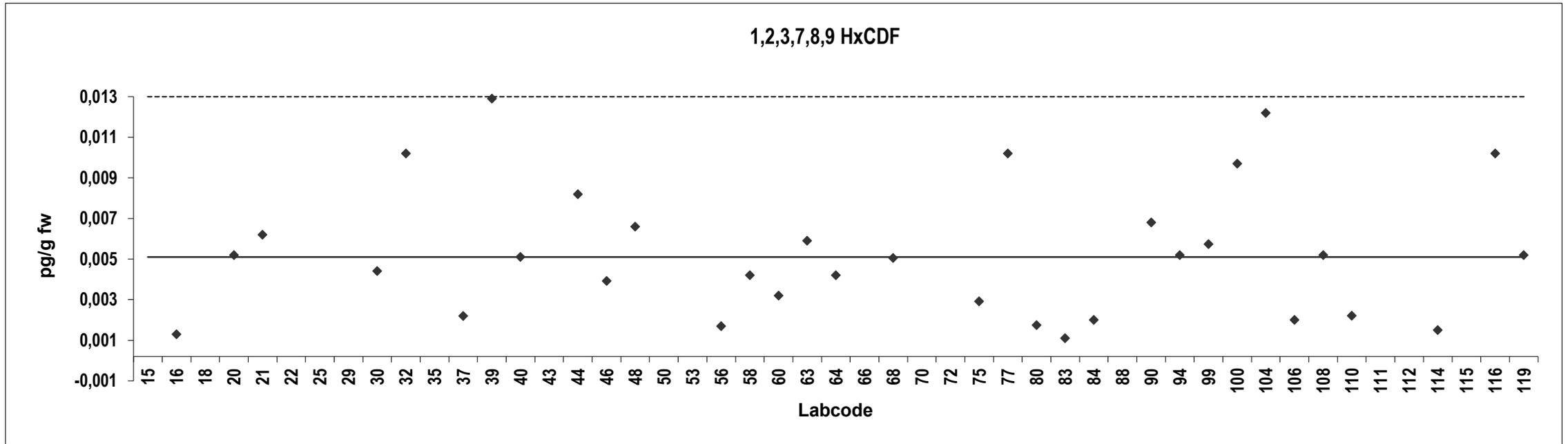
Consensus statistics	
Consensus median, pg/g	0,0090
Median all values pg/g	0,012
Consensus mean, pg/g	0,0087
Standard deviation, pg/g	0,0040
Relative standard deviation, %	46
No. of values reported	49
No. of values removed	16
No. of reported non-detects	20



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,040	36	Outlier,ND	114	0,0013	-3,7	ND
16	0,0011	-3,9	ND	115	0,18	181	Outlier,ND
18	0,014	9,3	Outlier,ND	116	0,010	5,2	
20	0,0050	0,10	ND	119	0,0050	0,10	ND
21	0,0060	1,1	ND				
22	0,088	85	Outlier				
25	0,050	46	Outlier,ND				
29	0,028	23	Outlier,ND				
30	0,0042	-0,70					
32	0,010	5,2	ND				
35	0,030	26	Outlier,ND				
37	0,0020	-3,0	ND				
39	0,013	8,0					
40	0,0049	0,00000	ND				
43	0,099	96	Outlier,ND				
44	0,0080	3,2	ND				
46	0,0037	-1,2					
48	0,0064	1,5	ND				
50	0,029	25	Outlier,ND				
53	0,040	36	Outlier,ND				
56	0,0015	-3,5					
58	0,0040	-0,92	ND				
60	0,0030	-1,9	ND				
63	0,0057	0,82	ND				
64	0,0040	-0,92					
66	0,023	19	Outlier,ND				
68	0,0049	-0,051	ND				
70	0,27	272	Outlier				
72	0,13	128	Outlier,ND				
75	0,0027	-2,2	ND				
77	0,010	5,2	ND				
80	0,0015	-3,4					
83	0,00090	-4,1					
84	0,0018	-3,2	ND				
88	0,16	156	Outlier,ND				
90	0,0066	1,7					
94	0,0050	0,10	ND				
99	0,0055	0,65	ND				
100	0,0095	4,7	ND				
104	0,012	7,2	ND				
106	0,0018	-3,2					
108	0,0050	0,10	ND				
110	0,0020	-2,9	ND				
111	0,050	46	Outlier,ND				
112	0,016	11	Outlier				

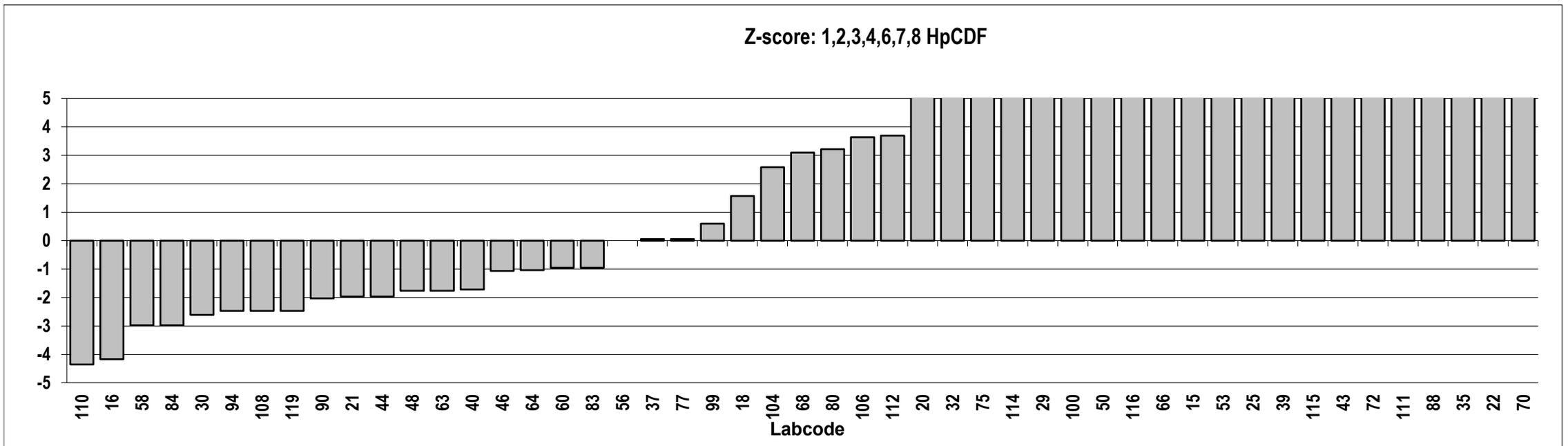
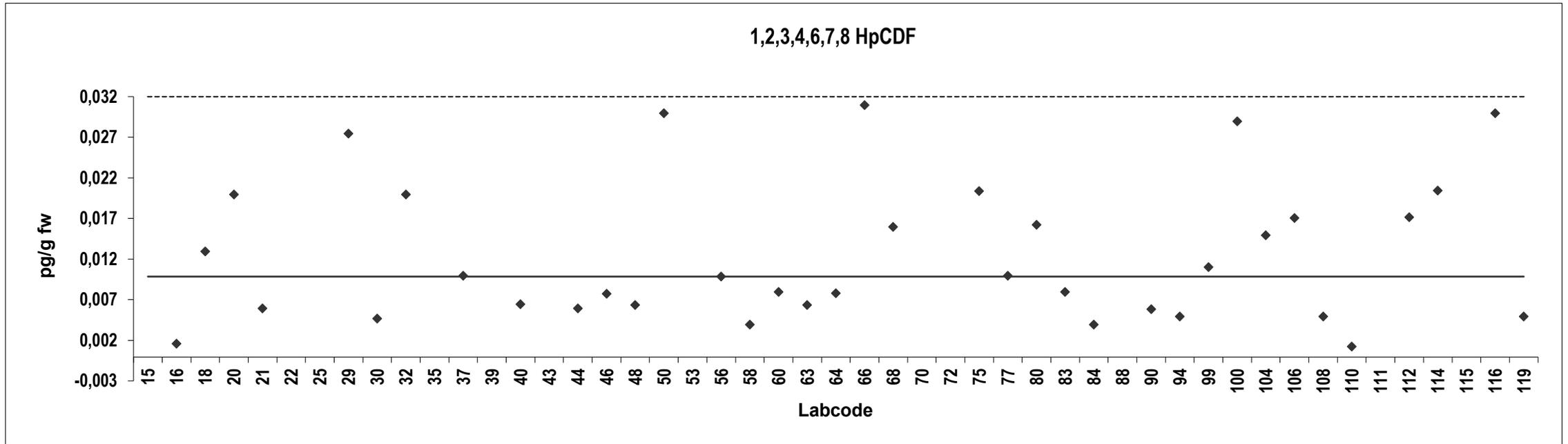
Consensus statistics	
Consensus median, pg/g	0,0049
Median all values pg/g	0,0064
Consensus mean, pg/g	0,0051
Standard deviation, pg/g	0,0033
Relative standard deviation, %	64
No. of values reported	49
No. of values removed	16
No. of reported non-detects	36



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,038	14	Outlier,ND	114	0,020	5,3	
16	0,0017	-4,2	ND	115	0,085	38	Outlier,ND
18	0,013	1,6	ND	116	0,030	10	
20	0,020	5,1		119	0,0050	-2,5	ND
21	0,0060	-2,0	ND				
22	0,42	208	Outlier				
25	0,050	20	Outlier,ND				
29	0,028	8,9	ND				
30	0,0047	-2,6					
32	0,020	5,1	ND				
35	0,20	96	Outlier,ND				
37	0,010	0,051					
39	0,083	37	Outlier				
40	0,0065	-1,7					
43	0,099	45	Outlier,ND				
44	0,0060	-2,0	ND				
46	0,0078	-1,1					
48	0,0064	-1,8	ND				
50	0,030	10					
53	0,040	15	Outlier,ND				
56	0,0099	0,00000					
58	0,0040	-3,0					
60	0,0080	-0,96	ND				
63	0,0064	-1,8					
64	0,0079	-1,0					
66	0,031	11					
68	0,016	3,1	ND				
70	16	7826	Outlier				
72	0,13	61	Outlier,ND				
75	0,020	5,3					
77	0,010	0,051	ND				
80	0,016	3,2					
83	0,0080	-0,96					
84	0,0040	-3,0					
88	0,19	89	Outlier				
90	0,0059	-2,0					
94	0,0050	-2,5	ND				
99	0,011	0,59	ND				
100	0,029	9,6	ND				
104	0,015	2,6					
106	0,017	3,6					
108	0,0050	-2,5	ND				
110	0,0013	-4,3	ND				
111	0,15	71	Outlier,ND				
112	0,017	3,7					

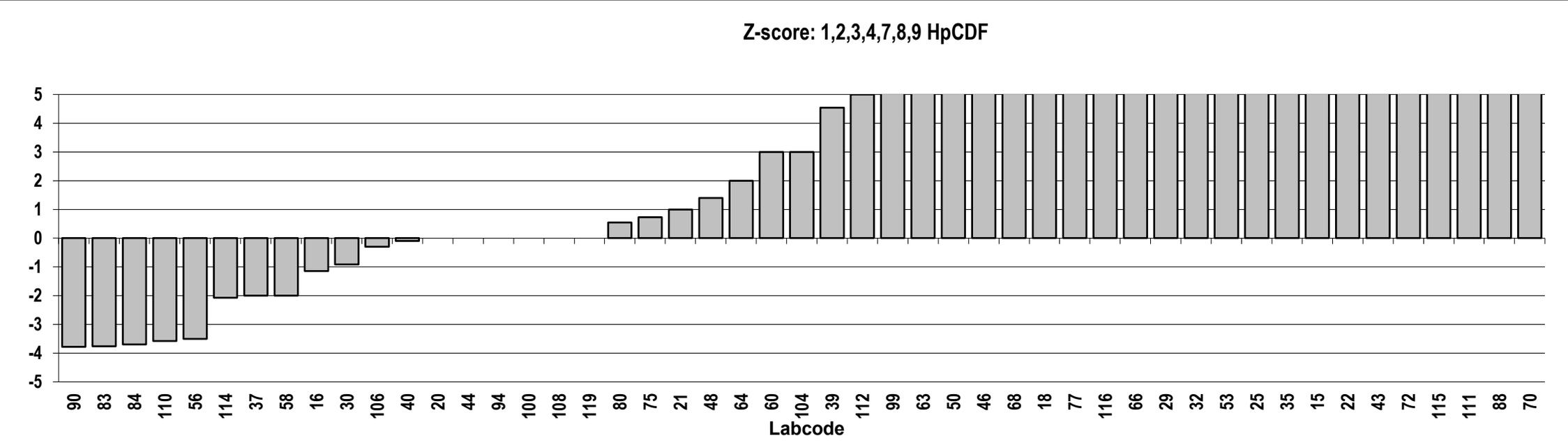
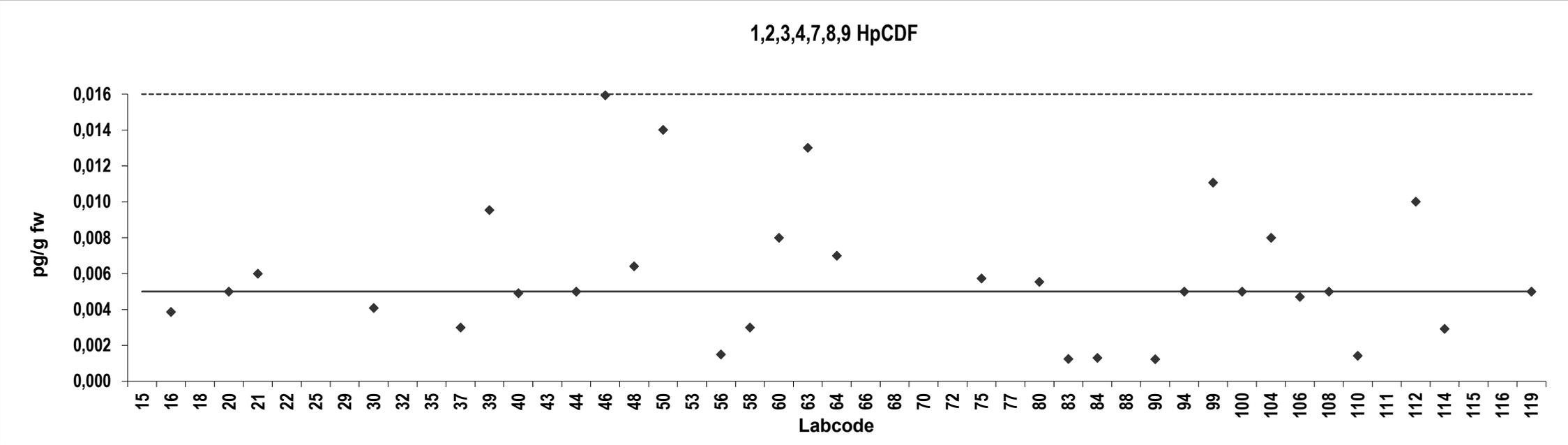
Consensus statistics	
Consensus median, pg/g	0,010
Median all values pg/g	0,016
Consensus mean, pg/g	0,013
Standard deviation, pg/g	0,0087
Relative standard deviation, %	70
No. of values reported	49
No. of values removed	12
No. of reported non-detects	24



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,064	59	Outlier	114	0,0029	-2,1	ND
16	0,0039	-1,1		115	0,14	131	Outlier,ND
18	0,018	13	Outlier,ND	116	0,020	15	Outlier
20	0,0050	0,00000	ND	119	0,0050	0,00000	ND
21	0,0060	1,0	ND				
22	0,069	64	Outlier				
25	0,050	45	Outlier,ND				
29	0,028	23	Outlier,ND				
30	0,0041	-0,91					
32	0,030	25	Outlier,ND				
35	0,050	45	Outlier,ND				
37	0,0030	-2,0					
39	0,0095	4,5					
40	0,0049	-0,10	ND				
43	0,099	94	Outlier,ND				
44	0,0050	0,00000	ND				
46	0,016	11					
48	0,0064	1,4	ND				
50	0,014	9	ND				
53	0,040	35	Outlier,ND				
56	0,0015	-3,5					
58	0,0030	-2,0	ND				
60	0,0080	3,0	ND				
63	0,013	8,0					
64	0,0070	2,0					
66	0,025	20	Outlier				
68	0,017	12	Outlier,ND				
70	0,87	861	Outlier				
72	0,13	125	Outlier,ND				
75	0,0057	0,73	ND				
77	0,020	15	Outlier,ND				
80	0,0055	0,54					
83	0,0012	-3,8					
84	0,0013	-3,7	ND				
88	0,16	154	Outlier,ND				
90	0,0012	-3,8	ND				
94	0,0050	0,00000	ND				
99	0,011	6,1	ND				
100	0,0050	0,00000					
104	0,0080	3,0	ND				
106	0,0047	-0,30					
108	0,0050	0,00000	ND				
110	0,0014	-3,6	ND				
111	0,15	145	Outlier,ND				
112	0,010	5,0	ND				

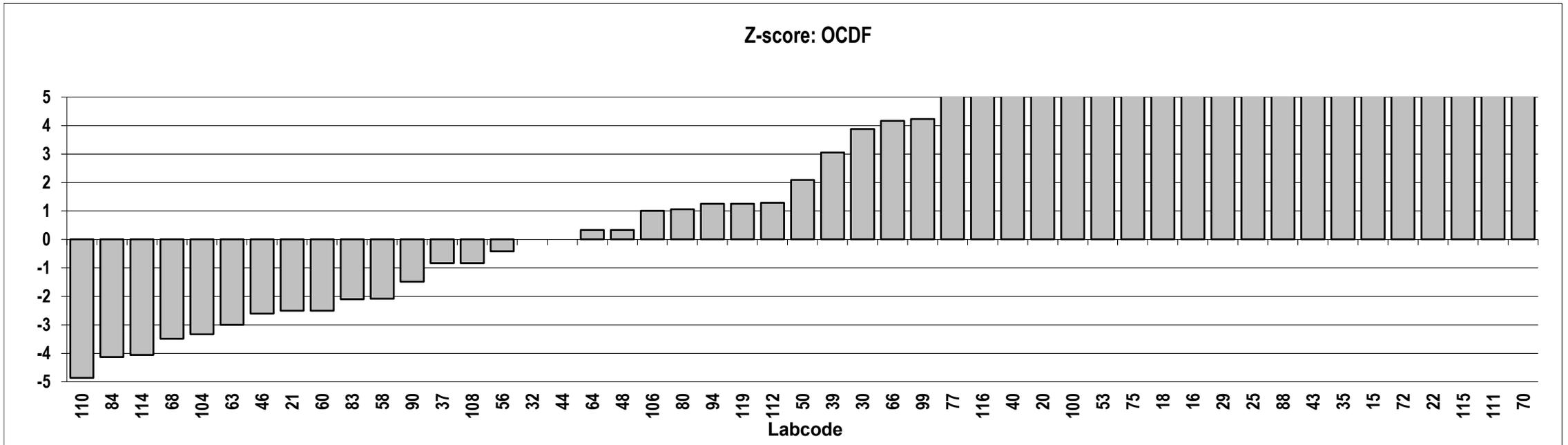
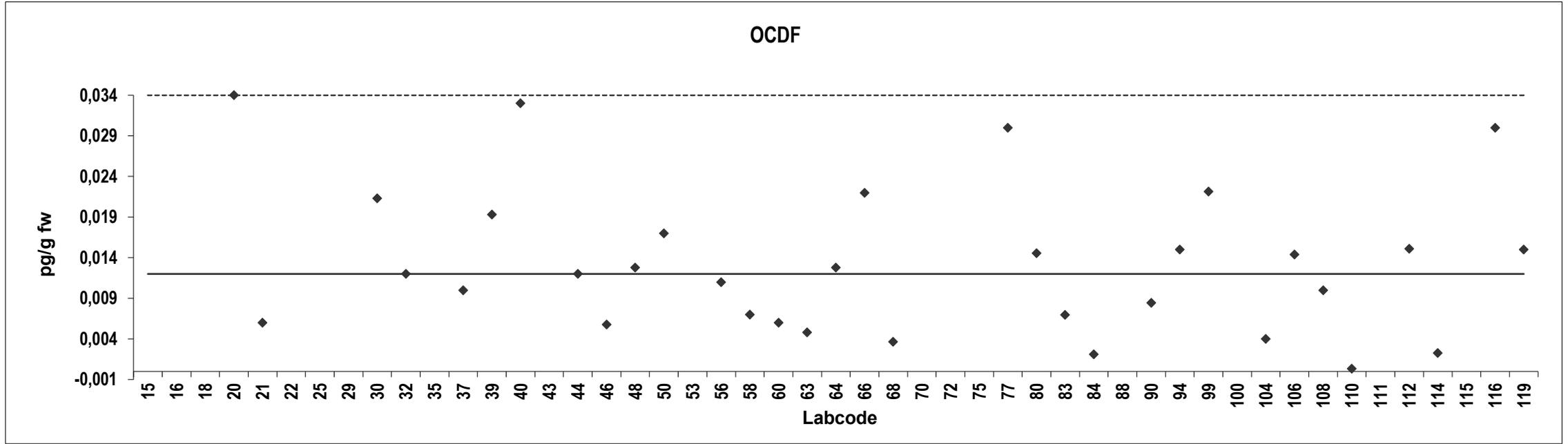
Consensus statistics	
Consensus median, pg/g	0,0050
Median all values pg/g	0,0080
Consensus mean, pg/g	0,0059
Standard deviation, pg/g	0,0038
Relative standard deviation, %	64
No. of values reported	49
No. of values removed	18
No. of reported non-detects	32



**Mackerel**  
**Congener: OCDF**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,24	93	Outlier	114	0,0023	-4,1	
16	0,064	22	Outlier	115	1,0	427	Outlier,ND
18	0,051	16	Outlier,ND	116	0,030	7,5	
20	0,034	9,2		119	0,015	1,3	ND
21	0,0060	-2,5	ND				
22	0,58	235	Outlier				
25	0,10	37	Outlier,ND				
29	0,069	24	Outlier,ND				
30	0,021	3,9					
32	0,012	0,00000					
35	0,20	78	Outlier,ND				
37	0,010	-0,83					
39	0,019	3,0					
40	0,033	8,8	ND				
43	0,20	78	Outlier,ND				
44	0,012	0,00000					
46	0,0058	-2,6					
48	0,013	0,33	ND				
50	0,017	2,1					
53	0,040	12	Outlier,ND				
56	0,011	-0,42					
58	0,0070	-2,1	ND				
60	0,0060	-2,5	ND				
63	0,0048	-3,0					
64	0,013	0,33					
66	0,022	4,2					
68	0,0036	-3,5	ND				
70	28	11610	Outlier				
72	0,31	124	Outlier,ND				
75	0,046	14	Outlier				
77	0,030	7,5	ND				
80	0,015	1,1					
83	0,0070	-2,1					
84	0,0021	-4,1	ND				
88	0,15	58	Outlier,ND				
90	0,0084	-1,5					
94	0,015	1,3	ND				
99	0,022	4,2	ND				
100	0,037	10	Outlier,ND				
104	0,0040	-3,3	ND				
106	0,014	1,0					
108	0,010	-0,83	ND				
110	0,00034	-4,9	ND				
111	2,0	828	Outlier,ND				
112	0,015	1,3					

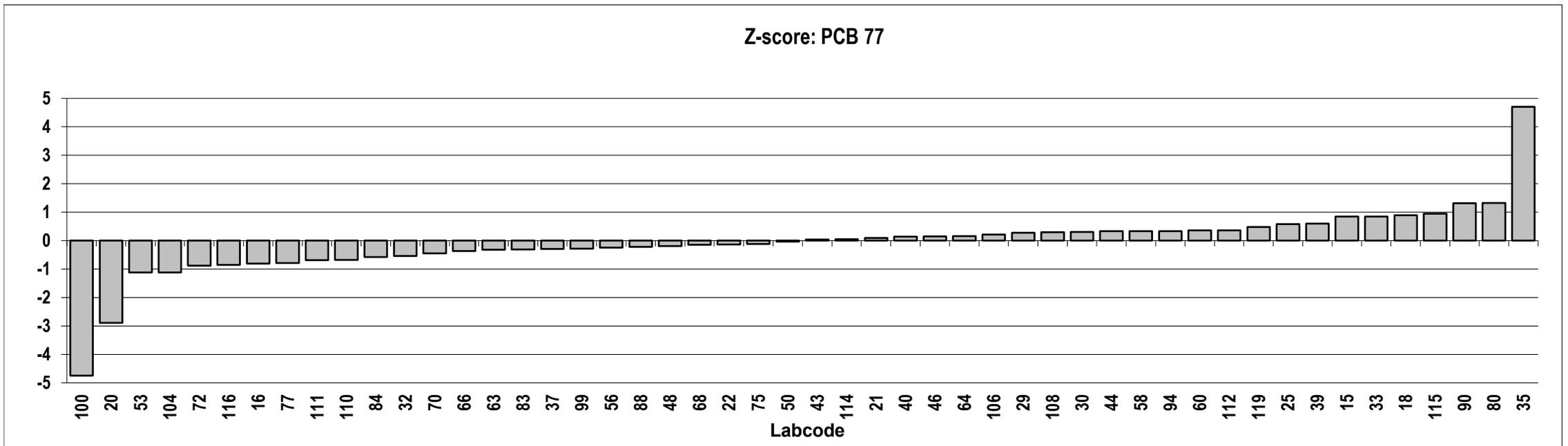
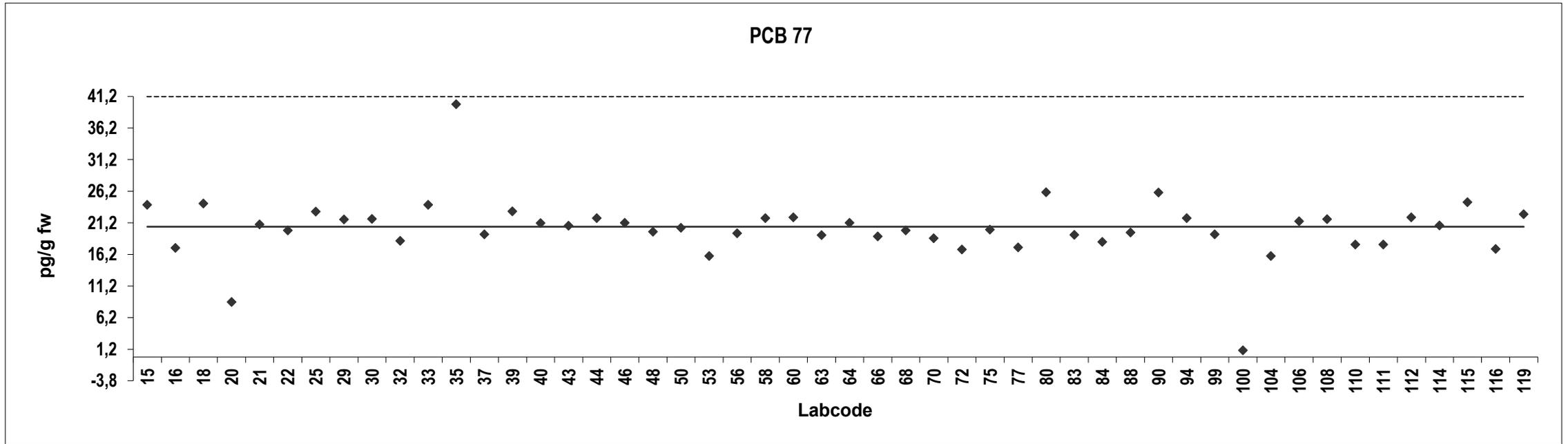
Consensus statistics	
Consensus median, pg/g	0,012
Median all values pg/g	0,017
Consensus mean, pg/g	0,013
Standard deviation, pg/g	0,0090
Relative standard deviation, %	68
No. of values reported	49
No. of values removed	16
No. of reported non-detects	25



**Mackerel**  
**Congener: PCB 77**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	24	0,85		112	22	0,36	
16	17	-0,81		114	21	0,047	
18	24	0,89		115	25	0,94	
20	8,7	-2,9		116	17	-0,85	
21	21	0,094		119	23	0,48	
22	20	-0,14					
25	23	0,58					
29	22	0,28					
30	22	0,30					
32	18	-0,54					
33	24	0,85					
35	40	4,7	ND				
37	19	-0,29					
39	23	0,60					
40	21	0,14					
43	21	0,037					
44	22	0,34					
46	21	0,15					
48	20	-0,19					
50	20	-0,037					
53	16	-1,1					
56	20	-0,25					
58	22	0,34					
60	22	0,36					
63	19	-0,32					
64	21	0,16					
66	19	-0,37					
68	20	-0,14					
70	19	-0,44					
72	17	-0,88					
75	20	-0,11					
77	17	-0,79					
80	26	1,3					
83	19	-0,31					
84	18	-0,58					
88	20	-0,22					
90	26	1,3					
94	22	0,34					
99	19	-0,29					
100	1,1	-4,7	ND				
104	16	-1,1					
106	21	0,21					
108	22	0,29					
110	18	-0,68					
111	18	-0,69					

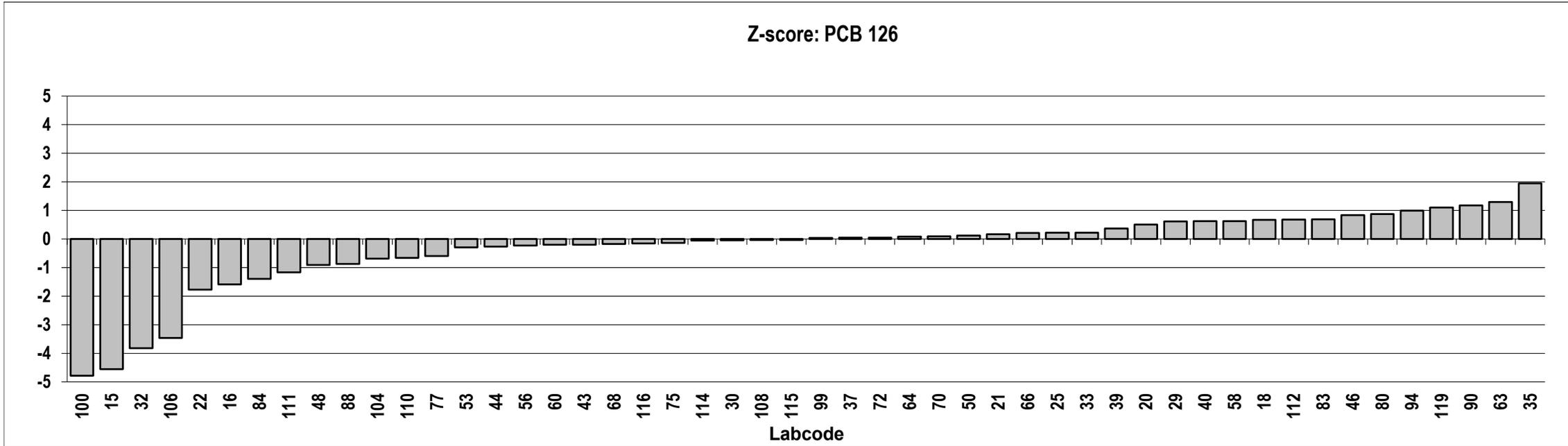
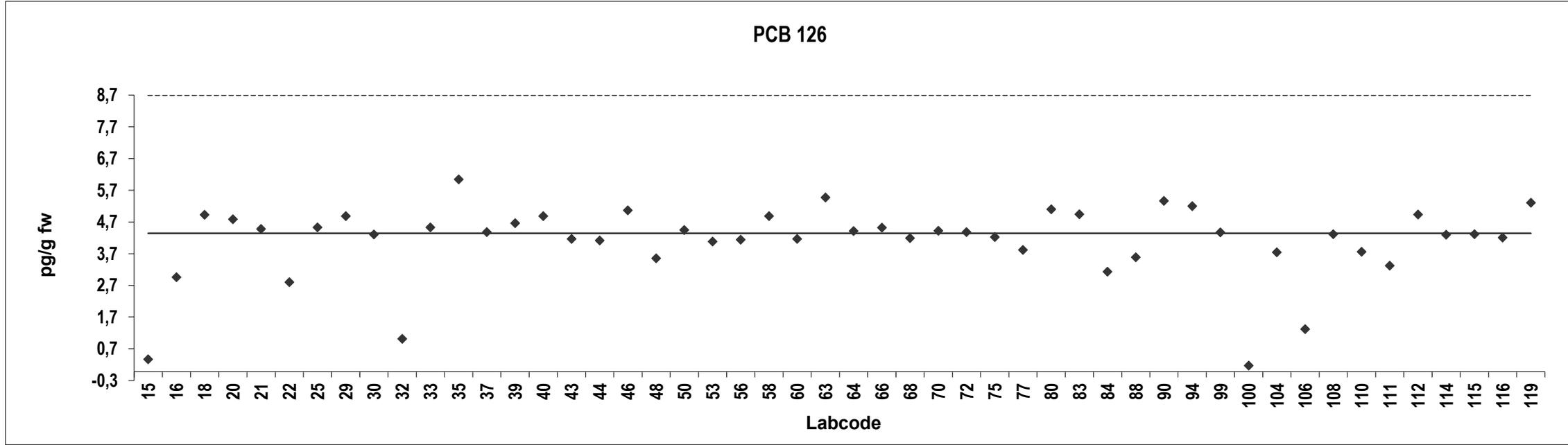
Consensus statistics	
Consensus median, pg/g	21
Median all values pg/g	21
Consensus mean, pg/g	20
Standard deviation, pg/g	4,9
Relative standard deviation, %	24
No. of values reported	50
No. of values removed	0
No. of reported non-detects	2



**Mackerel**  
**Congener: PCB 126**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,39	-4,6	ND	112	5,0	0,68	
16	3,0	-1,6		114	4,3	-0,056	
18	4,9	0,67		115	4,3	-0,034	
20	4,8	0,50		116	4,2	-0,16	
21	4,5	0,16		119	5,3	1,1	
22	2,8	-1,8					
25	4,6	0,22					
29	4,9	0,62					
30	4,3	-0,044					
32	1,0	-3,8					
33	4,6	0,22					
35	6,1	1,9					
37	4,4	0,046					
39	4,7	0,37					
40	4,9	0,62					
43	4,2	-0,21					
44	4,1	-0,26					
46	5,1	0,83					
48	3,6	-0,91					
50	4,5	0,12					
53	4,1	-0,30					
56	4,2	-0,23					
58	4,9	0,62					
60	4,2	-0,21					
63	5,5	1,3					
64	4,4	0,079					
66	4,5	0,21					
68	4,2	-0,18					
70	4,4	0,087					
72	4,4	0,046					
75	4,2	-0,14					
77	3,8	-0,60					
80	5,1	0,87					
83	5,0	0,69					
84	3,1	-1,4					
88	3,6	-0,87					
90	5,4	1,2					
94	5,2	1,0					
99	4,4	0,034					
100	0,19	-4,8					
104	3,8	-0,69					
106	1,3	-3,5					
108	4,3	-0,037					
110	3,8	-0,67					
111	3,3	-1,2					

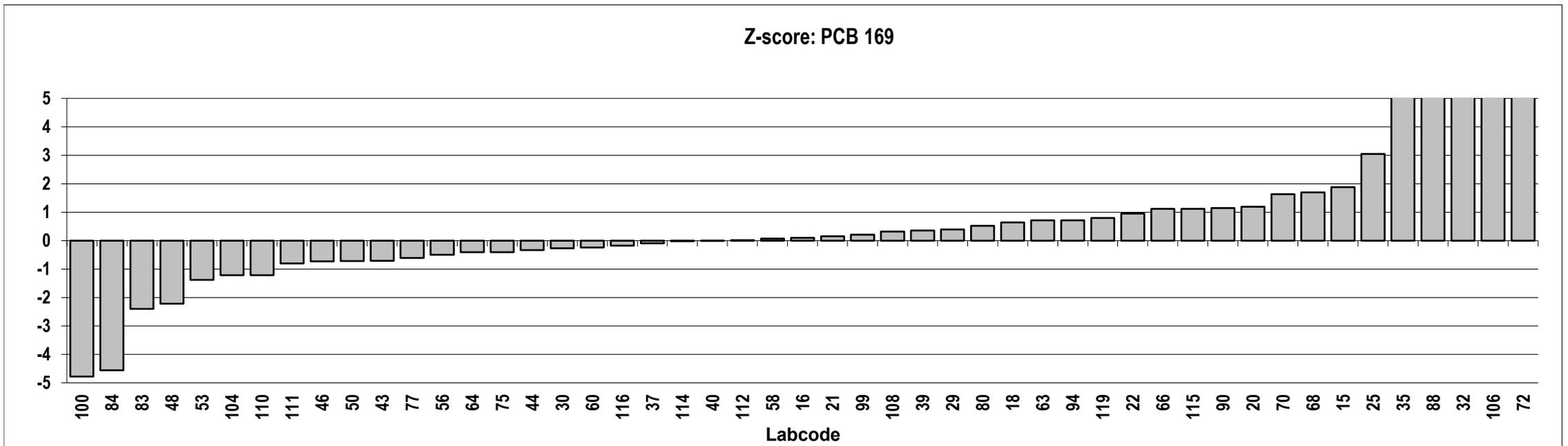
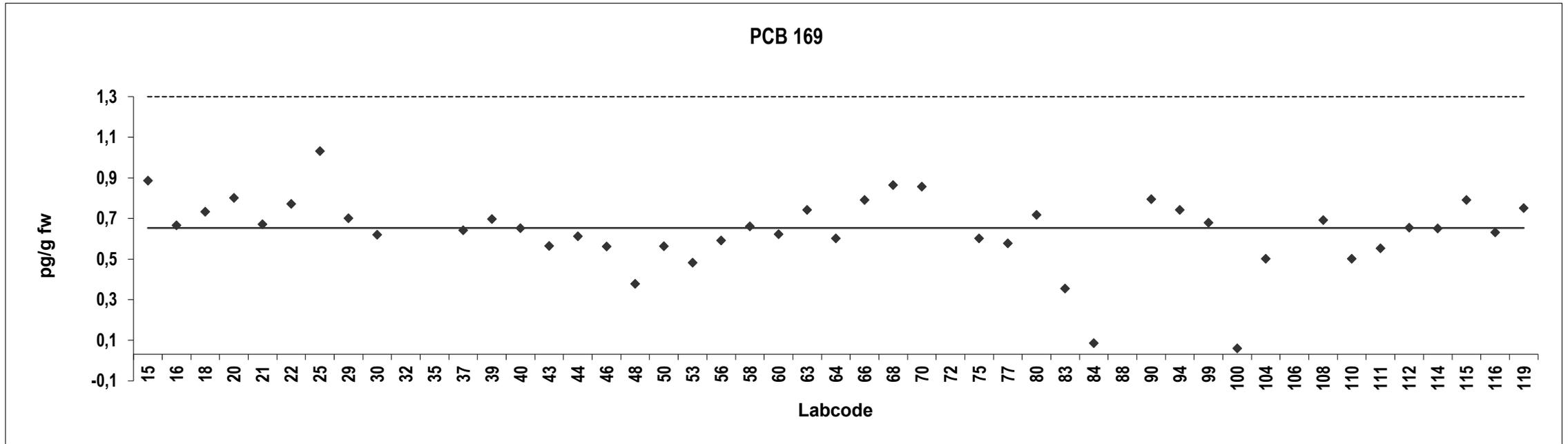
Consensus statistics	
Consensus median, pg/g	4,4
Median all values pg/g	4,4
Consensus mean, pg/g	4,1
Standard deviation, pg/g	1,2
Relative standard deviation, %	29
No. of values reported	50
No. of values removed	0
No. of reported non-detects	1



**Mackerel**  
**Congener: PCB 169**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	0,86	1,9		114	0,62	-0,019	
16	0,63	0,10	ND	115	0,76	1,1	
18	0,70	0,64		116	0,60	-0,17	
20	0,77	1,2		119	0,72	0,79	
21	0,64	0,15					
22	0,74	0,96					
25	1,0	3,0	ND				
29	0,67	0,39					
30	0,59	-0,27					
32	4,0	27	Outlier				
35	2,0	11	Outlier,ND				
37	0,61	-0,093					
39	0,67	0,36					
40	0,62	-0,012					
43	0,53	-0,71					
44	0,58	-0,33					
46	0,53	-0,73					
48	0,35	-2,2					
50	0,53	-0,72					
53	0,45	-1,4					
56	0,56	-0,49					
58	0,63	0,068					
60	0,59	-0,25					
63	0,71	0,71					
64	0,57	-0,41					
66	0,76	1,1					
68	0,83	1,7					
70	0,82	1,6					
72	5,0	35	Outlier,ND				
75	0,57	-0,41					
77	0,55	-0,61					
80	0,69	0,52					
83	0,32	-2,4					
84	0,055	-4,6	ND				
88	2,2	12	Outlier,ND				
90	0,76	1,1					
94	0,71	0,71					
99	0,65	0,21					
100	0,028	-4,8					
104	0,47	-1,2					
106	4,6	32	Outlier				
108	0,66	0,32					
110	0,47	-1,2					
111	0,52	-0,80					
112	0,62	0,012					

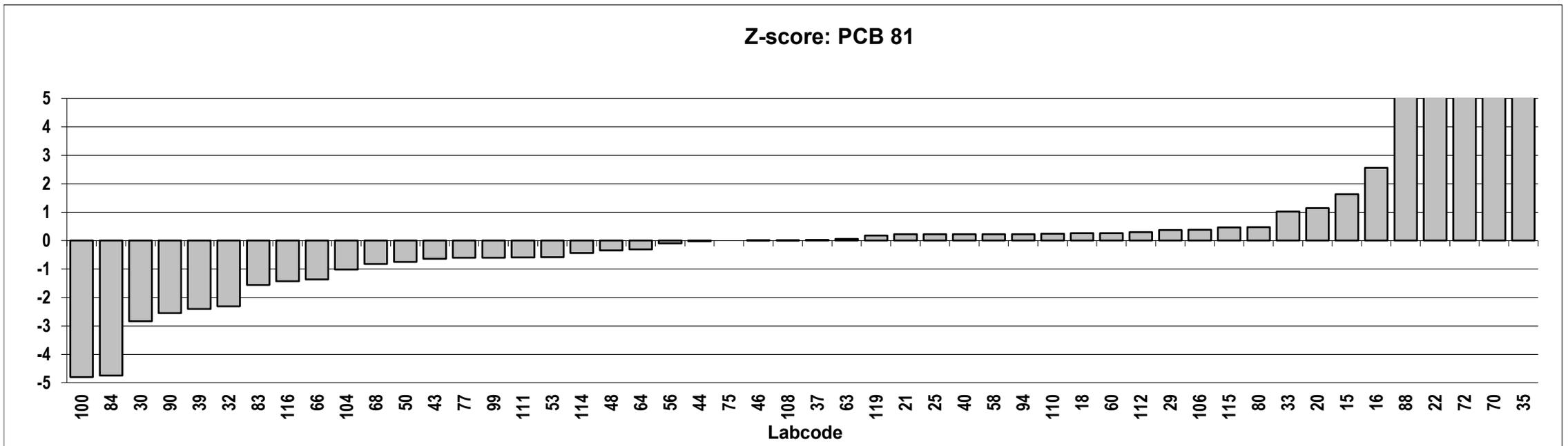
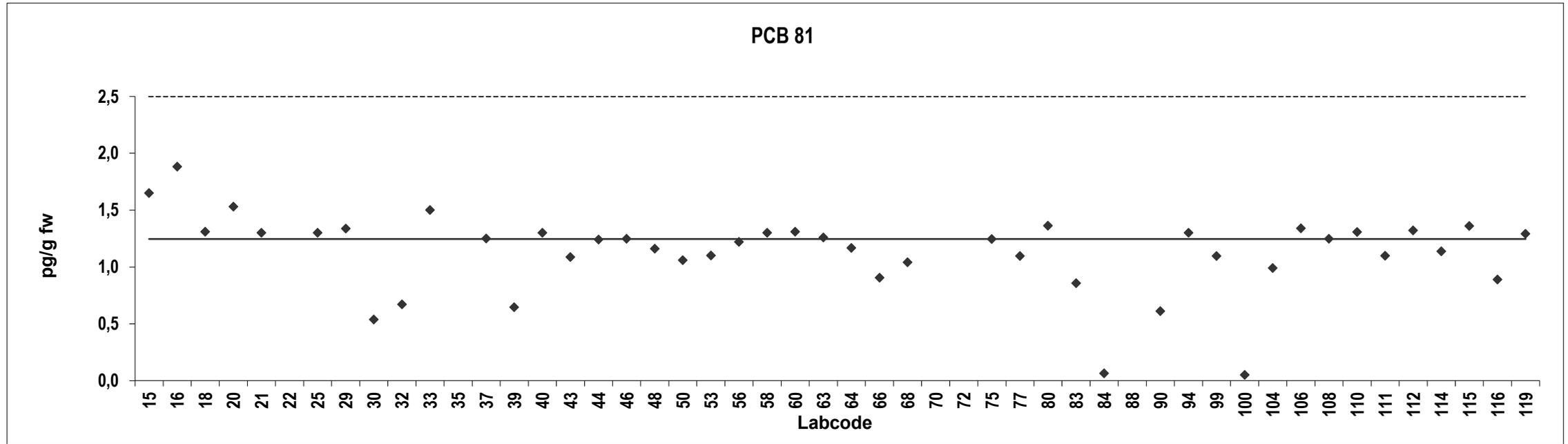
Consensus statistics	
Consensus median, pg/g	0,62
Median all values pg/g	0,63
Consensus mean, pg/g	0,61
Standard deviation, pg/g	0,18
Relative standard deviation, %	29
No. of values reported	49
No. of values removed	5
No. of reported non-detects	6



**Mackerel**  
**Congener: PCB 81**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	1,7	1,6		112	1,3	0,30	
16	1,9	2,6		114	1,1	-0,43	
18	1,3	0,26		115	1,4	0,46	
20	1,5	1,1		116	0,89	-1,4	
21	1,3	0,22		119	1,3	0,18	
22	4,7	14	Outlier				
25	1,3	0,22					
29	1,3	0,37					
30	0,54	-2,8					
32	0,67	-2,3					
33	1,5	1,0					
35	10	35	Outlier,ND				
37	1,3	0,021					
39	0,65	-2,4					
40	1,3	0,22					
43	1,1	-0,64					
44	1,2	-0,019					
46	1,2	0,010					
48	1,2	-0,34					
50	1,1	-0,75					
53	1,1	-0,58					
56	1,2	-0,10					
58	1,3	0,22					
60	1,3	0,26					
63	1,3	0,061					
64	1,2	-0,31					
66	0,91	-1,4					
68	1,0	-0,82					
70	7,0	23	Outlier				
72	5,0	15	Outlier,ND				
75	1,2	0,00000					
77	1,1	-0,60					
80	1,4	0,47					
83	0,86	-1,6					
84	0,064	-4,7	ND				
88	3,3	8,1	Outlier,ND				
90	0,61	-2,5					
94	1,3	0,22					
99	1,1	-0,60					
100	0,051	-4,8					
104	0,99	-1,0					
106	1,3	0,4					
108	1,2	0,013					
110	1,3	0,25					
111	1,1	-0,59					

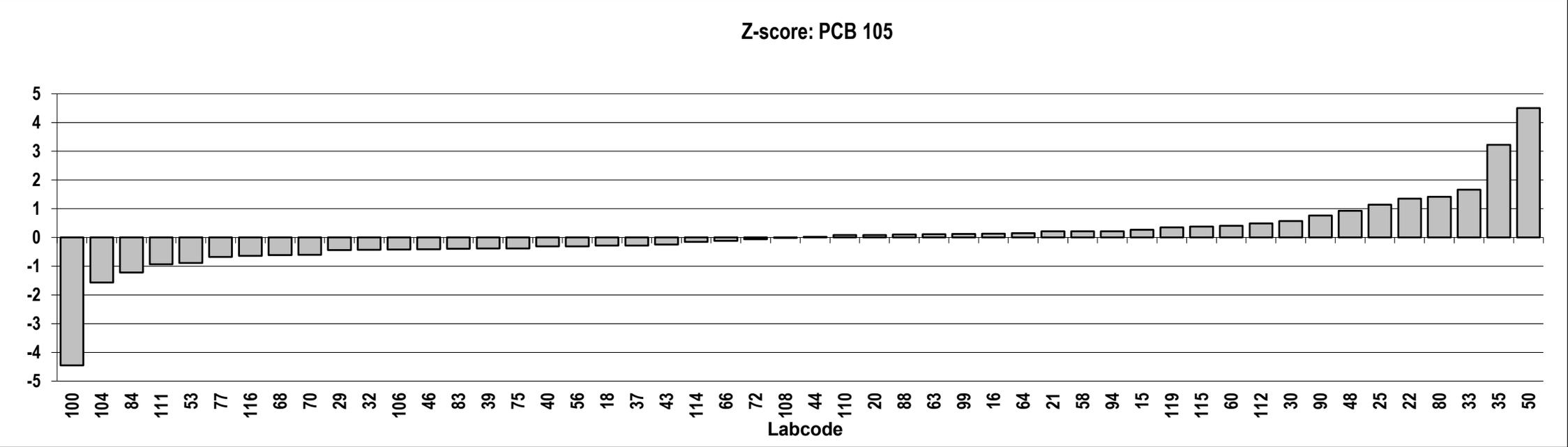
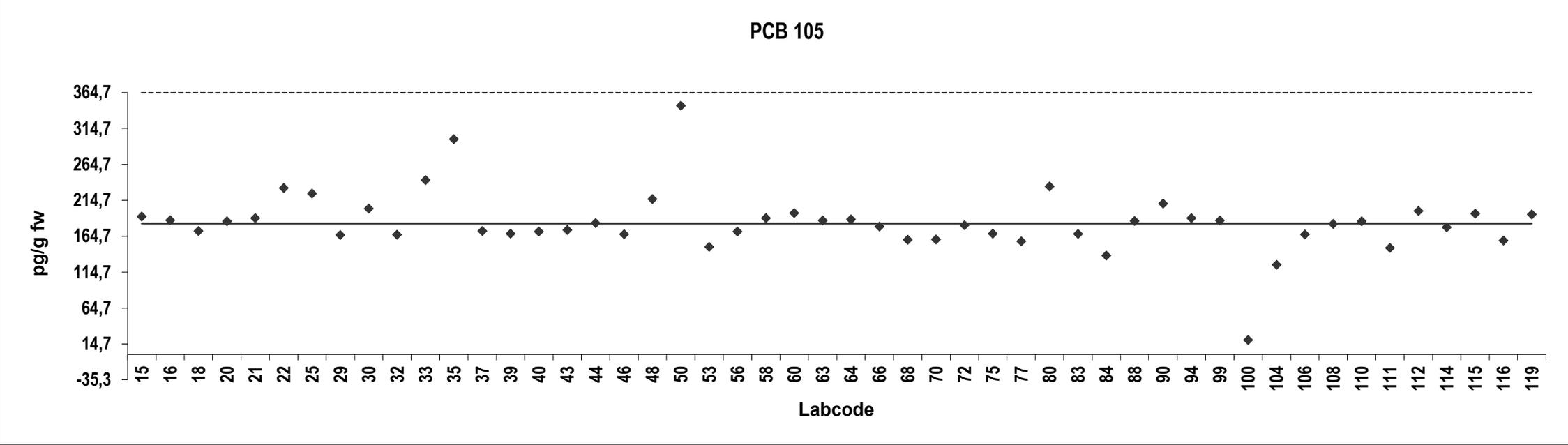
Consensus statistics	
Consensus median, pg/g	1,2
Median all values pg/g	1,2
Consensus mean, pg/g	1,1
Standard deviation, pg/g	0,35
Relative standard deviation, %	31
No. of values reported	50
No. of values removed	5
No. of reported non-detects	4



**Mackerel**  
**Congener: PCB 105**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	192	0,26		112	200	0,48	
16	187	0,13		114	177	-0,15	
18	172	-0,28		115	196	0,37	
20	186	0,087		116	159	-0,64	
21	190	0,21		119	195	0,35	
22	232	1,4					
25	224	1,1					
29	166	-0,44					
30	203	0,57					
32	167	-0,43					
33	243	1,7					
35	300	3,2	ND				
37	172	-0,28					
39	168	-0,38					
40	171	-0,31					
43	173	-0,24					
44	183	0,018					
46	167	-0,41					
48	216	0,93					
50	346	4,5					
53	150	-0,89					
56	171	-0,31					
58	190	0,21					
60	197	0,40					
63	187	0,12					
64	188	0,15					
66	178	-0,12					
68	160	-0,62					
70	160	-0,61					
72	180	-0,064					
75	168	-0,38					
77	158	-0,68					
80	234	1,4					
83	168	-0,40					
84	138	-1,2					
88	186	0,10					
90	210	0,77					
94	190	0,21					
99	187	0,12					
100	20	-4,5					
104	125	-1,6					
106	167	-0,42					
108	182	-0,018					
110	185	0,084					
111	148	-0,93					

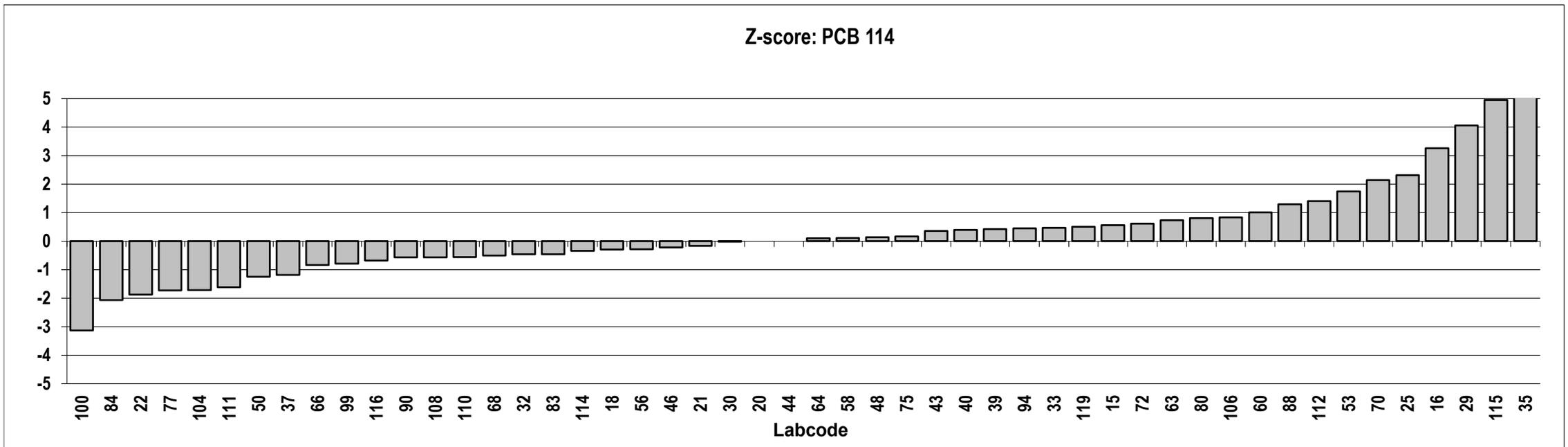
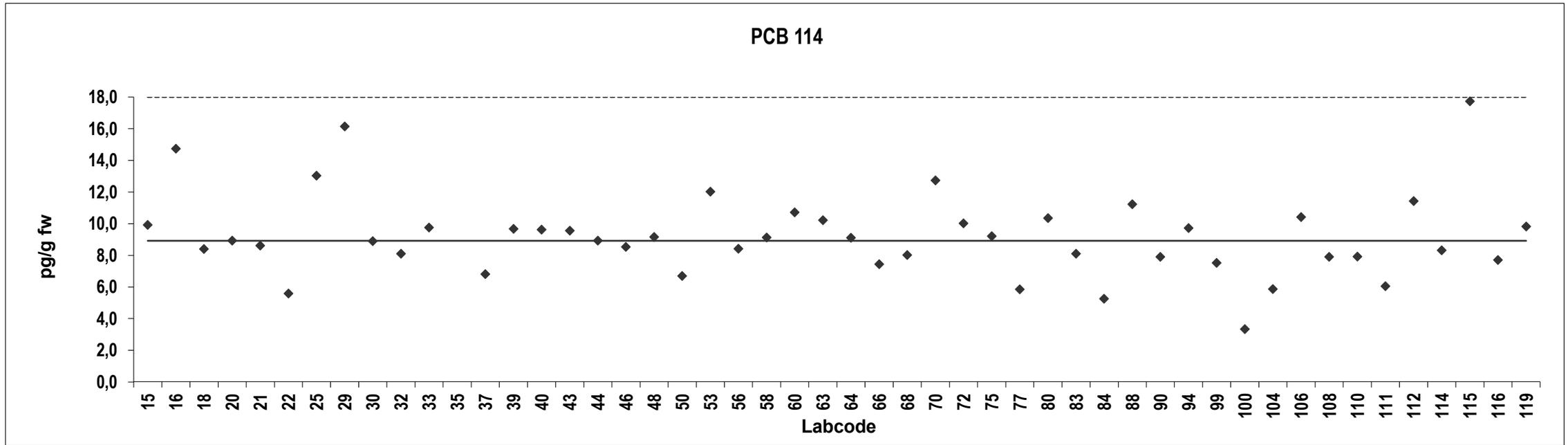
Consensus statistics	
Consensus median, pg/g	182
Median all values pg/g	182
Consensus mean, pg/g	184
Standard deviation, pg/g	44
Relative standard deviation, %	24
No. of values reported	50
No. of values removed	0
No. of reported non-detects	1



**Mackerel**  
**Congener: PCB 114**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	9,9	0,56		112	11	1,4	
16	15	3,3		114	8,3	-0,34	
18	8,4	-0,30		115	18	4,9	
20	8,9	0,00000		116	7,7	-0,68	
21	8,6	-0,17		119	9,8	0,51	
22	5,6	-1,9					
25	13	2,3					
29	16	4,1					
30	8,9	-0,015					
32	8,1	-0,46					
33	9,7	0,47					
35	20	6,2	Outlier,ND				
37	6,8	-1,2					
39	9,6	0,42					
40	9,6	0,39					
43	9,5	0,36					
44	8,9	0,00000					
46	8,5	-0,22					
48	9,1	0,13					
50	6,7	-1,2					
53	12	1,7					
56	8,4	-0,28					
58	9,1	0,11					
60	11	1,0					
63	10	0,73					
64	9,1	0,10					
66	7,4	-0,83					
68	8,0	-0,51					
70	13	2,1					
72	10	0,62					
75	9,2	0,16					
77	5,8	-1,7					
80	10	0,81					
83	8,1	-0,46					
84	5,2	-2,1					
88	11	1,3					
90	7,9	-0,57					
94	9,7	0,45					
99	7,5	-0,79					
100	3,3	-3,1	ND				
104	5,9	-1,7					
106	10	0,84					
108	7,9	-0,57					
110	7,9	-0,56					
111	6,0	-1,6					

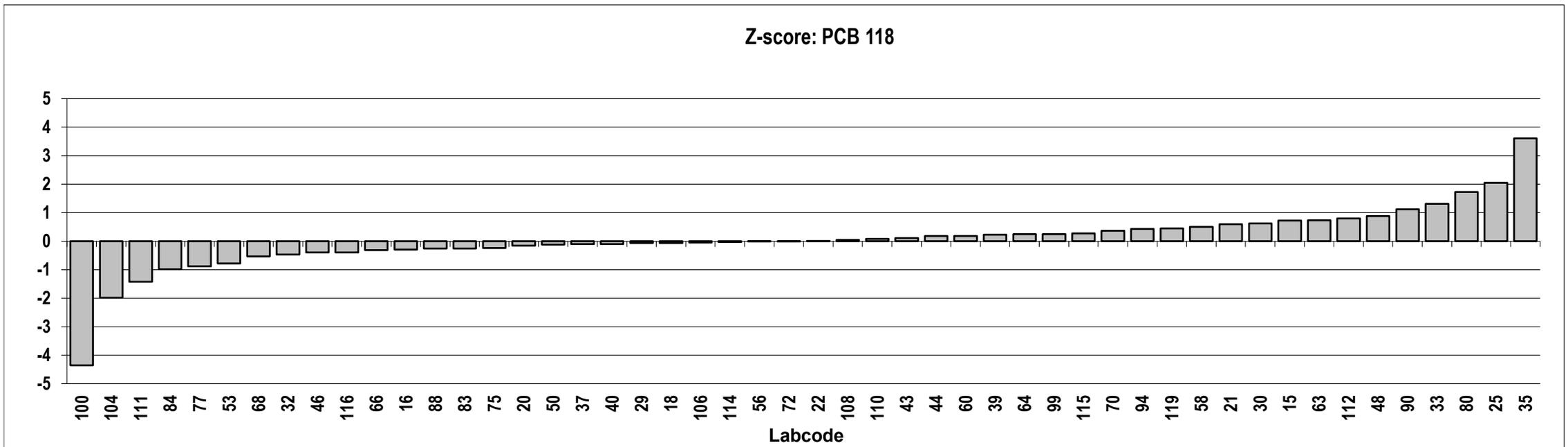
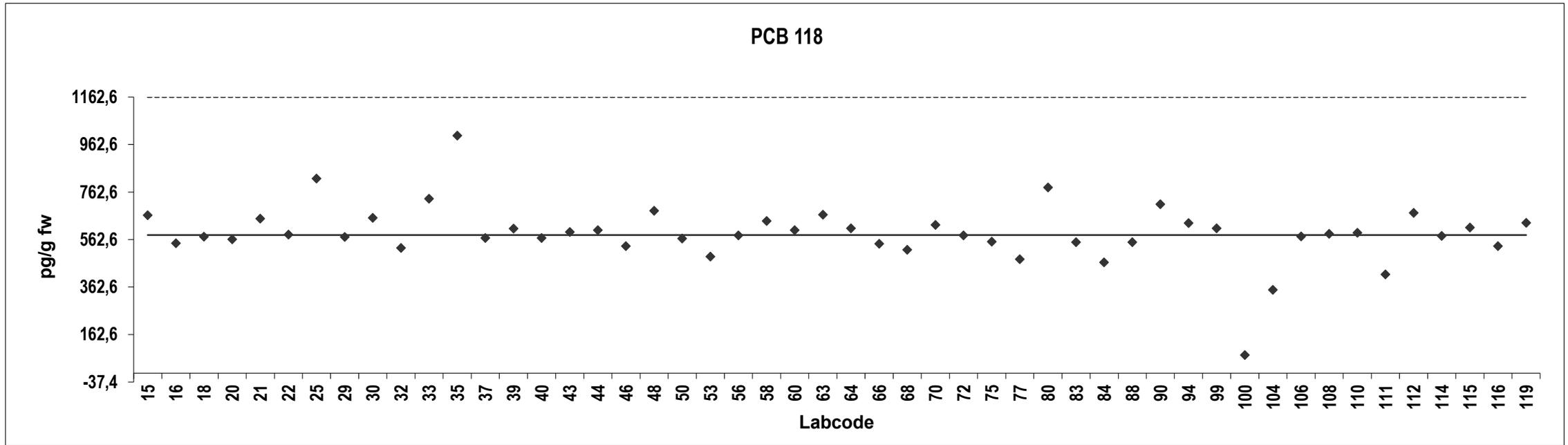
Consensus statistics	
Consensus median, pg/g	8,9
Median all values pg/g	9,0
Consensus mean, pg/g	9,2
Standard deviation, pg/g	2,6
Relative standard deviation, %	29
No. of values reported	50
No. of values removed	1
No. of reported non-detects	2



**Mackerel**  
**Congener: PCB 118**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	665	0,72		112	674	0,80	
16	547	-0,29		114	578	-0,028	
18	574	-0,063		115	613	0,27	
20	563	-0,15		116	535	-0,40	
21	650	0,59		119	633	0,44	
22	583	0,011					
25	819	2,0					
29	573	-0,071					
30	654	0,63					
32	527	-0,47					
33	734	1,3					
35	1000	3,6	ND				
37	569	-0,11					
39	608	0,23					
40	569	-0,11					
43	594	0,11					
44	602	0,18					
46	535	-0,40					
48	683	0,87					
50	567	-0,13					
53	490	-0,79					
56	580	-0,011					
58	640	0,50					
60	602	0,18					
63	666	0,73					
64	610	0,24					
66	545	-0,31					
68	519	-0,54					
70	624	0,36					
72	580	-0,011					
75	553	-0,24					
77	479	-0,88					
80	782	1,7					
83	552	-0,26					
84	467	-0,99					
88	551	-0,26					
90	711	1,1					
94	631	0,43					
99	610	0,25					
100	76	-4,4					
104	350	-2,0					
106	576	-0,050					
108	587	0,047					
110	591	0,080					
111	416	-1,4					

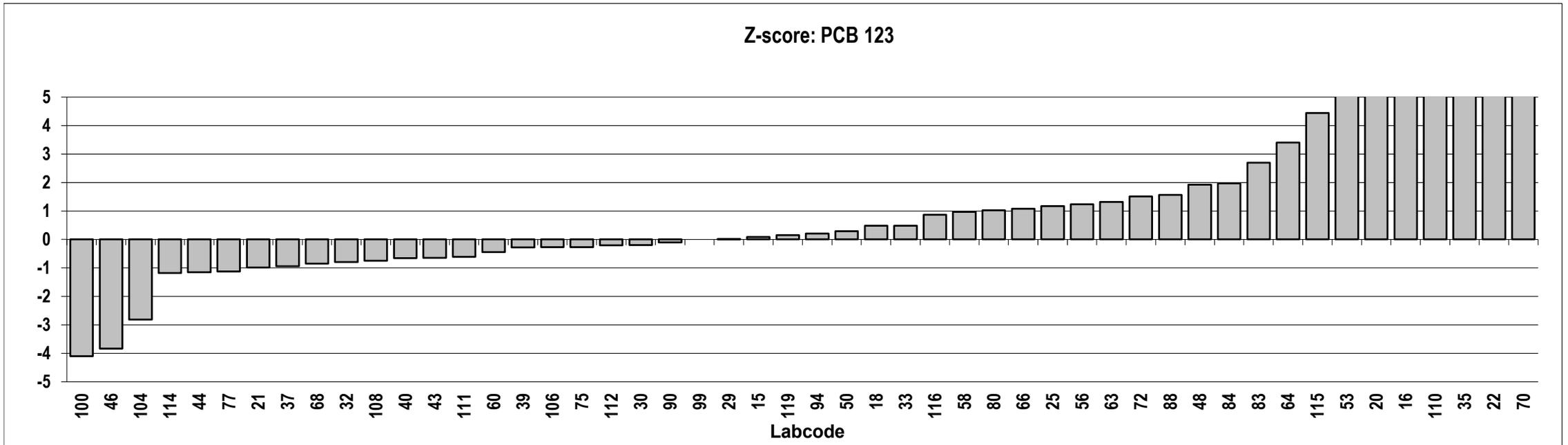
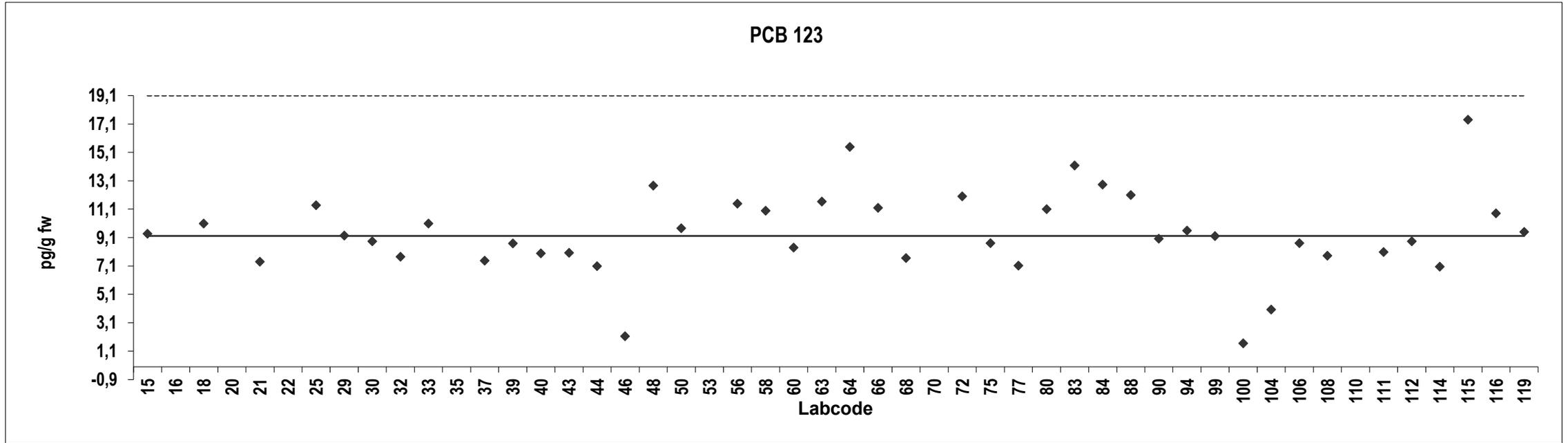
Consensus statistics	
Consensus median, pg/g	581
Median all values pg/g	581
Consensus mean, pg/g	589
Standard deviation, pg/g	124
Relative standard deviation, %	21
No. of values reported	50
No. of values removed	0
No. of reported non-detects	1



**Mackerel**  
**Congener: PCB 123**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	9,4	0,088		112	8,8	-0,20	
16	27	9,9	Outlier	114	7,0	-1,2	
18	10	0,48		115	17	4,4	
20	22	6,9	Outlier	116	11	0,86	
21	7,4	-0,99		119	9,5	0,15	
22	96	47	Outlier				
25	11	1,2					
29	9,2	0,016					
30	8,8	-0,20					
32	7,7	-0,80					
33	10	0,48					
35	30	11	Outlier,ND				
37	7,5	-0,94					
39	8,7	-0,28					
40	8,0	-0,66					
43	8,0	-0,65					
44	7,1	-1,1					
46	2,2	-3,8					
48	13	1,9					
50	9,8	0,29					
53	21	6,4	Outlier				
56	12	1,2					
58	11	0,97					
60	8,4	-0,44					
63	12	1,3					
64	15	3,4					
66	11	1,1					
68	7,7	-0,84					
70	122	61	Outlier				
72	12	1,5					
75	8,7	-0,27					
77	7,1	-1,1					
80	11	1,0					
83	14	2,7					
84	13	2,0					
88	12	1,6					
90	9,0	-0,10					
94	9,6	0,21					
99	9,2	0,00000					
100	1,7	-4,1	ND				
104	4,0	-2,8					
106	8,7	-0,27					
108	7,8	-0,75					
110	28	10	Outlier				
111	8,1	-0,62					

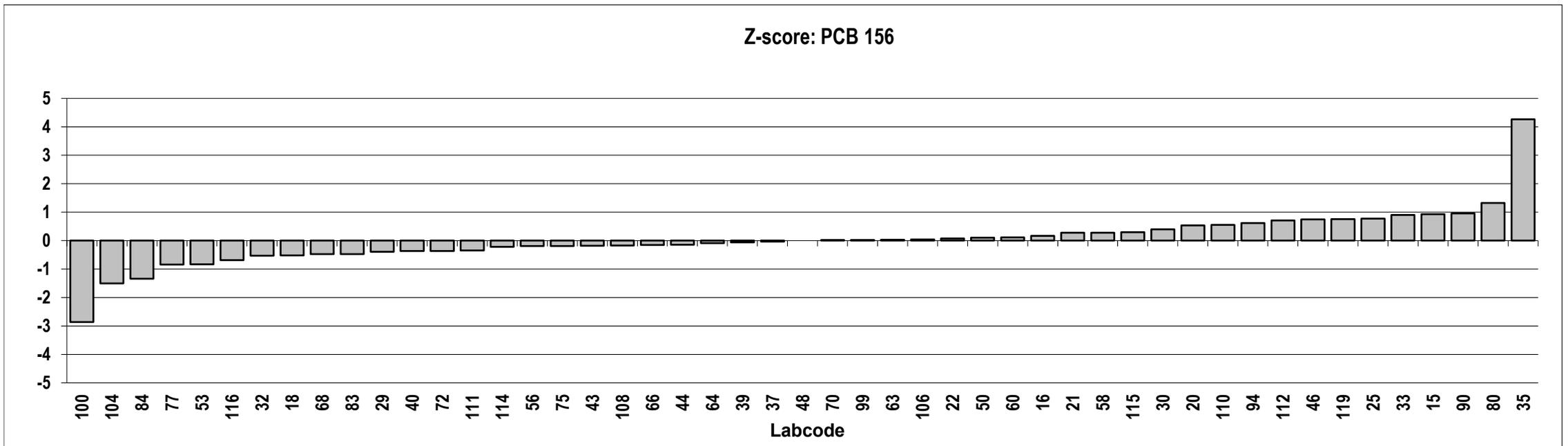
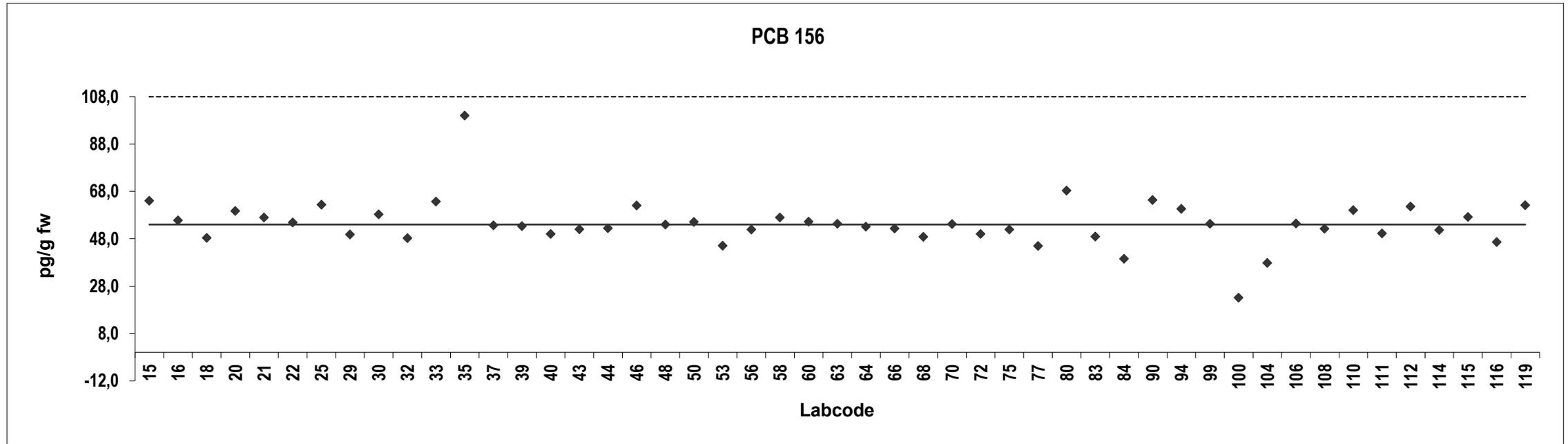
Consensus statistics	
Consensus median, pg/g	9,2
Median all values pg/g	9,6
Consensus mean, pg/g	9,4
Standard deviation, pg/g	3,0
Relative standard deviation, %	31
No. of values reported	50
No. of values removed	7
No. of reported non-detects	2



**Mackerel**  
**Congener: PCB 156**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	64	0,93		114	52	-0,22	
16	56	0,17		115	57	0,30	
18	48	-0,52		116	47	-0,69	
20	60	0,53		119	62	0,75	
21	57	0,28					
22	55	0,077					
25	62	0,78					
29	50	-0,39					
30	58	0,40					
32	48	-0,53					
33	64	0,90					
35	100	4,3	ND				
37	54	-0,035					
39	53	-0,060					
40	50	-0,37					
43	52	-0,18					
44	52	-0,15					
46	62	0,74					
48	54	0,00000					
50	55	0,10					
53	45	-0,83					
56	52	-0,19					
58	57	0,28					
60	55	0,11					
63	54	0,026					
64	53	-0,087					
66	52	-0,16					
68	49	-0,48					
70	54	0,018					
72	50	-0,37					
75	52	-0,19					
77	45	-0,84					
80	68	1,3					
83	49	-0,47					
84	40	-1,3					
90	64	0,96					
94	61	0,61					
99	54	0,025					
100	23	-2,9					
104	38	-1,5					
106	54	0,043					
108	52	-0,17					
110	60	0,56					
111	50	-0,34					
112	62	0,71					

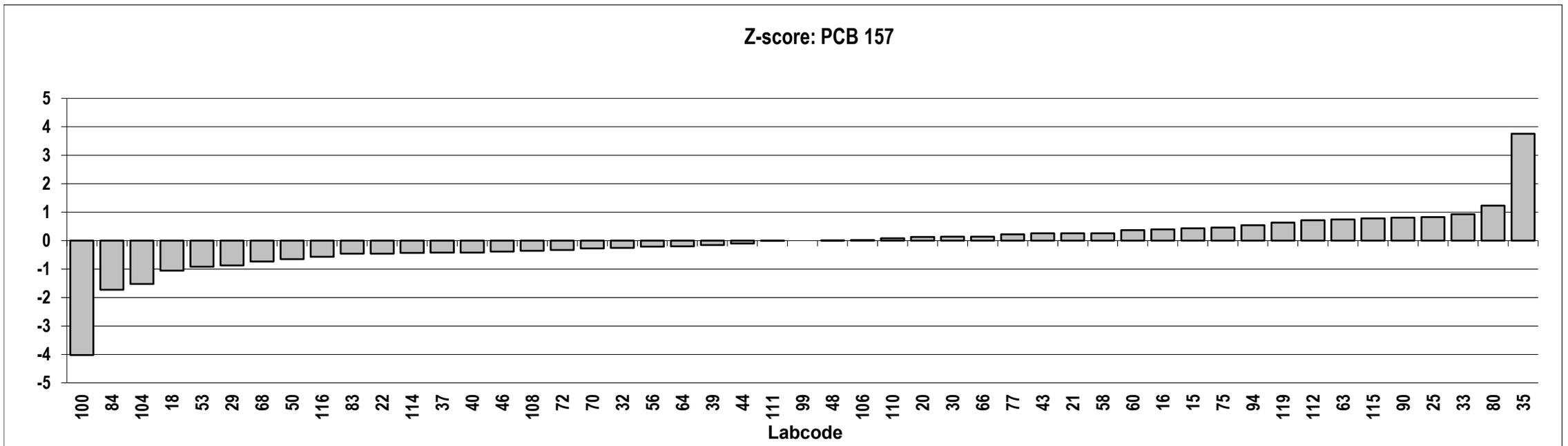
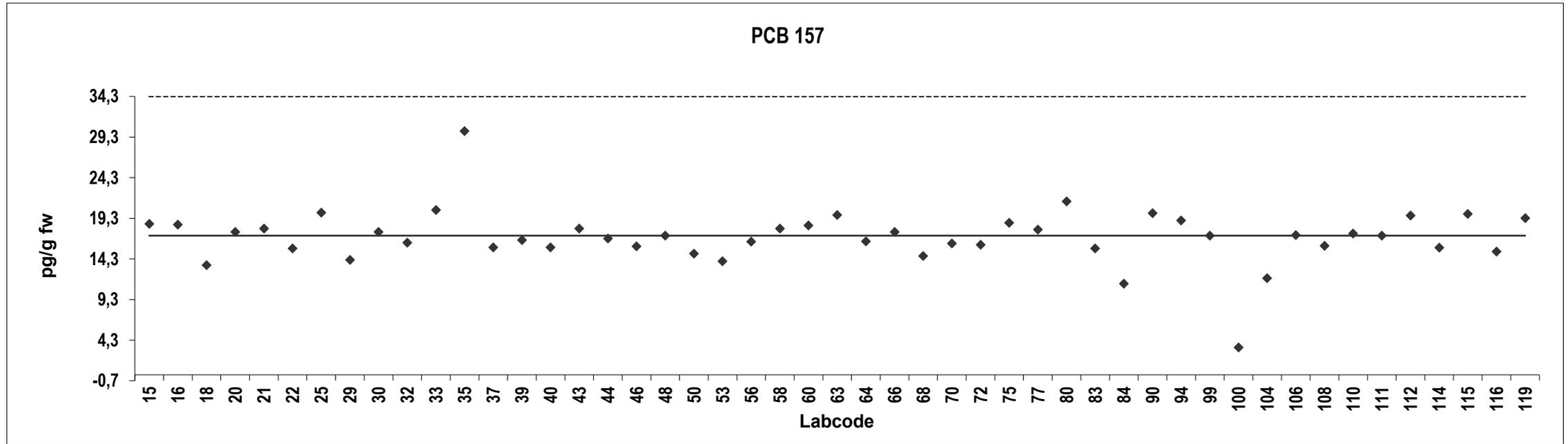
Consensus statistics	
Consensus median, pg/g	54
Median all values pg/g	54
Consensus mean, pg/g	54
Standard deviation, pg/g	10
Relative standard deviation, %	19
No. of values reported	49
No. of values removed	0
No. of reported non-detects	1



**Mackerel**  
**Congener: PCB 157**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	19	0,43		114	16	-0,43	
16	18	0,40		115	20	0,78	
18	14	-1,1		116	15	-0,57	
20	18	0,13		119	19	0,63	
21	18	0,25					
22	16	-0,46					
25	20	0,83					
29	14	-0,87					
30	18	0,13					
32	16	-0,26					
33	20	0,92					
35	30	3,8	ND				
37	16	-0,42					
39	17	-0,16					
40	16	-0,42					
43	18	0,25					
44	17	-0,10					
46	16	-0,38					
48	17	0,0056					
50	15	-0,65					
53	14	-0,91					
56	16	-0,21					
58	18	0,25					
60	18	0,37					
63	20	0,75					
64	16	-0,20					
66	18	0,14					
68	15	-0,73					
70	16	-0,28					
72	16	-0,33					
75	19	0,46					
77	18	0,22					
80	21	1,2					
83	16	-0,46					
84	11	-1,7					
90	20	0,81					
94	19	0,55					
99	17	0,00000					
100	3,4	-4,0	ND				
104	12	-1,5					
106	17	0,021					
108	16	-0,36					
110	17	0,079					
111	17	-0,00086					
112	20	0,72					

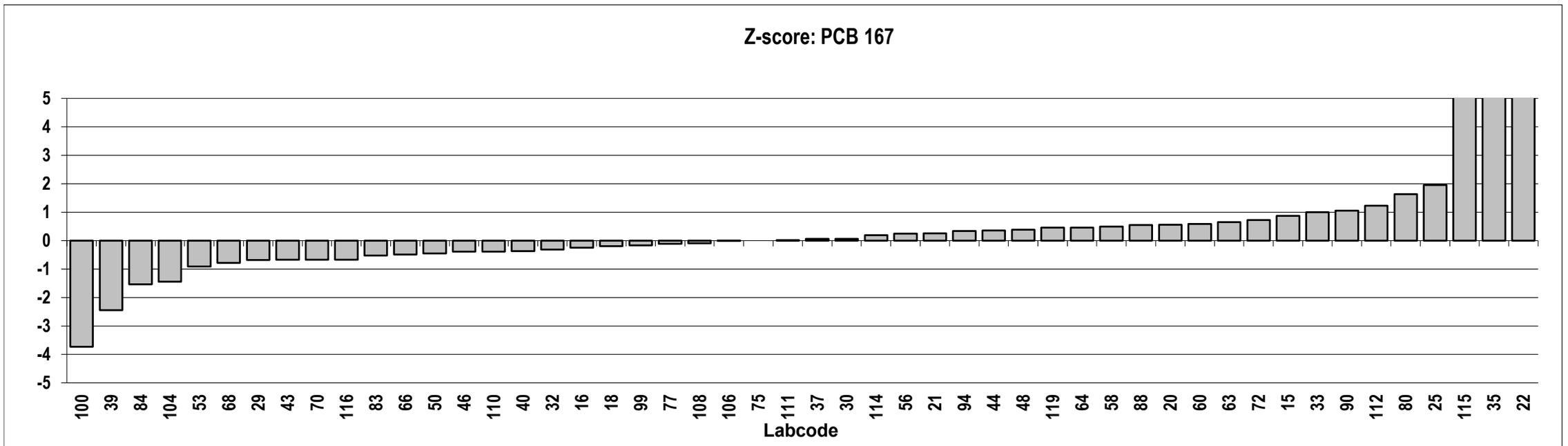
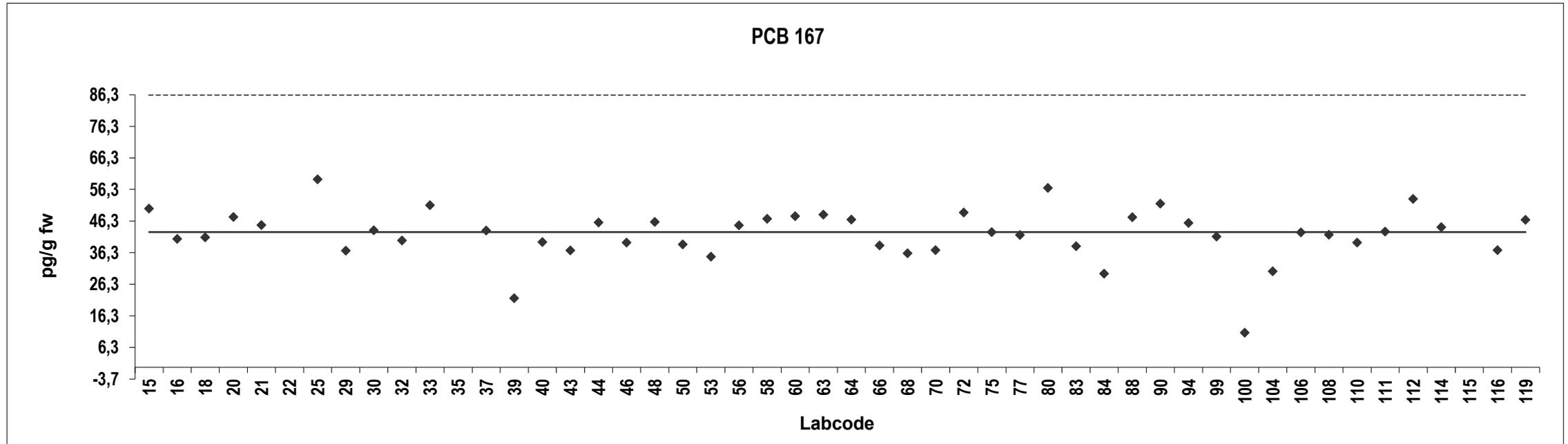
Consensus statistics	
Consensus median, pg/g	17
Median all values pg/g	17
Consensus mean, pg/g	17
Standard deviation, pg/g	3,4
Relative standard deviation, %	20
No. of values reported	49
No. of values removed	0
No. of reported non-detects	2



**Mackerel**  
**Congener: PCB 167**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	50	0,87		112	53	1,2	
16	41	-0,25		114	44	0,19	
18	41	-0,20		115	87	5,2	Outlier
20	48	0,56		116	37	-0,67	
21	45	0,26		119	47	0,46	
22	163	14	Outlier				
25	59	1,9					
29	37	-0,68					
30	43	0,066					
32	40	-0,31					
33	51	1,0					
35	100	6,7	Outlier,ND				
37	43	0,060					
39	22	-2,4					
40	40	-0,37					
43	37	-0,68					
44	46	0,35					
46	39	-0,39					
48	46	0,38					
50	39	-0,46					
53	35	-0,91					
56	45	0,25					
58	47	0,49					
60	48	0,59					
63	48	0,65					
64	47	0,46					
66	39	-0,49					
68	36	-0,79					
70	37	-0,67					
72	49	0,73					
75	43	0,00000					
77	42	-0,11					
80	57	1,6					
83	38	-0,52					
84	30	-1,5					
88	48	0,55					
90	52	1,1					
94	46	0,34					
99	41	-0,17					
100	11	-3,7					
104	30	-1,4					
106	43	-0,010					
108	42	-0,092					
110	40	-0,38					
111	43	0,020					

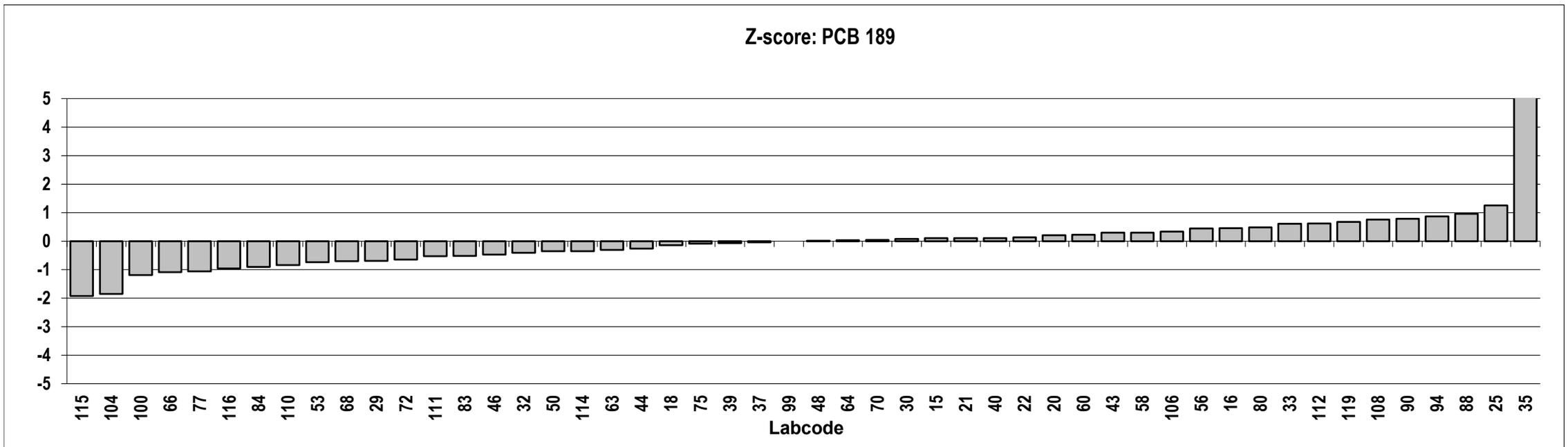
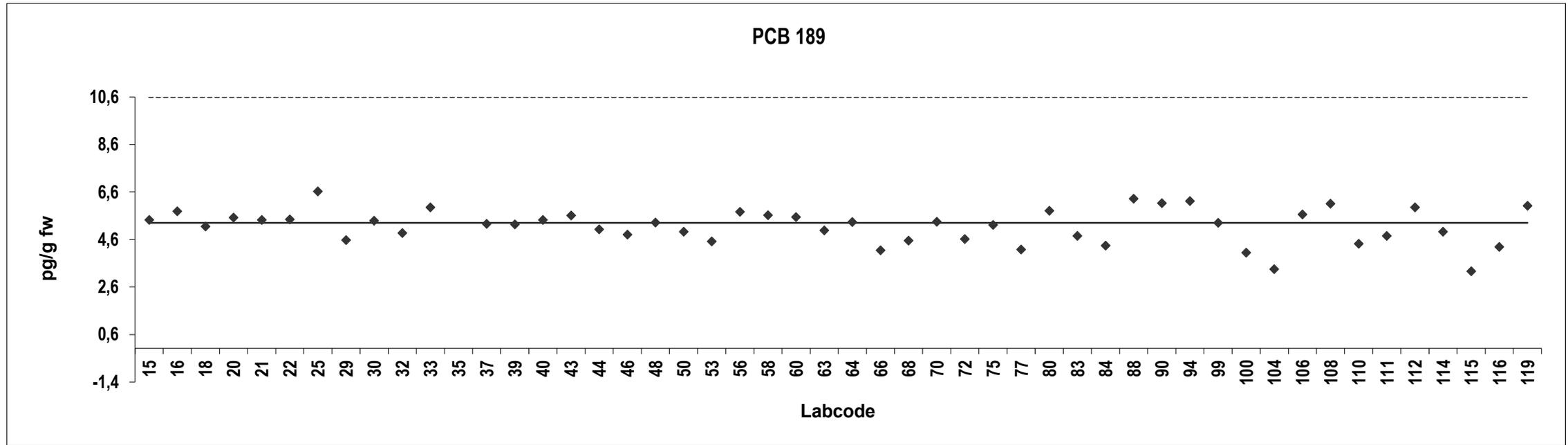
Consensus statistics	
Consensus median, pg/g	43
Median all values pg/g	43
Consensus mean, pg/g	42
Standard deviation, pg/g	8,2
Relative standard deviation, %	20
No. of values reported	50
No. of values removed	3
No. of reported non-detects	1



**Mackerel**  
**Congener: PCB 189**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	5,4	0,11		112	5,9	0,62	
16	5,8	0,45		114	4,9	-0,35	
18	5,1	-0,15		115	3,3	-1,9	
20	5,5	0,20		116	4,3	-0,96	
21	5,4	0,11		119	6,0	0,68	
22	5,4	0,13					
25	6,6	1,3					
29	4,6	-0,69					
30	5,4	0,082					
32	4,9	-0,41					
33	5,9	0,61					
35	15	9,2	Outlier,ND				
37	5,2	-0,042					
39	5,2	-0,066					
40	5,4	0,11					
43	5,6	0,30					
44	5,0	-0,26					
46	4,8	-0,47					
48	5,3	0,015					
50	4,9	-0,35					
53	4,5	-0,74					
56	5,8	0,44					
58	5,6	0,30					
60	5,5	0,23					
63	5,0	-0,31					
64	5,3	0,029					
66	4,1	-1,1					
68	4,5	-0,71					
70	5,3	0,041					
72	4,6	-0,65					
75	5,2	-0,088					
77	4,2	-1,1					
80	5,8	0,48					
83	4,7	-0,52					
84	4,3	-0,91					
88	6,3	0,96					
90	6,1	0,78					
94	6,2	0,87					
99	5,3	0,00000					
100	4,0	-1,2	ND				
104	3,3	-1,8					
106	5,6	0,33					
108	6,1	0,76					
110	4,4	-0,84					
111	4,7	-0,53					

Consensus statistics	
Consensus median, pg/g	5,3
Median all values pg/g	5,3
Consensus mean, pg/g	5,1
Standard deviation, pg/g	0,72
Relative standard deviation, %	14
No. of values reported	50
No. of values removed	1
No. of reported non-detects	2

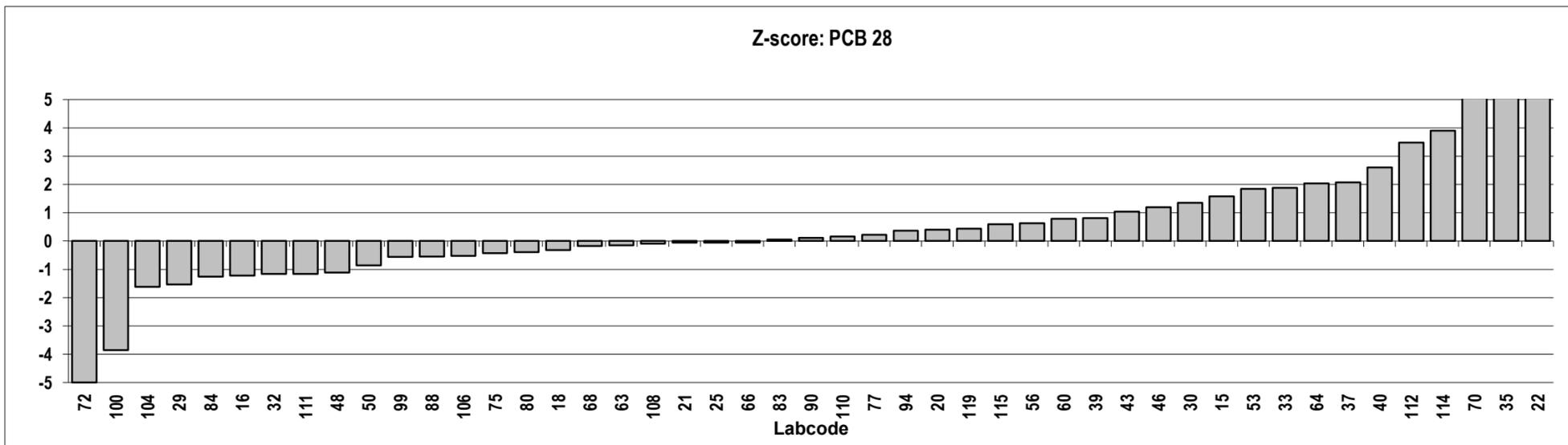
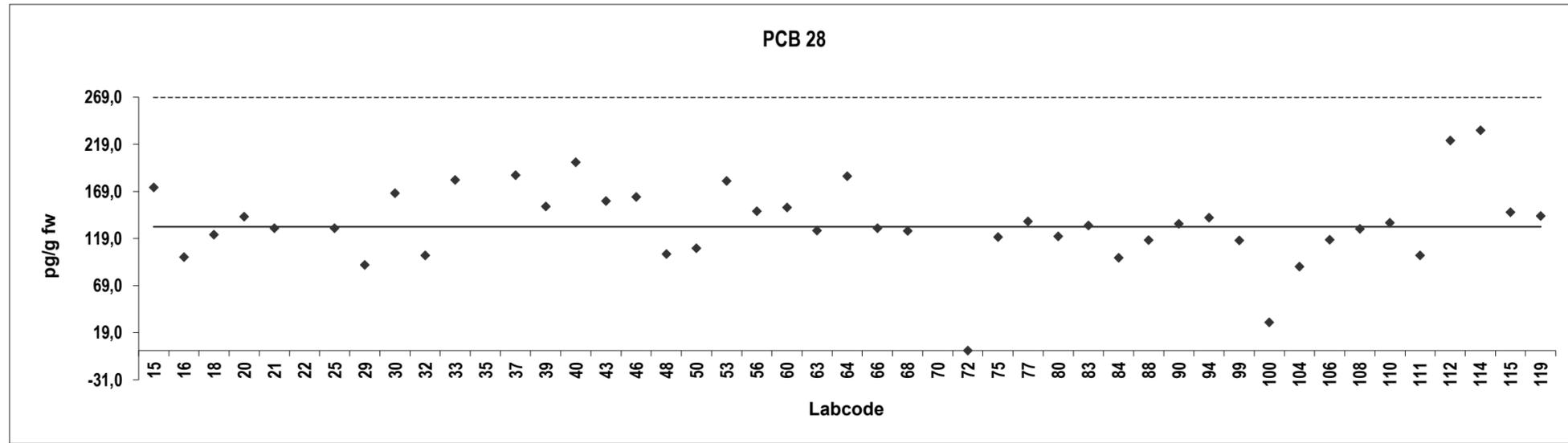


**Mackerel**  
Congener: PCB 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	173	1,6		115	147	0,59	
16	99	-1,2		119	143	0,44	
18	123	-0,32					
20	142	0,40					
21	130	-0,055					
22	469	13	Outlier				
25	130	-0,055					
29	91	-1,5					
30	167	1,3					
32	101	-1,2					
33	181	1,9					
35	400	10	Outlier,ND				
37	186	2,1					
39	153	0,82					
40	200	2,6	ND				
43	159	1,0					
46	163	1,2					
48	102	-1,1					
50	109	-0,87					
53	180	1,8					
56	148	0,63					
60	152	0,78					
63	127	-0,16					
64	185	2,0					
66	130	-0,055					
68	127	-0,17					
70	323	7,3	Outlier				
72	0,15	-5,0					
75	120	-0,42					
77	137	0,22					
80	121	-0,39					
83	133	0,055					
84	99	-1,3					
88	117	-0,55					
90	134	0,12					
94	141	0,36					
99	117	-0,56					
100	30	-3,9	ND				
104	89	-1,6					
106	118	-0,52					
108	129	-0,089					
110	136	0,16					
111	101	-1,2					
112	223	3,5					
114	234	3,9					

**Consensus statistics**

Consensus median, pg/g	131
Median all values pg/g	134
Consensus mean, pg/g	135
Standard deviation, pg/g	42
Relative standard deviation, %	32
No. of values reported	47
No. of values removed	3
No. of reported non-detects	3

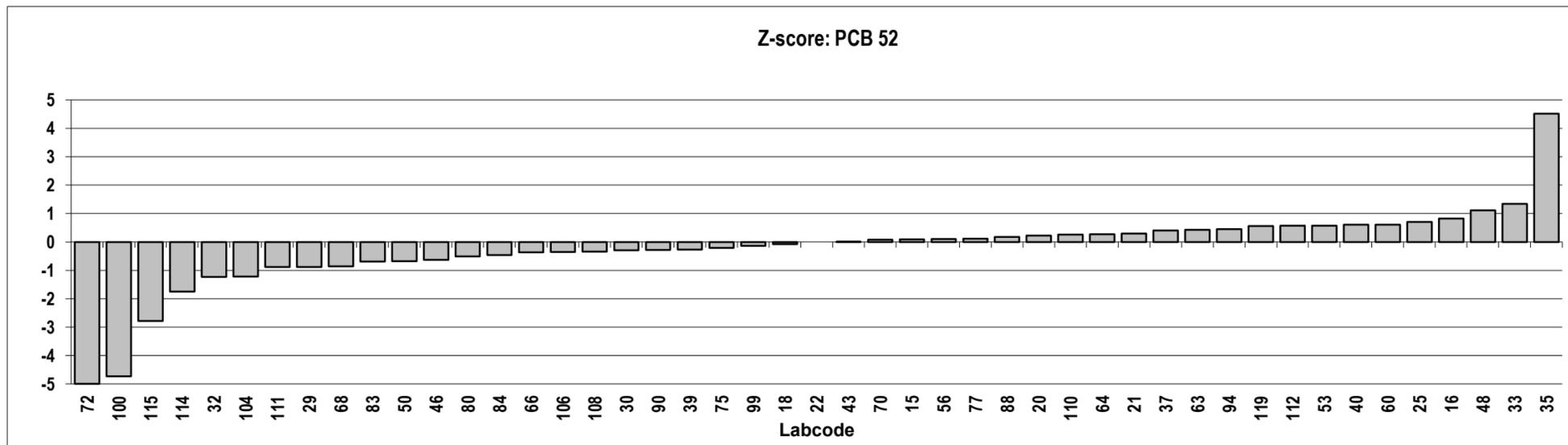
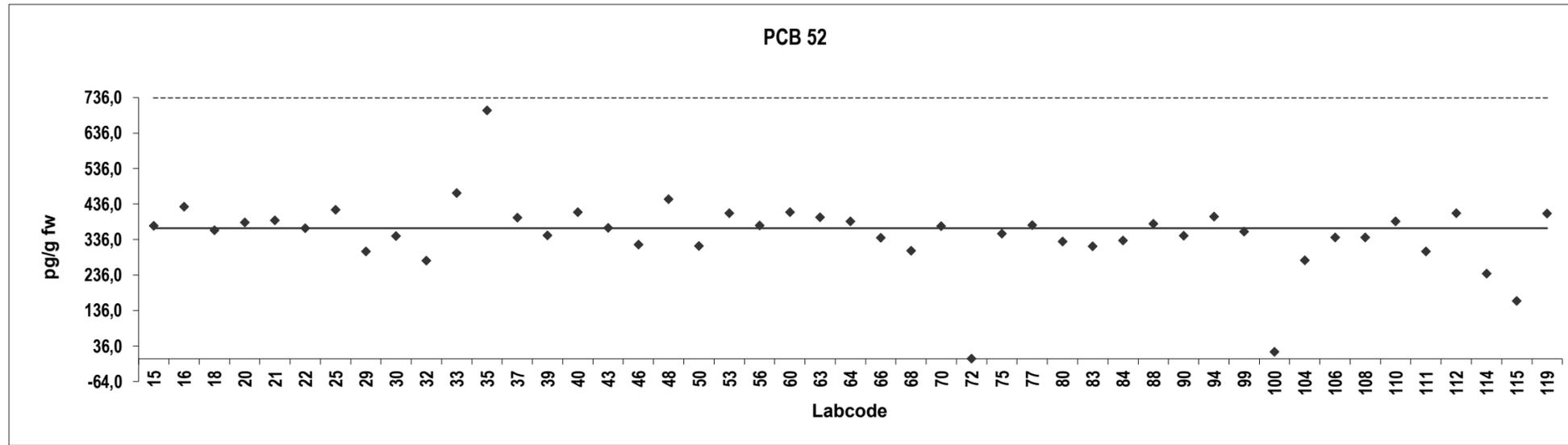


**Mackerel**  
Congener: PCB 52

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	375	0,095		115	163	-2,8	
16	429	0,83		119	409	0,56	
18	362	-0,081					
20	384	0,22					
21	390	0,30					
22	368	0,00000					
25	420	0,71					
29	303	-0,88					
30	346	-0,30					
32	277	-1,2					
33	467	1,3					
35	700	4,5	ND				
37	398	0,41					
39	348	-0,27					
40	413	0,61					
43	369	0,012					
46	322	-0,63					
48	450	1,1					
50	318	-0,68					
53	410	0,57					
56	376	0,11					
60	413	0,61					
63	399	0,42					
64	388	0,27					
66	341	-0,37					
68	305	-0,86					
70	373	0,073					
72	0,38	-5,0					
75	353	-0,21					
77	376	0,12					
80	331	-0,51					
83	317	-0,69					
84	334	-0,47					
88	381	0,17					
90	347	-0,29					
94	401	0,45					
99	358	-0,13					
100	20	-4,7	ND				
104	278	-1,2					
106	342	-0,35					
108	342	-0,35					
110	387	0,26					
111	303	-0,88					
112	410	0,57					
114	240	-1,7					

**Consensus statistics**

Consensus median, pg/g	368
Median all values pg/g	368
Consensus mean, pg/g	352
Standard deviation, pg/g	103
Relative standard deviation, %	29
No. of values reported	47
No. of values removed	0
No. of reported non-detects	2

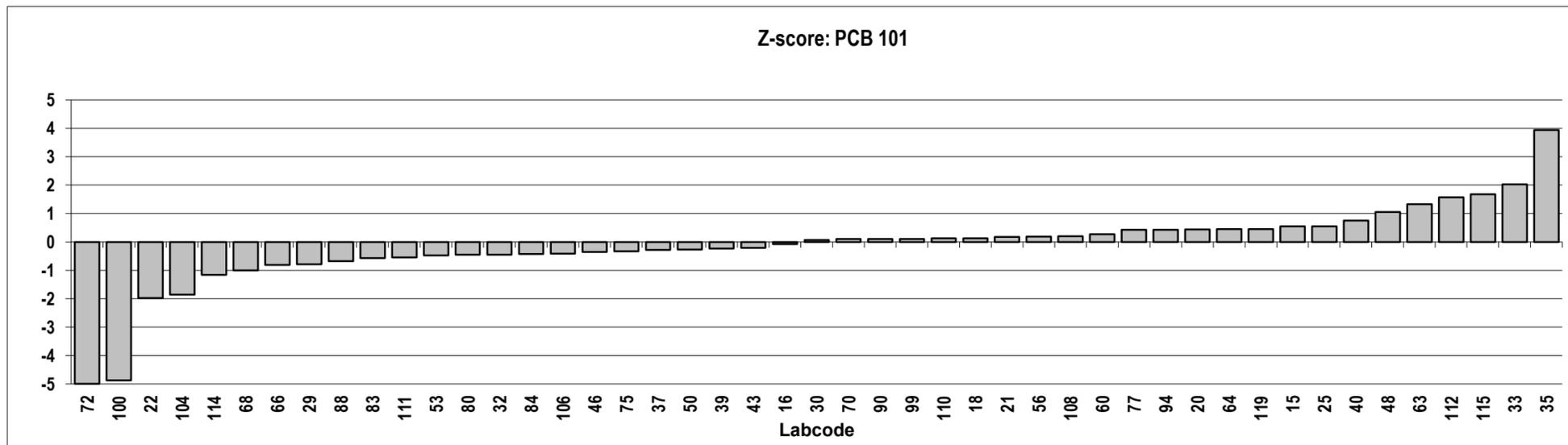
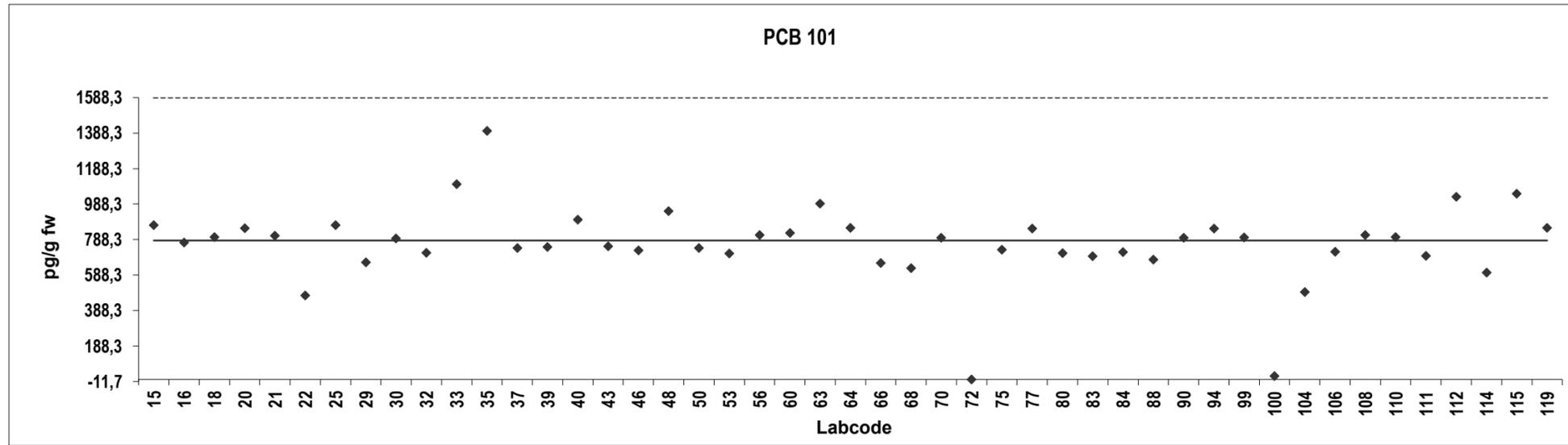


**Mackerel**  
Congener: PCB 101

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	870	0,55		115	1046	1,7	
16	772	-0,070		119	854	0,45	
18	803	0,13					
20	852	0,44					
21	810	0,17					
22	473	-2,0					
25	870	0,55					
29	660	-0,79					
30	794	0,070					
32	713	-0,45					
33	1100	2,0					
35	1400	3,9	ND				
37	740	-0,28					
39	747	-0,23					
40	901	0,75					
43	750	-0,21					
46	727	-0,36					
48	948	1,1					
50	742	-0,26					
53	710	-0,47					
56	813	0,19					
60	825	0,27					
63	991	1,3					
64	853	0,45					
66	657	-0,81					
68	627	-1,0					
70	799	0,10					
72	0,77	-5,0					
75	731	-0,33					
77	850	0,43					
80	712	-0,45					
83	694	-0,57					
84	717	-0,42					
88	676	-0,68					
90	799	0,10					
94	851	0,43					
99	800	0,11					
100	20	-4,9					
104	493	-1,9					
106	719	-0,41					
108	814	0,20					
110	802	0,12					
111	697	-0,55					
112	1030	1,6					
114	601	-1,2					

**Consensus statistics**

Consensus median, pg/g	783
Median all values pg/g	794
Consensus mean, pg/g	763
Standard deviation, pg/g	221
Relative standard deviation, %	29
No. of values reported	47
No. of values removed	0
No. of reported non-detects	1

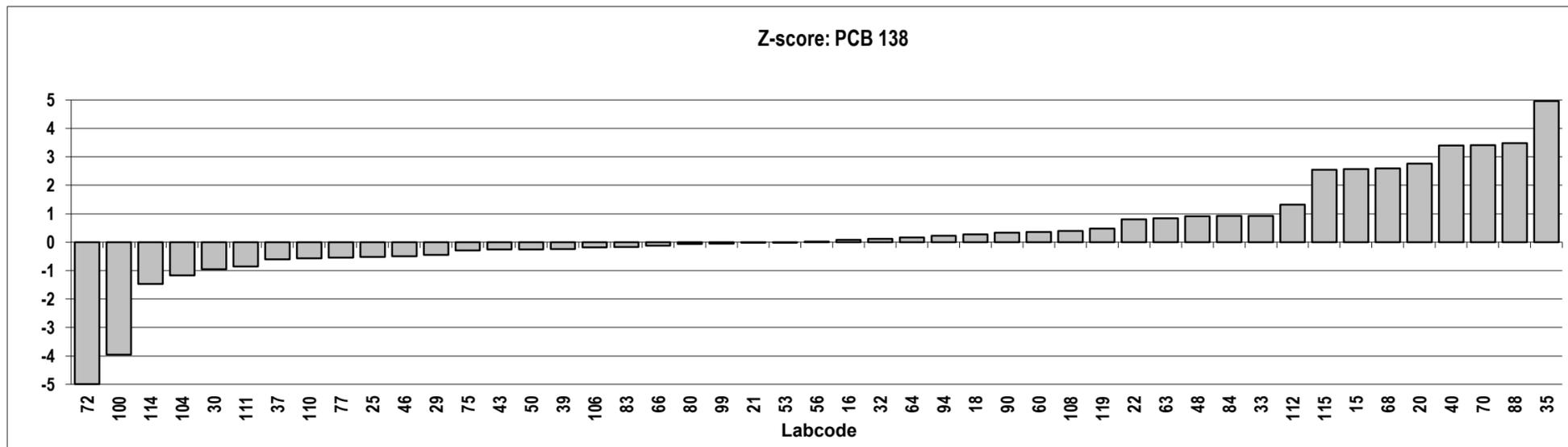
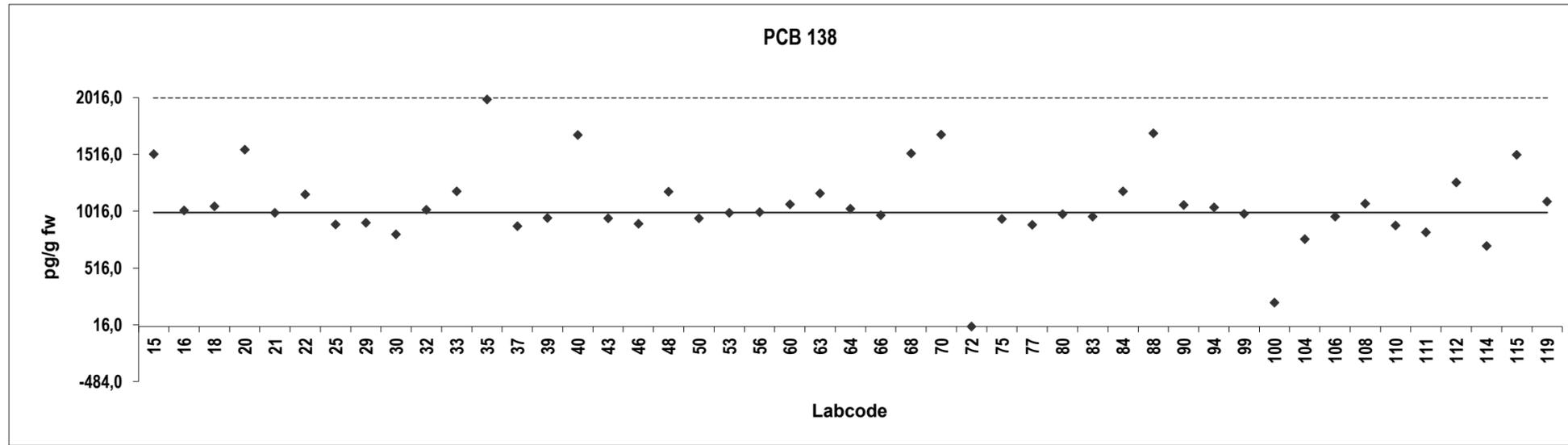


**Mackerel**  
Congener: PCB 138

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	1520	2,6		115	1514	2,5	
16	1021	0,085		119	1100	0,48	
18	1060	0,28					
20	1558	2,8					
21	1000	-0,020					
22	1164	0,80					
25	900	-0,52					
29	915	-0,44					
30	812	-0,96					
32	1028	0,12					
33	1190	0,93					
35	2000	5,0	ND				
37	883	-0,60					
39	955	-0,24					
40	1686	3,4					
43	953	-0,26					
46	904	-0,50					
48	1188	0,92					
50	953	-0,25					
53	1000	-0,020					
56	1008	0,020					
60	1077	0,36					
63	1173	0,84					
64	1036	0,16					
66	980	-0,12					
68	1524	2,6					
70	1690	3,4					
72	0,99	-5,0					
75	946	-0,29					
77	895	-0,54					
80	990	-0,069					
83	969	-0,18					
84	1190	0,92					
88	1703	3,5					
90	1071	0,33					
94	1050	0,23					
99	993	-0,054					
100	210	-4,0					
104	770	-1,2					
106	967	-0,18					
108	1083	0,39					
110	889	-0,57					
111	831	-0,86					
112	1270	1,3					
114	709	-1,5					

**Consensus statistics**

Consensus median, pg/g	1004
Median all values pg/g	1008
Consensus mean, pg/g	1071
Standard deviation, pg/g	346
Relative standard deviation, %	32
No. of values reported	47
No. of values removed	0
No. of reported non-detects	1

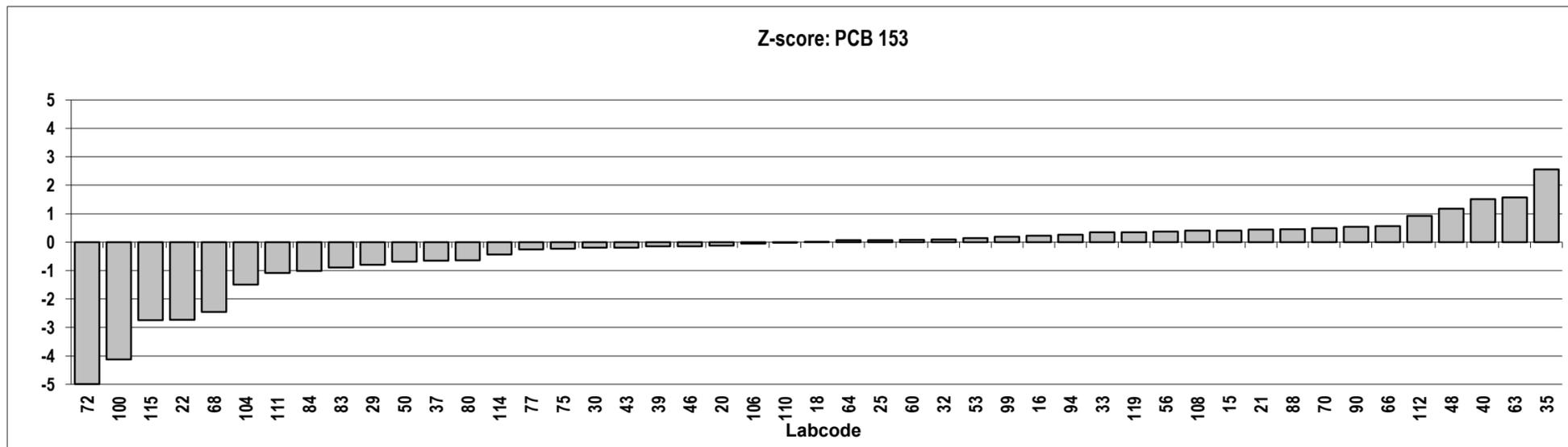
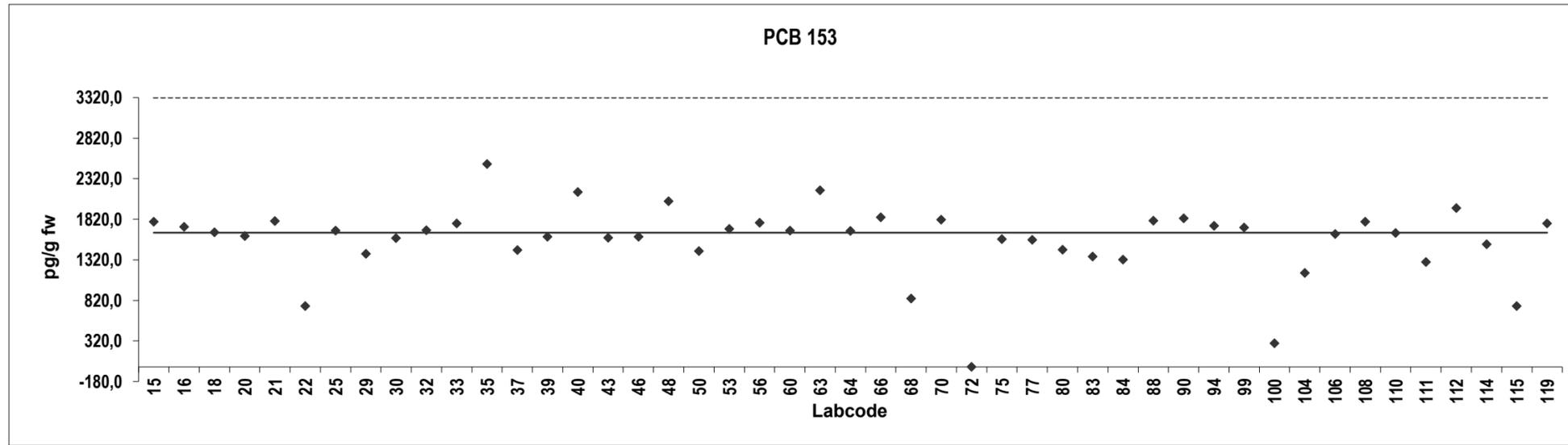


**Mackerel**  
Congener: PCB 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	1790	0,41		115	749	-2,7	
16	1728	0,22		119	1770	0,35	
18	1660	0,016					
20	1614	-0,12					
21	1800	0,44					
22	750	-2,7					
25	1680	0,076					
29	1392	-0,79					
30	1589	-0,20					
32	1686	0,094					
33	1770	0,35					
35	2500	2,6	ND				
37	1440	-0,65					
39	1605	-0,15					
40	2156	1,5					
43	1592	-0,19					
46	1606	-0,15					
48	2045	1,2					
50	1427	-0,69					
53	1700	0,14					
56	1776	0,37					
60	1681	0,078					
63	2177	1,6					
64	1677	0,067					
66	1843	0,57					
68	842	-2,5					
70	1816	0,49					
72	1,6	-5,0					
75	1577	-0,23					
77	1569	-0,26					
80	1445	-0,63					
83	1360	-0,89					
84	1322	-1,0					
88	1804	0,45					
90	1833	0,54					
94	1740	0,26					
99	1719	0,19					
100	290	-4,1					
104	1160	-1,5					
106	1638	-0,050					
108	1790	0,41					
110	1650	-0,016					
111	1295	-1,1					
112	1960	0,92					
114	1512	-0,43					

**Consensus statistics**

Consensus median, pg/g	1655
Median all values pg/g	1660
Consensus mean, pg/g	1564
Standard deviation, pg/g	444
Relative standard deviation, %	28
No. of values reported	47
No. of values removed	0
No. of reported non-detects	1

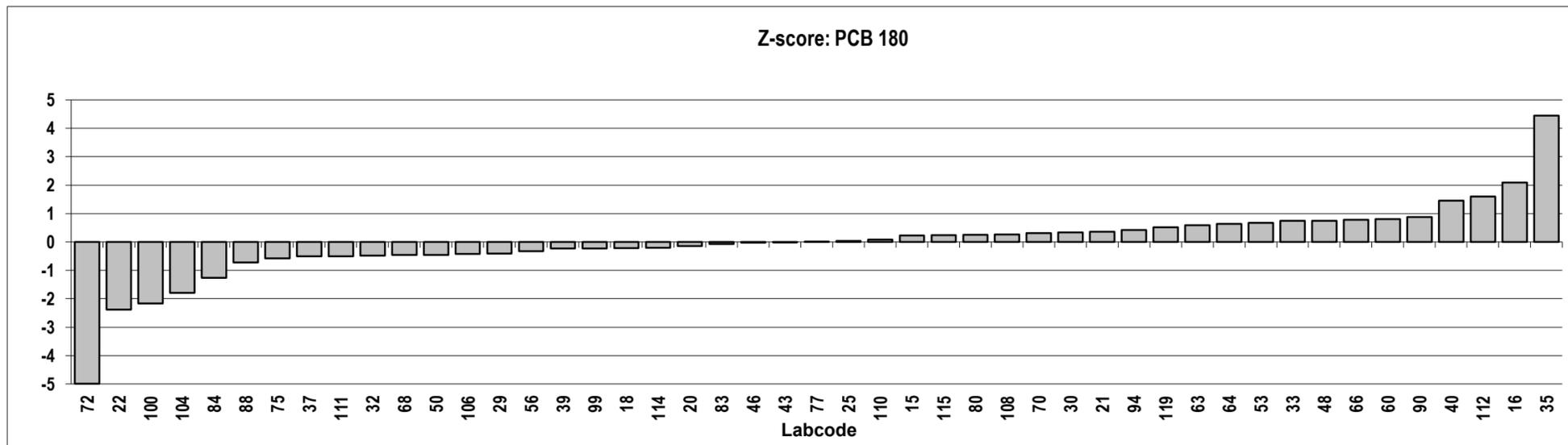
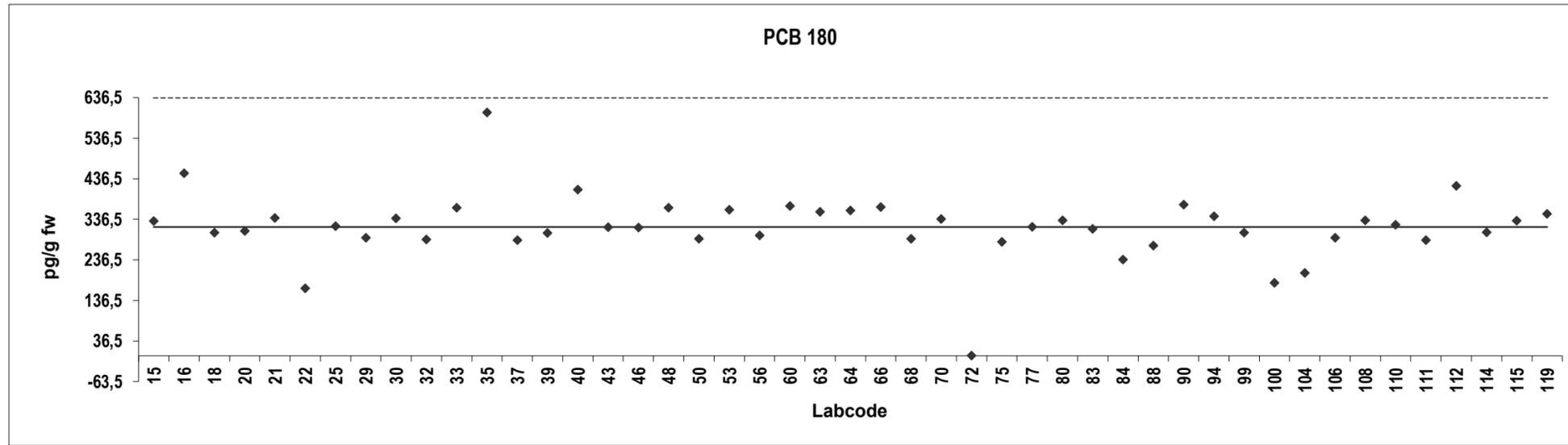


**Mackerel**  
Congener: PCB 180

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	332	0,23		115	333	0,24	
16	450	2,1		119	350	0,51	
18	304	-0,21					
20	308	-0,15					
21	340	0,35					
22	166	-2,4					
25	320	0,040					
29	291	-0,42					
30	339	0,34					
32	287	-0,48					
33	365	0,75					
35	600	4,4	ND				
37	285	-0,51					
39	303	-0,23					
40	410	1,5					
43	317	-0,012					
46	316	-0,022					
48	365	0,75					
50	289	-0,45					
53	360	0,67					
56	297	-0,32					
60	369	0,81					
63	355	0,59					
64	358	0,64					
66	367	0,78					
68	289	-0,45					
70	337	0,31					
72	0,32	-5,0					
75	281	-0,58					
77	318	0,012					
80	334	0,26					
83	313	-0,075					
84	237	-1,3					
88	272	-0,72					
90	373	0,87					
94	344	0,42					
99	303	-0,22					
100	180	-2,2					
104	204	-1,8					
106	291	-0,42					
108	334	0,26					
110	323	0,089					
111	285	-0,51					
112	419	1,6					
114	304	-0,21					

**Consensus statistics**

Consensus median, pg/g	317
Median all values pg/g	318
Consensus mean, pg/g	317
Standard deviation, pg/g	82
Relative standard deviation, %	26
No. of values reported	47
No. of values removed	0
No. of reported non-detects	1

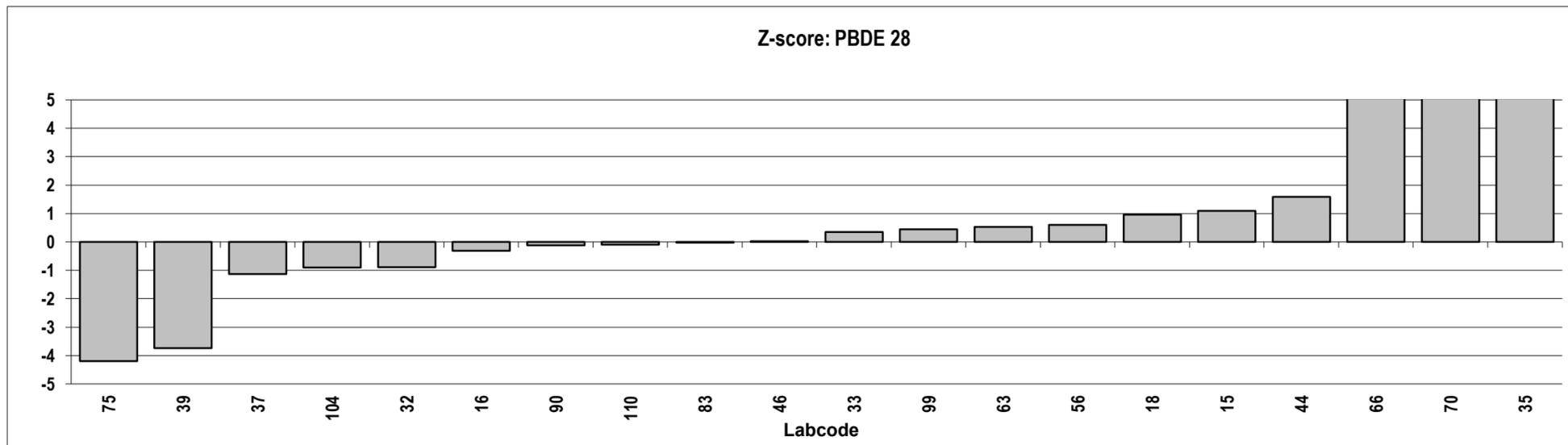
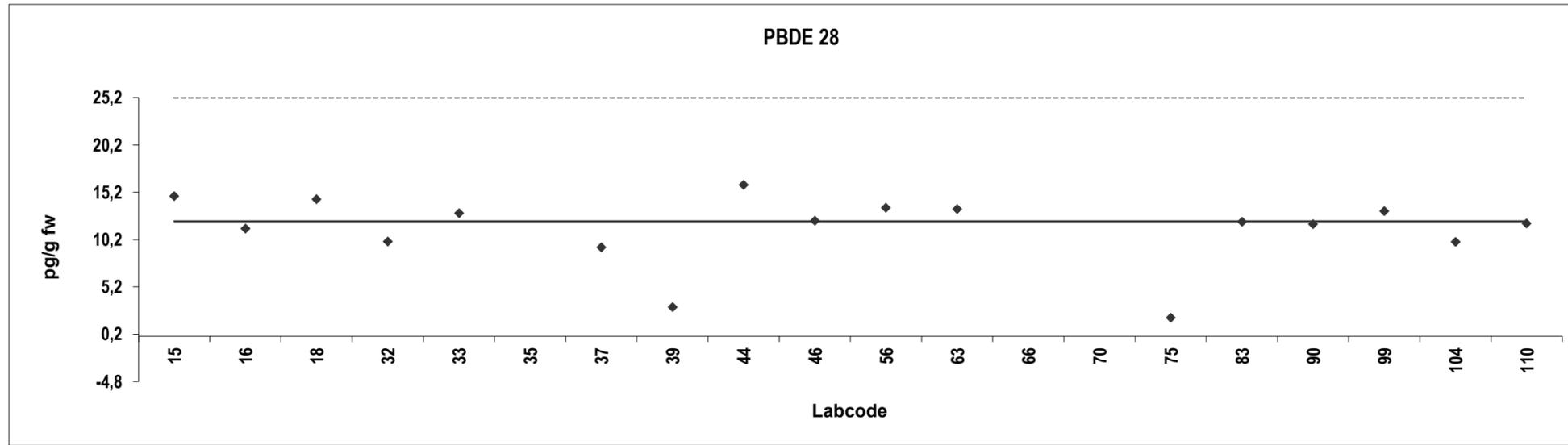


**Mackerel**  
Congener: PBDE 28

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	15	1,1					
16	11	-0,31					
18	15	0,97					
32	10	-0,89					
33	13	0,35					
35	35	9,4	Outlier,ND				
37	9,4	-1,1					
39	3,1	-3,7					
44	16	1,6					
46	12	0,027					
56	14	0,60					
63	13	0,53					
66	28	6,6	Outlier				
70	35	9,2	Outlier				
75	2,0	-4,2	ND				
83	12	-0,027					
90	12	-0,12					
99	13	0,44					
104	10,0	-0,90					
110	12	-0,10					

**Consensus statistics**

Consensus median, pg/g	12
Median all values pg/g	13
Consensus mean, pg/g	11
Standard deviation, pg/g	3,8
Relative standard deviation, %	33
No. of values reported	20
No. of values removed	3
No. of reported non-detects	2

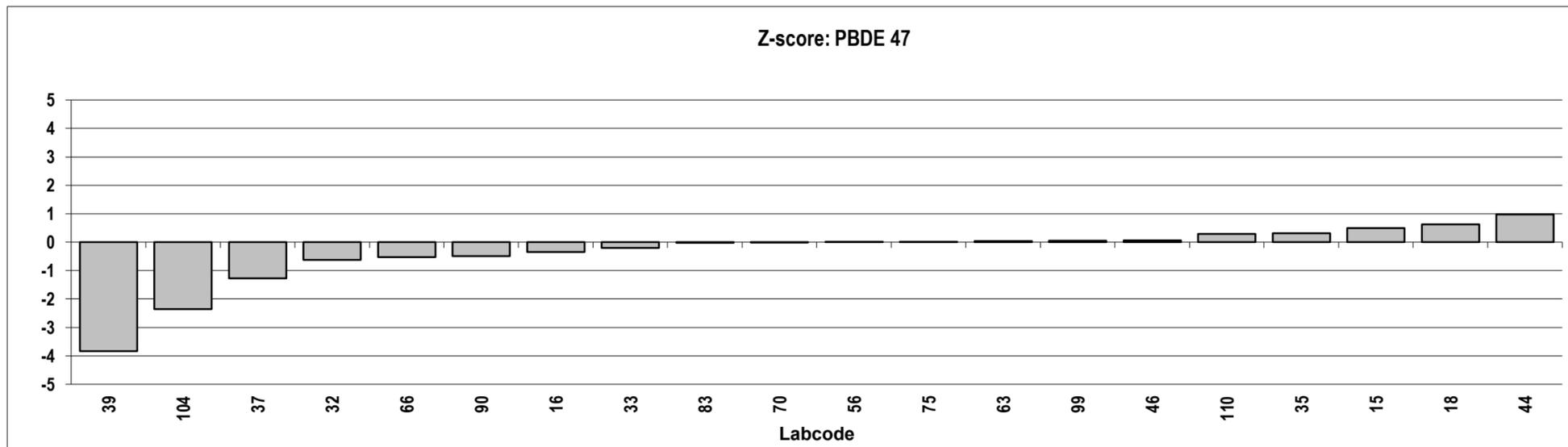
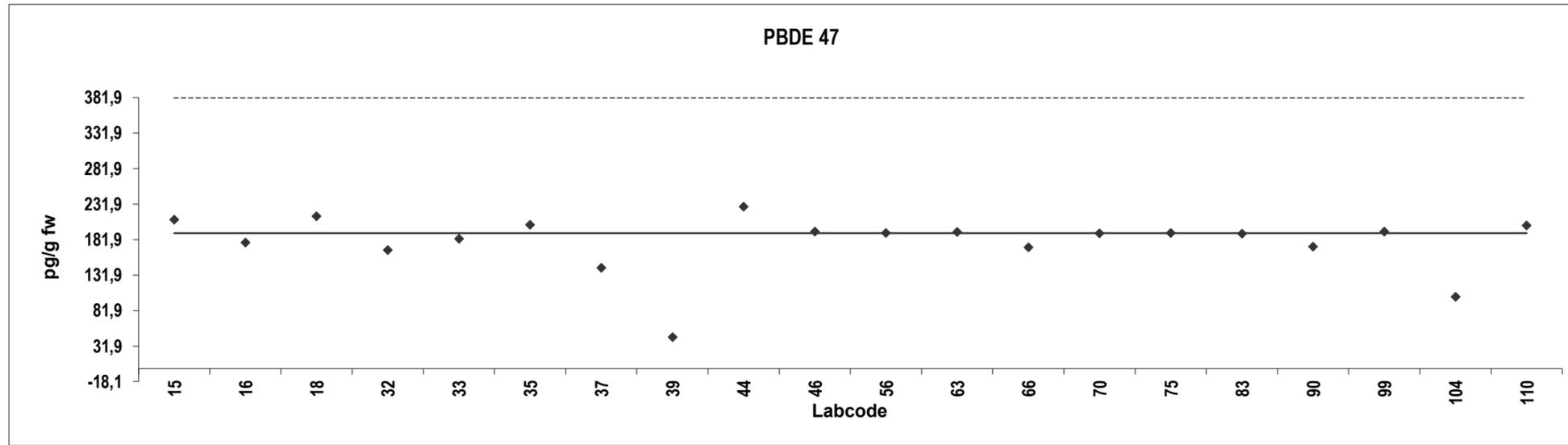


**Mackerel**  
Congener: PBDE 47

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	210	0,50					
16	178	-0,35					
18	215	0,63					
32	167	-0,63					
33	183	-0,21					
35	203	0,31					
37	142	-1,3					
39	45	-3,8					
44	228	0,97					
46	193	0,058					
56	191	0,0011					
63	193	0,042					
66	171	-0,52					
70	191	-0,0011					
75	191	0,010					
83	190	-0,023					
90	172	-0,50					
99	193	0,055					
104	101	-2,4					
110	202	0,29					

**Consensus statistics**

Consensus median, pg/g	191
Median all values pg/g	191
Consensus mean, pg/g	178
Standard deviation, pg/g	41
Relative standard deviation, %	23
No. of values reported	20
No. of values removed	0
No. of reported non-detects	0

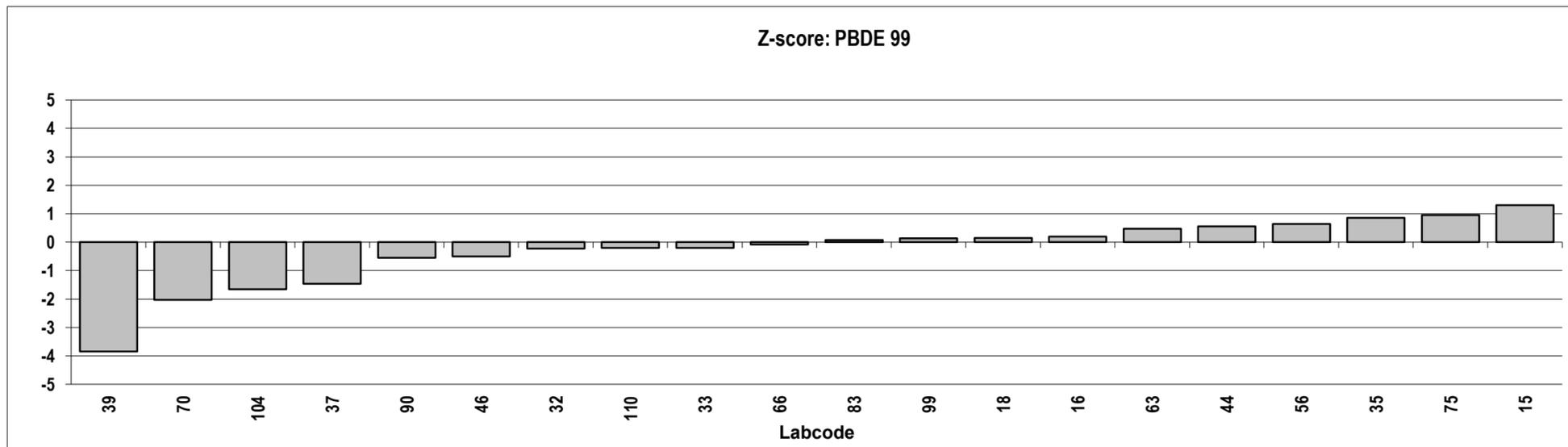
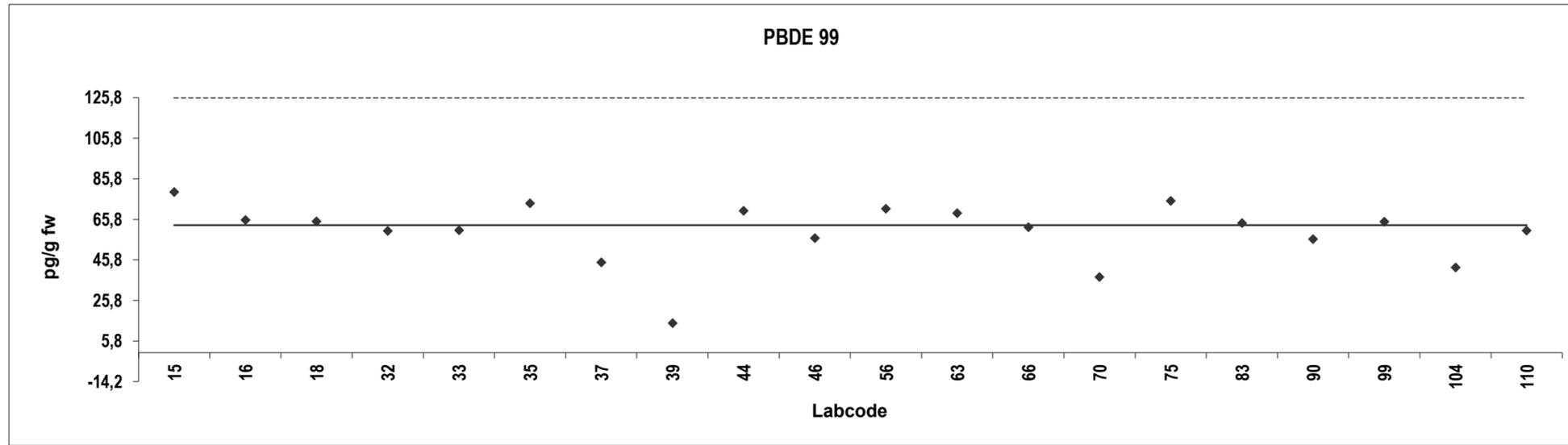


**Mackerel**  
Congener: PBDE 99

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	79	1,3					
16	65	0,20					
18	65	0,14					
32	60	-0,23					
33	60	-0,20					
35	74	0,86					
37	45	-1,5					
39	15	-3,8					
44	70	0,56					
46	57	-0,50					
56	71	0,64					
63	69	0,47					
66	62	-0,079					
70	37	-2,0					
75	75	0,95					
83	64	0,079					
90	56	-0,55					
99	65	0,13					
104	42	-1,7					
110	60	-0,21					

**Consensus statistics**

Consensus median, pg/g	63
Median all values pg/g	63
Consensus mean, pg/g	59
Standard deviation, pg/g	15
Relative standard deviation, %	25
No. of values reported	20
No. of values removed	0
No. of reported non-detects	0

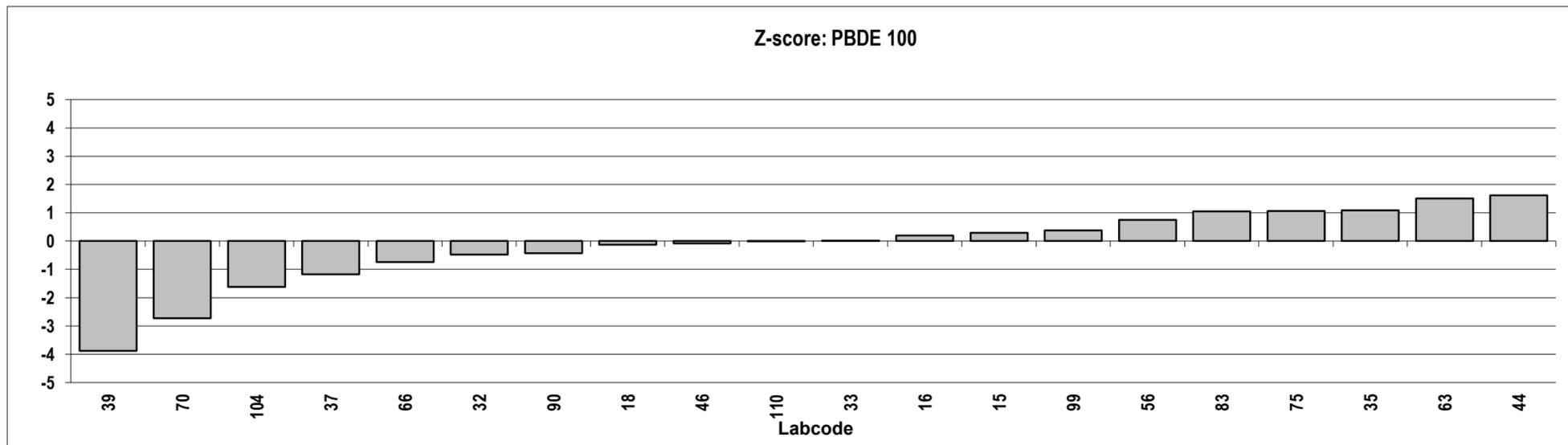
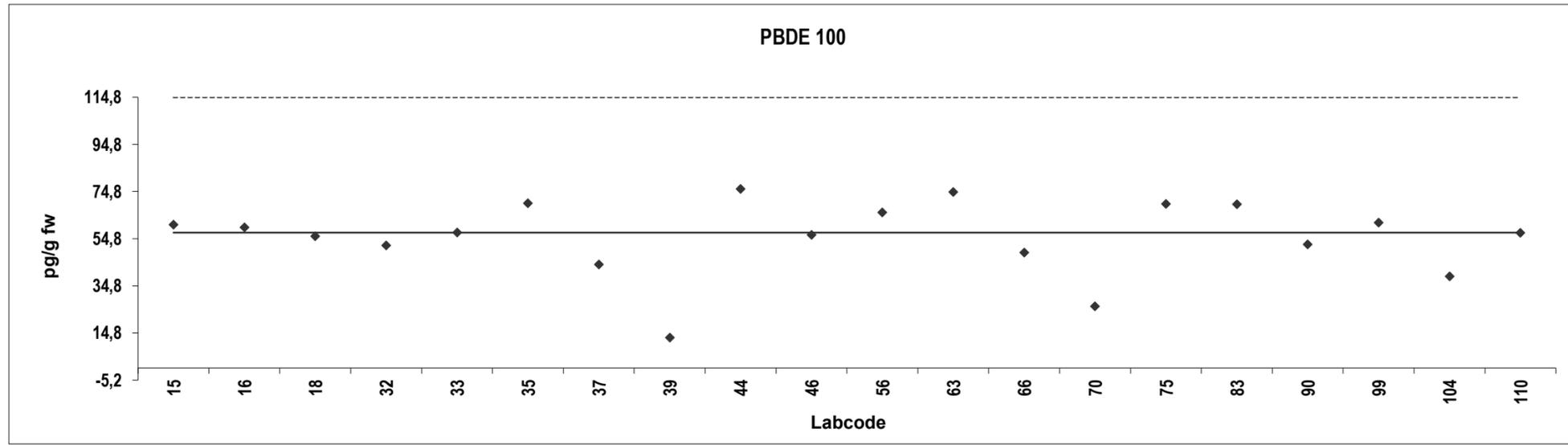


**Mackerel**  
Congener: PBDE 100

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	61	0,29					
16	60	0,19					
18	56	-0,13					
32	52	-0,47					
33	58	0,0074					
35	70	1,1					
37	44	-1,2					
39	13	-3,9					
44	76	1,6					
46	56	-0,083					
56	66	0,75					
63	75	1,5					
66	49	-0,74					
70	26	-2,7					
75	70	1,1					
83	69	1,0					
90	52	-0,43					
99	62	0,37					
104	39	-1,6					
110	57	-0,0074					

**Consensus statistics**

Consensus median, pg/g	57
Median all values pg/g	57
Consensus mean, pg/g	55
Standard deviation, pg/g	16
Relative standard deviation, %	28
No. of values reported	20
No. of values removed	0
No. of reported non-detects	0

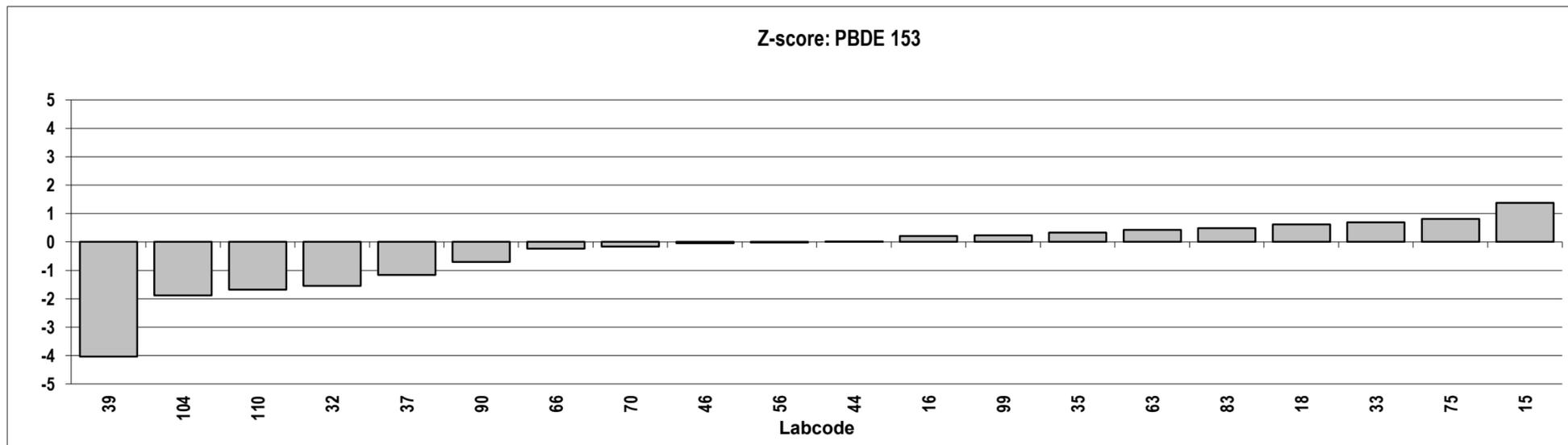
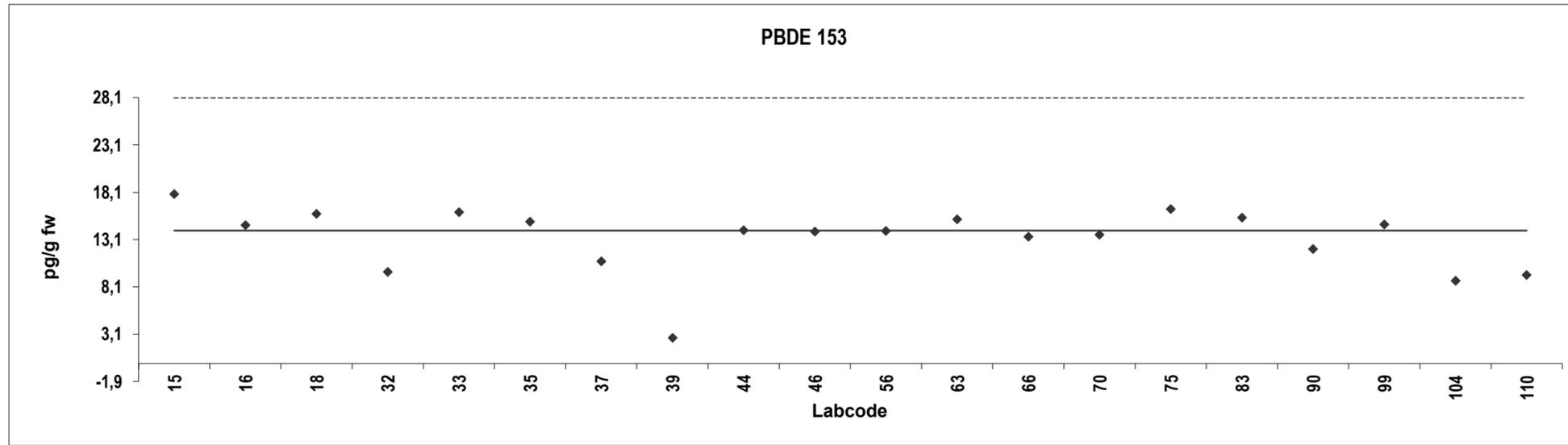


**Mackerel**  
Congener: PBDE 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	18	1,4					
16	15	0,21					
18	16	0,62					
32	9,7	-1,5					
33	16	0,69					
35	15	0,33					
37	11	-1,2					
39	2,7	-4,0					
44	14	0,018					
46	14	-0,041					
56	14	-0,018					
63	15	0,42					
66	13	-0,23					
70	14	-0,16					
75	16	0,81					
83	15	0,48					
90	12	-0,70					
99	15	0,23					
104	8,8	-1,9					
110	9,4	-1,7					

**Consensus statistics**

Consensus median, pg/g	14
Median all values pg/g	14
Consensus mean, pg/g	13
Standard deviation, pg/g	3,5
Relative standard deviation, %	26
No. of values reported	20
No. of values removed	0
No. of reported non-detects	0

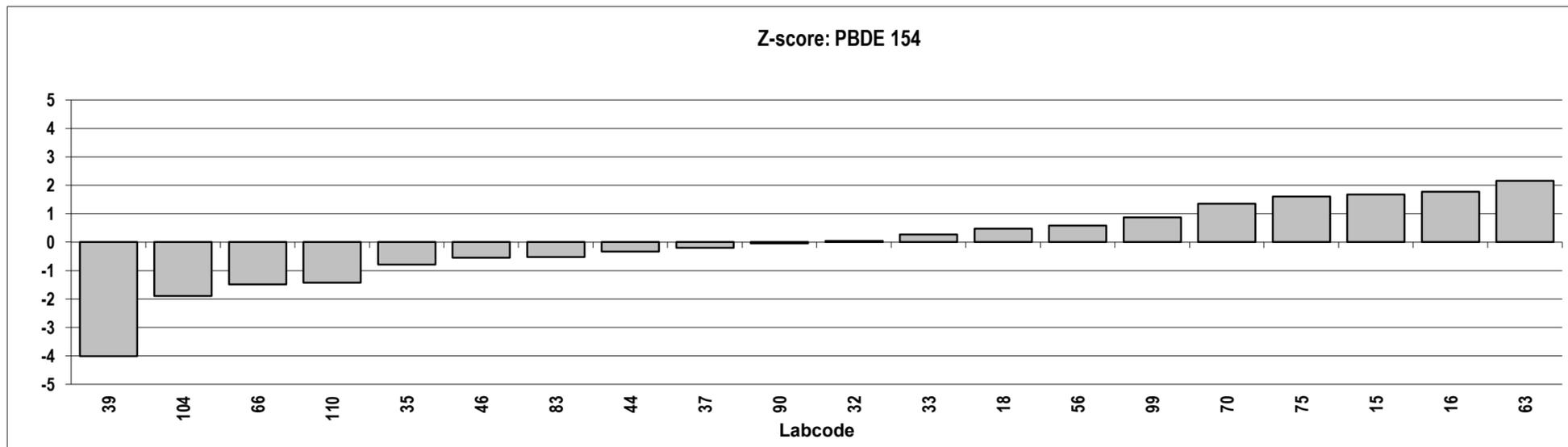
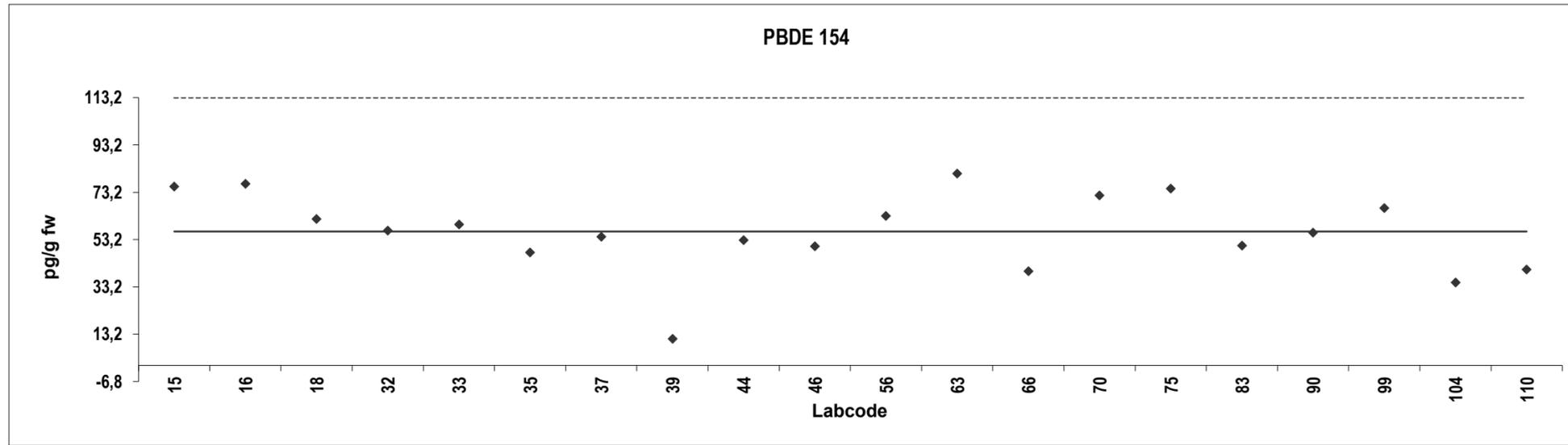


**Mackerel**  
Congener: PBDE 154

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	76	1,7					
16	77	1,8					
18	62	0,47					
32	57	0,037					
33	60	0,27					
35	48	-0,79					
37	54	-0,20					
39	11	-4,0					
44	53	-0,33					
46	50	-0,55					
56	63	0,58					
63	81	2,2					
66	40	-1,5					
70	72	1,3					
75	75	1,6					
83	51	-0,53					
90	56	-0,037					
99	66	0,87					
104	35	-1,9					
110	40	-1,4					

**Consensus statistics**

Consensus median, pg/g	57
Median all values pg/g	57
Consensus mean, pg/g	56
Standard deviation, pg/g	17
Relative standard deviation, %	30
No. of values reported	20
No. of values removed	0
No. of reported non-detects	0

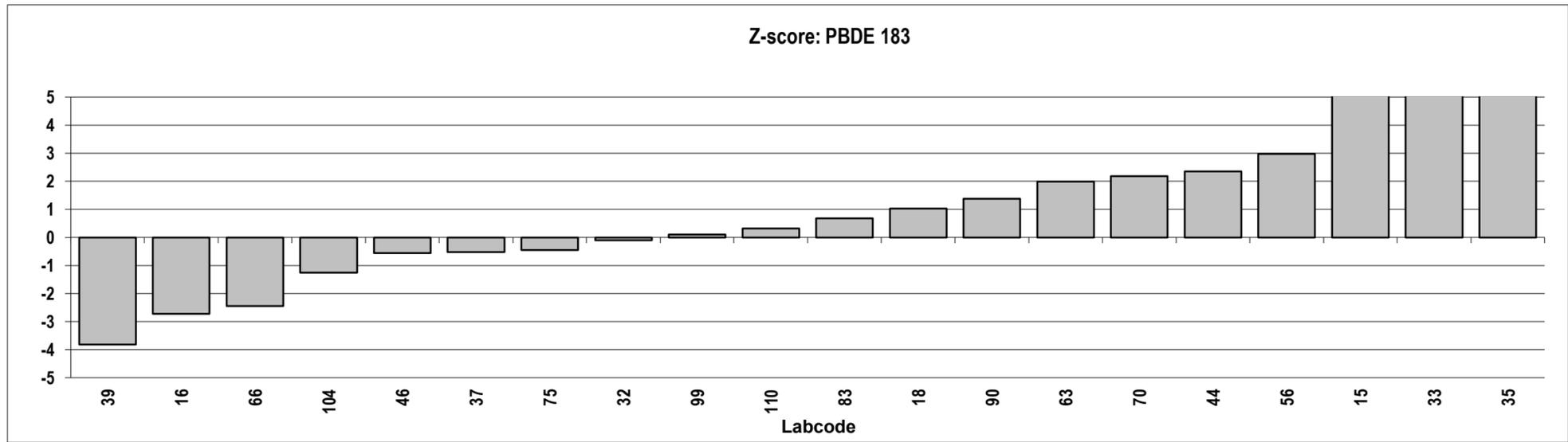
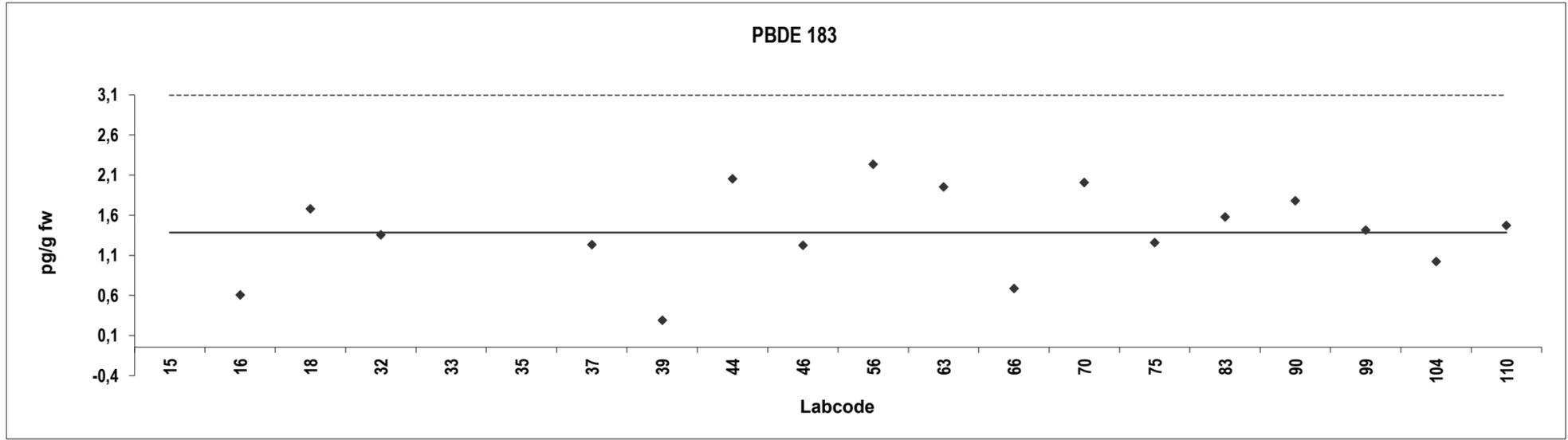


**Mackerel**  
Congener: PBDE 183

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	3,4	6,7	Outlier				
16	0,65	-2,7					
18	1,7	1,0	ND				
32	1,4	-0,10					
33	10	30	Outlier,ND				
35	10	30	Outlier,ND				
37	1,3	-0,52					
39	0,34	-3,8					
44	2,1	2,3					
46	1,3	-0,56					
56	2,3	3,0					
63	2,0	2,0					
66	0,73	-2,4					
70	2,1	2,2					
75	1,3	-0,44					
83	1,6	0,69					
90	1,8	1,4					
99	1,5	0,10					
104	1,1	-1,3					
110	1,5	0,32					

**Consensus statistics**

Consensus median, pg/g	1,4
Median all values pg/g	1,6
Consensus mean, pg/g	1,4
Standard deviation, pg/g	0,54
Relative standard deviation, %	37
No. of values reported	20
No. of values removed	3
No. of reported non-detects	3

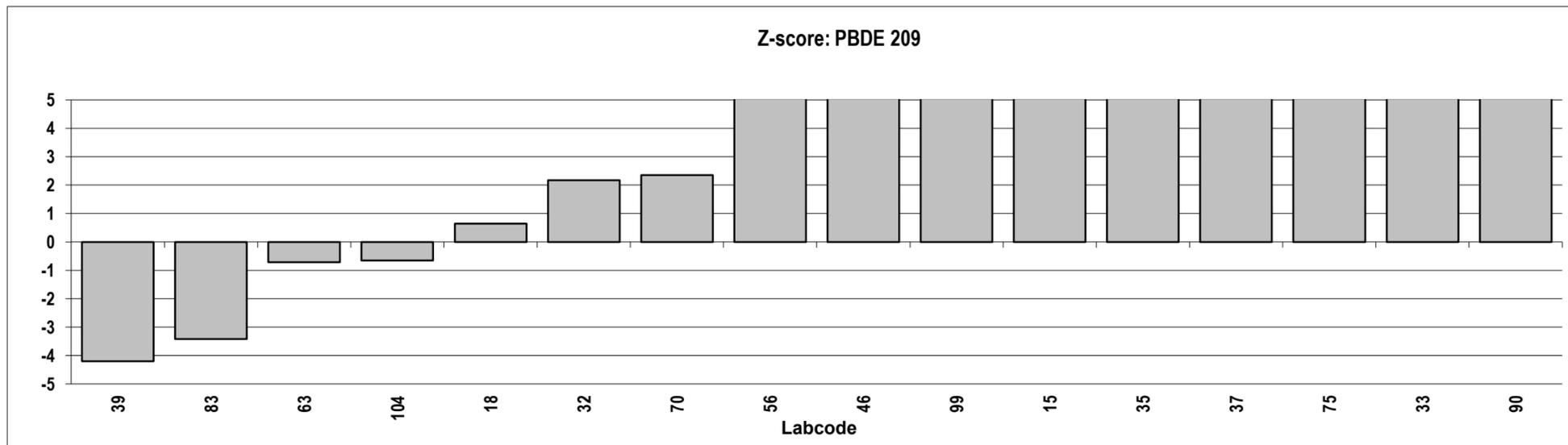
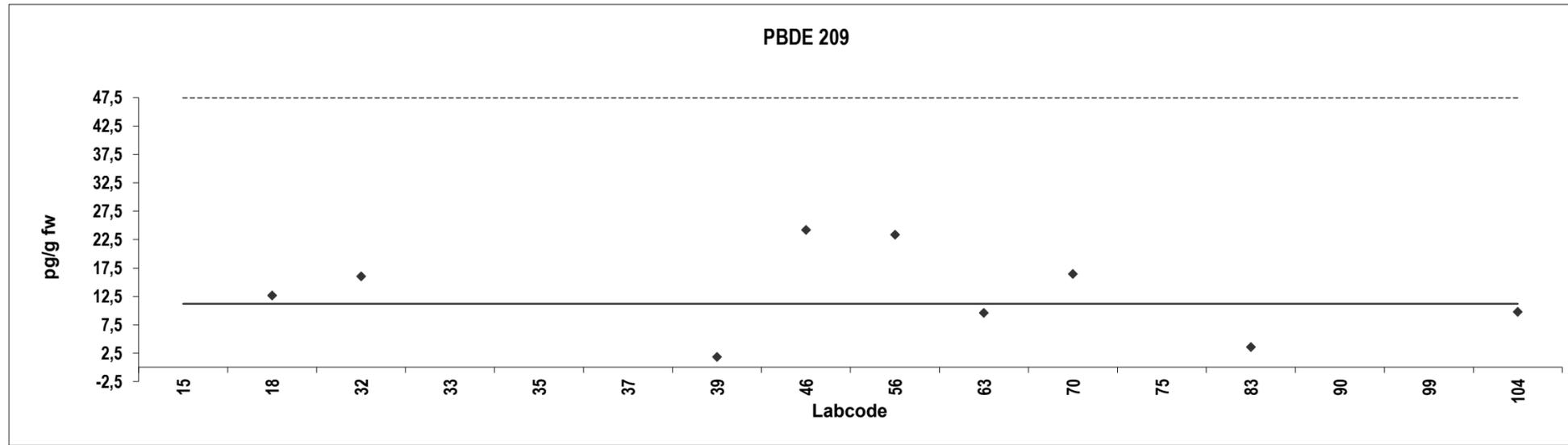


**Mackerel**  
Congener: PBDE 209

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
15	93	37	Outlier				
18	13	0,65					
32	16	2,2	ND				
33	199	84	Outlier,ND				
35	100	40	Outlier,ND				
37	120	49	Outlier,ND				
39	1,8	-4,2					
46	24	5,8					
56	23	5,4					
63	9,6	-0,72					
70	16	2,4					
75	195	82	Outlier				
83	3,5	-3,4					
90	226	96	Outlier				
99	89	35	Outlier,ND				
104	9,7	-0,65					

**Consensus statistics**

Consensus median, pg/g	11
Median all values pg/g	24
Consensus mean, pg/g	13
Standard deviation, pg/g	7,8
Relative standard deviation, %	60
No. of values reported	16
No. of values removed	7
No. of reported non-detects	5

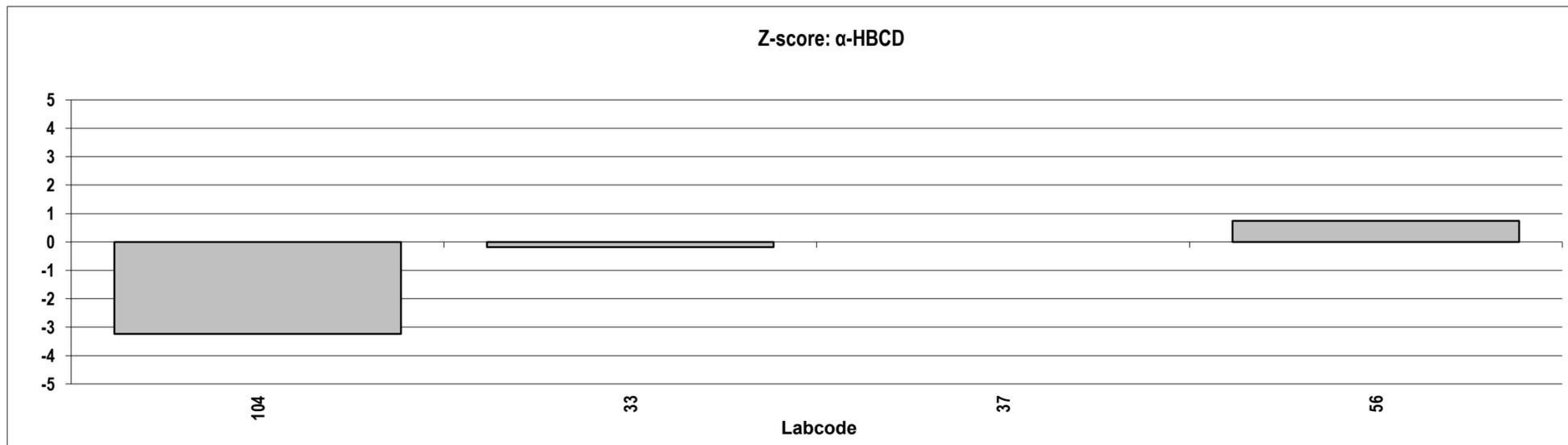
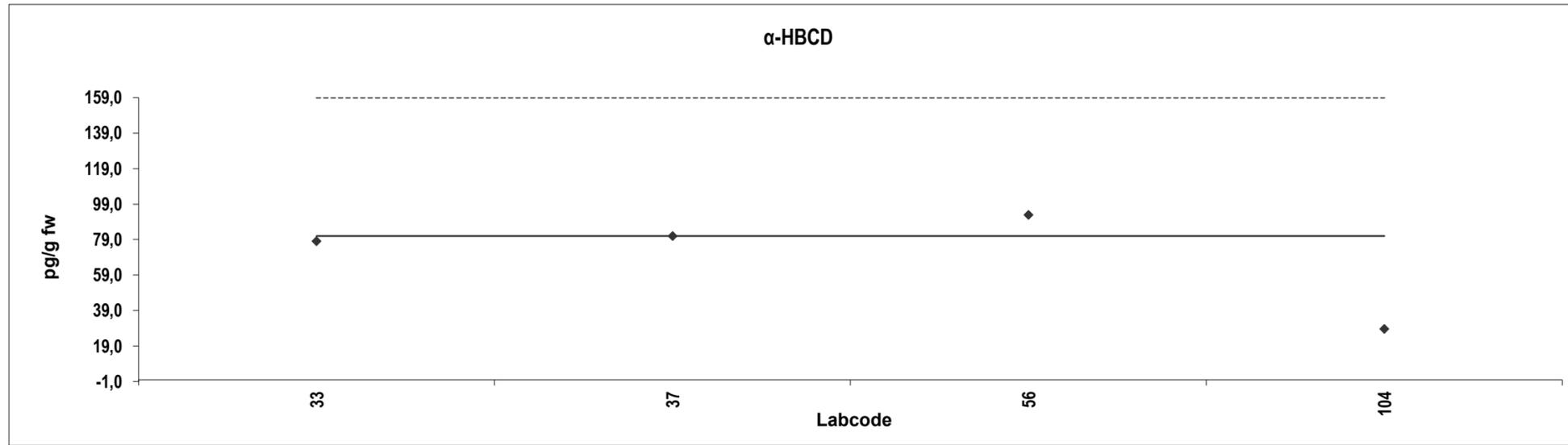


**Mackerel**  
Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
33	78	-0,19					
37	81	0,00000					
56	93	0,74					
104	29	-3,2	ND				

**Consensus statistics**

Consensus median, pg/g	81
Median all values pg/g	80
Consensus mean, pg/g	70
Standard deviation, pg/g	28
Relative standard deviation, %	41
No. of values reported	4
No. of values removed	0
No. of reported non-detects	1

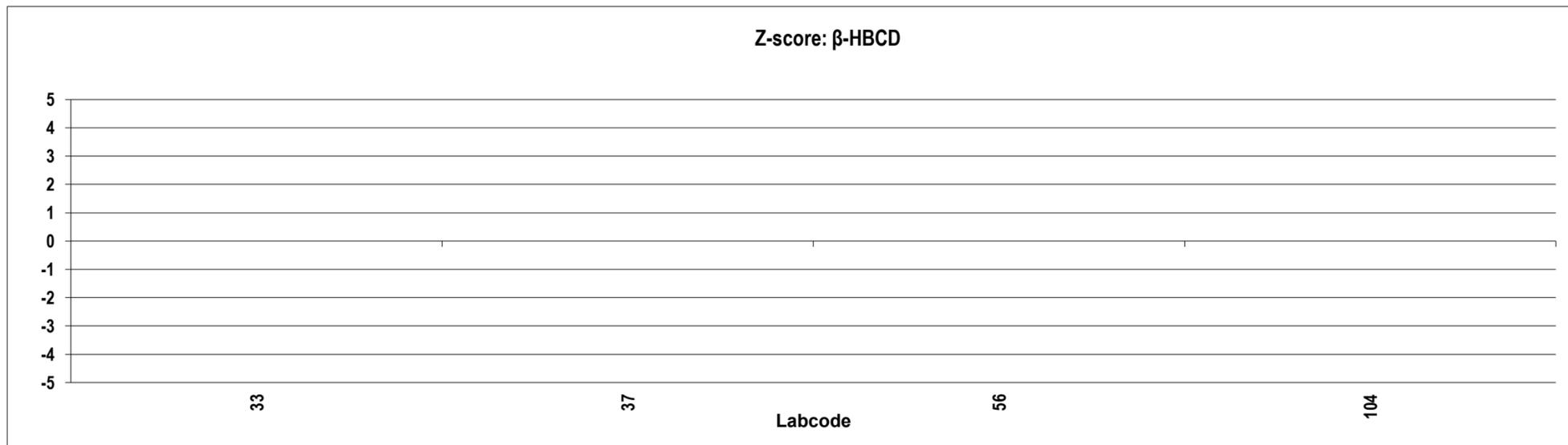
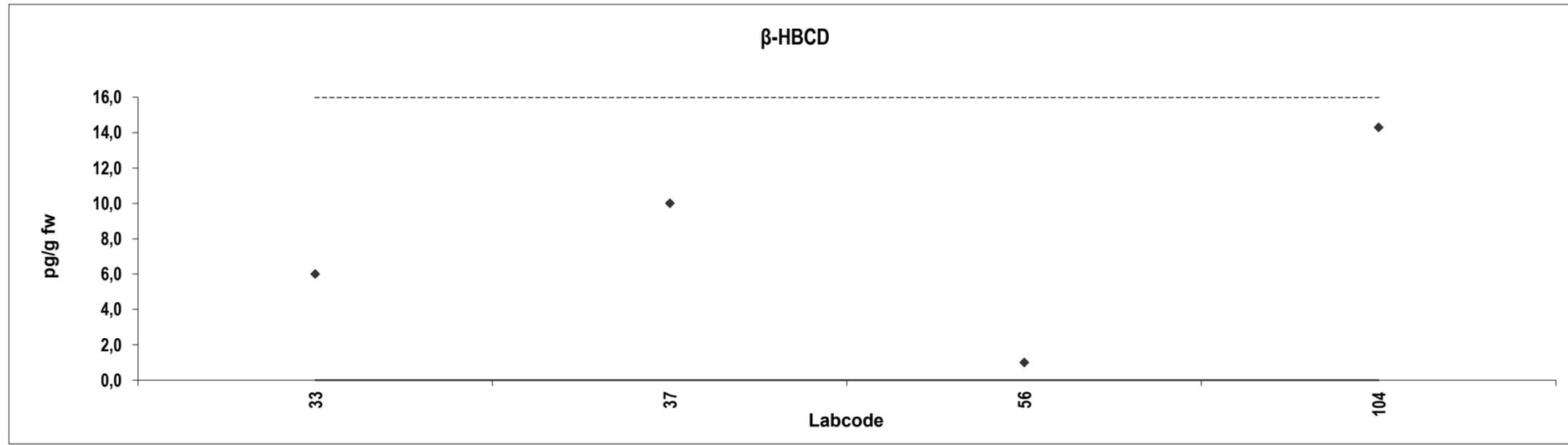


**Mackerel**  
Congener:  $\beta$ -HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
33	6,0	**	ND				
37	10	**	ND				
56	1,0	**	ND				
104	14	**	ND				

**Consensus statistics**

Consensus median, pg/g	**
Median all values pg/g	8,0
Consensus mean, pg/g	7,8
Standard deviation, pg/g	5,7
Relative standard deviation, %	73
No. of values reported	4
No. of values removed	0
No. of reported non-detects	4

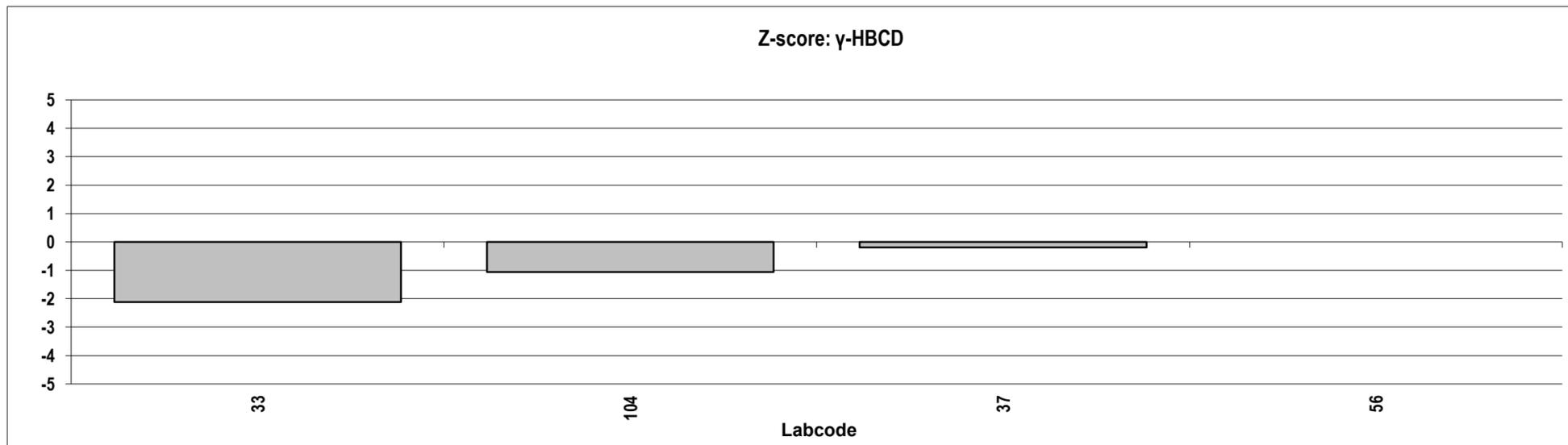
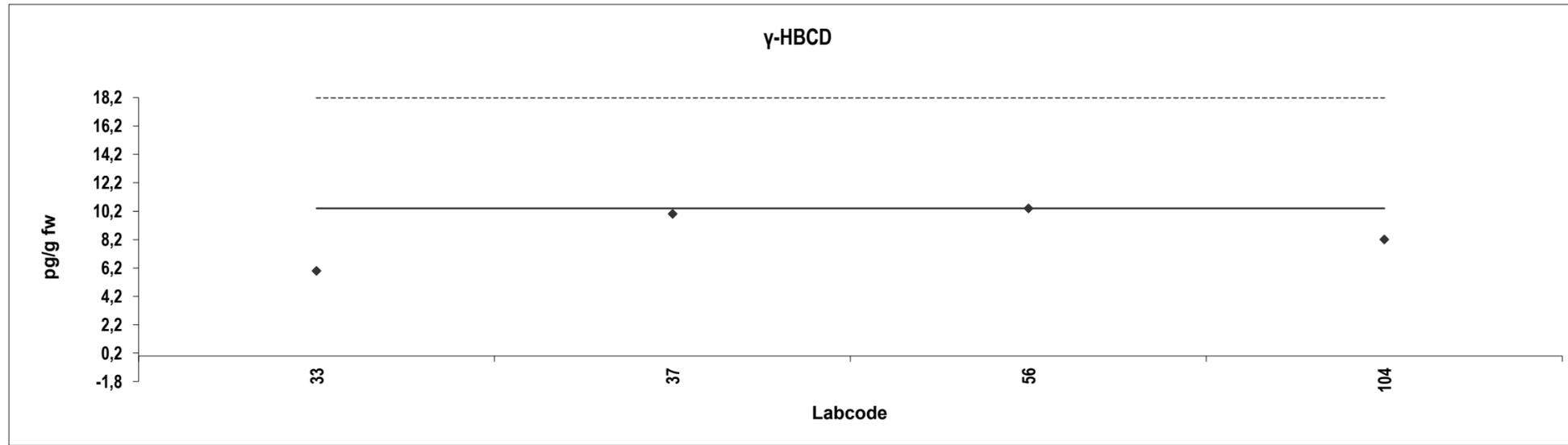


**Mackerel**  
Congener:  $\gamma$ -HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
33	6,0	-2,1	ND				
37	10	-0,19	ND				
56	10	0,00000					
104	8,2	-1,1	ND				

**Consensus statistics**

Consensus median, pg/g	10
Median all values pg/g	9,1
Consensus mean, pg/g	8,7
Standard deviation, pg/g	2,0
Relative standard deviation, %	23
No. of values reported	4
No. of values removed	0
No. of reported non-detects	3

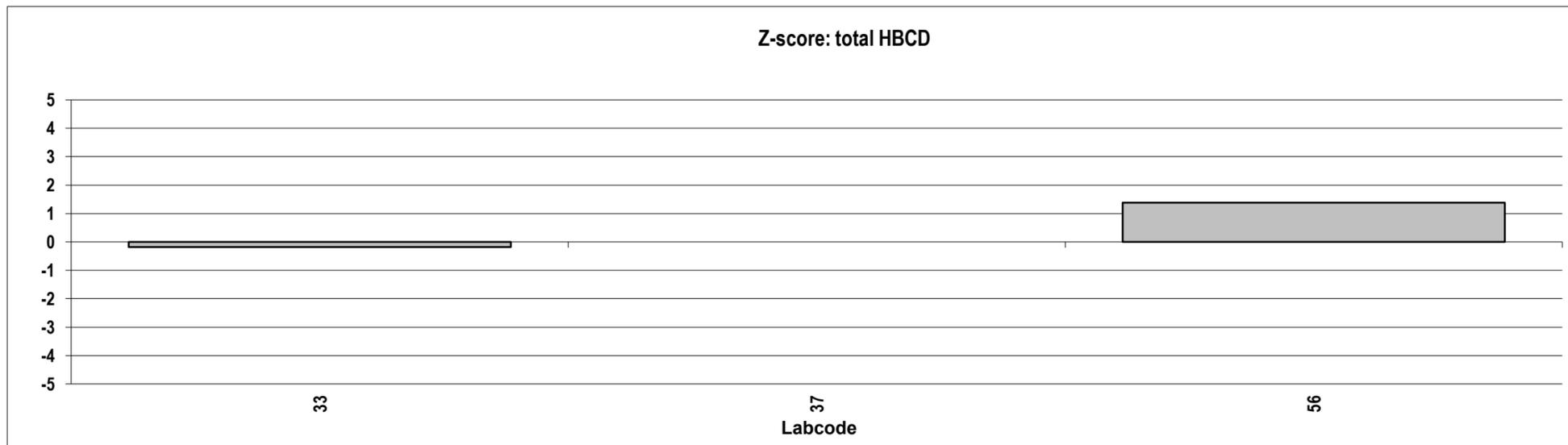
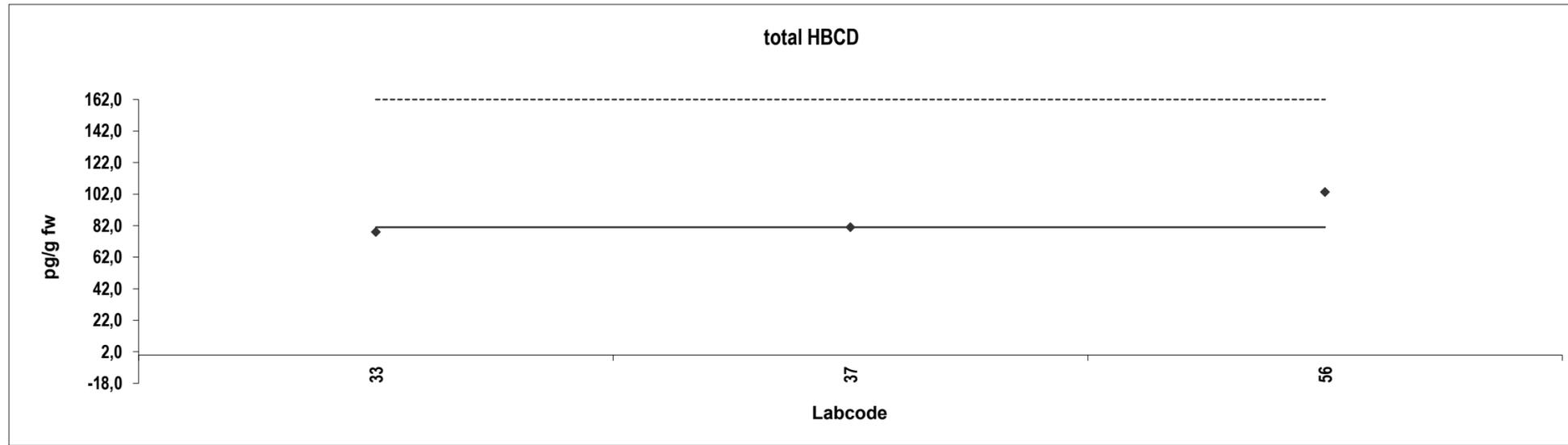


**Mackerel**  
Congener: total HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Z-score	Notes
33	78	-0,19					
37	81	0,00000					
56	103	1,4					

**Consensus statistics**

Consensus median, pg/g	81
Median all values pg/g	81
Consensus mean, pg/g	87
Standard deviation, pg/g	14
Relative standard deviation, %	16
No. of values reported	3
No. of values removed	0
No. of reported non-detects	0





## **Appendix 3:**



Presentation of results for  
Cream 2024



## Appendix 3: Presentation of results: Cream 2024

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

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

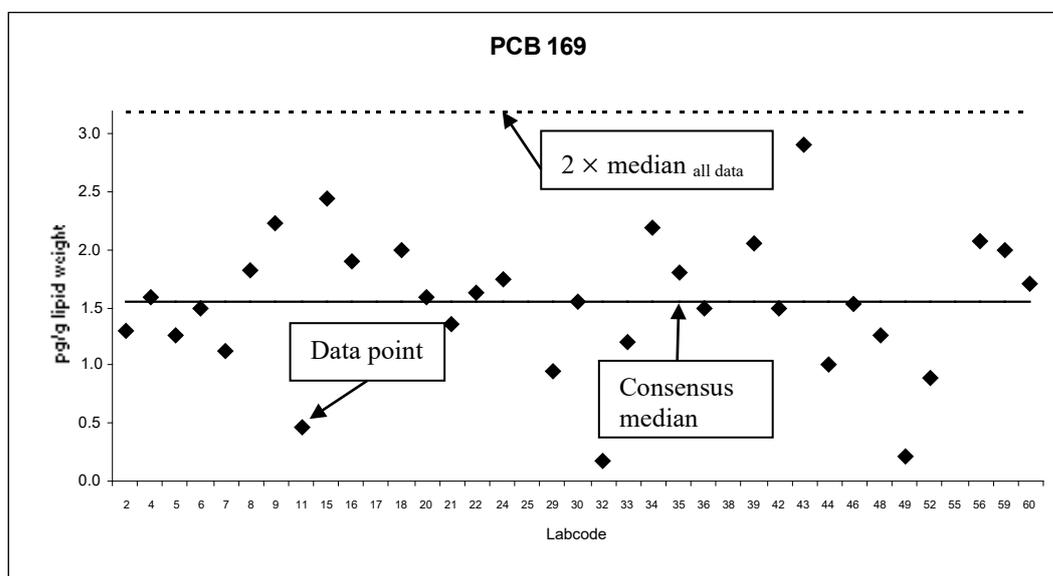
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding  $2 \times$  this median were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

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

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

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

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



### Z-Scores of individual congeners

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

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

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

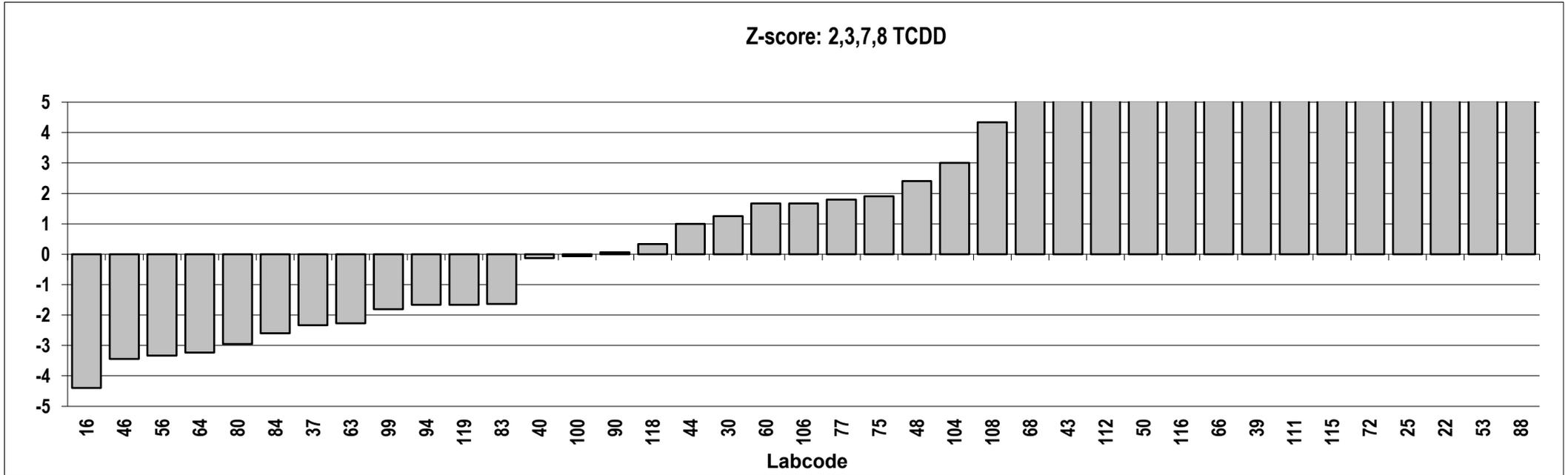
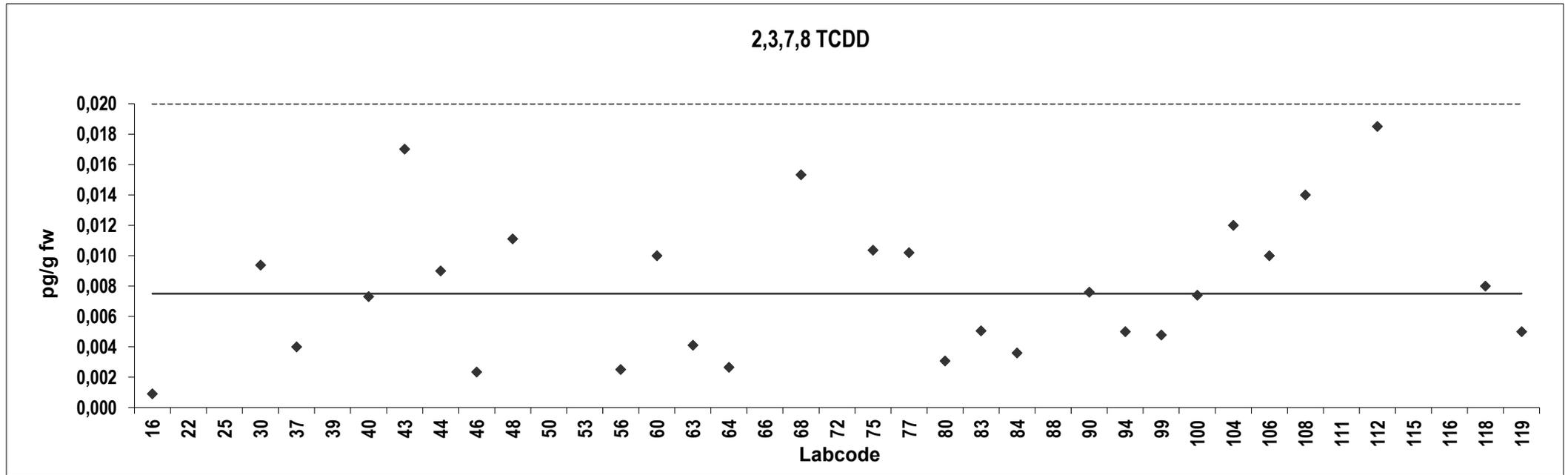


**Cream**  
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00090	-4,4	ND			
22	0,078	47	Outlier			
25	0,050	28	Outlier,ND			
30	0,0094	1,2				
37	0,0040	-2,3				
39	0,035	18	Outlier			
40	0,0073	-0,13	ND			
43	0,017	6,3	ND			
44	0,0090	1,0	ND			
46	0,0023	-3,4				
48	0,011	2,4	ND			
50	0,023	10	Outlier,ND			
53	0,080	48	Outlier,ND			
56	0,0025	-3,3				
60	0,010	1,7	ND			
63	0,0041	-2,3	ND			
64	0,0027	-3,2				
66	0,031	16	Outlier			
68	0,015	5,2	ND			
72	0,048	27	Outlier,ND			
75	0,010	1,9	ND			
77	0,010	1,8				
80	0,0031	-3,0				
83	0,0050	-1,6				
84	0,0036	-2,6				
88	0,17	108	Outlier,ND			
90	0,0076	0,066				
94	0,0050	-1,7	ND			
99	0,0048	-1,8	ND			
100	0,0074	-0,066				
104	0,012	3,0				
106	0,010	1,7				
108	0,014	4,3				
111	0,040	22	Outlier,ND			
112	0,019	7,3				
115	0,040	22	Outlier,ND			
116	0,024	11	Outlier			
118	0,0080	0,33	ND			
119	0,0050	-1,7	ND			

**Consensus statistics**

Consensus median, pg/g	0,0075
Median all values pg/g	0,010
Consensus mean, pg/g	0,0079
Standard deviation, pg/g	0,0046
Relative standard deviation, %	59
No. of values reported	39
No. of values removed	11
No. of reported non-detects	20

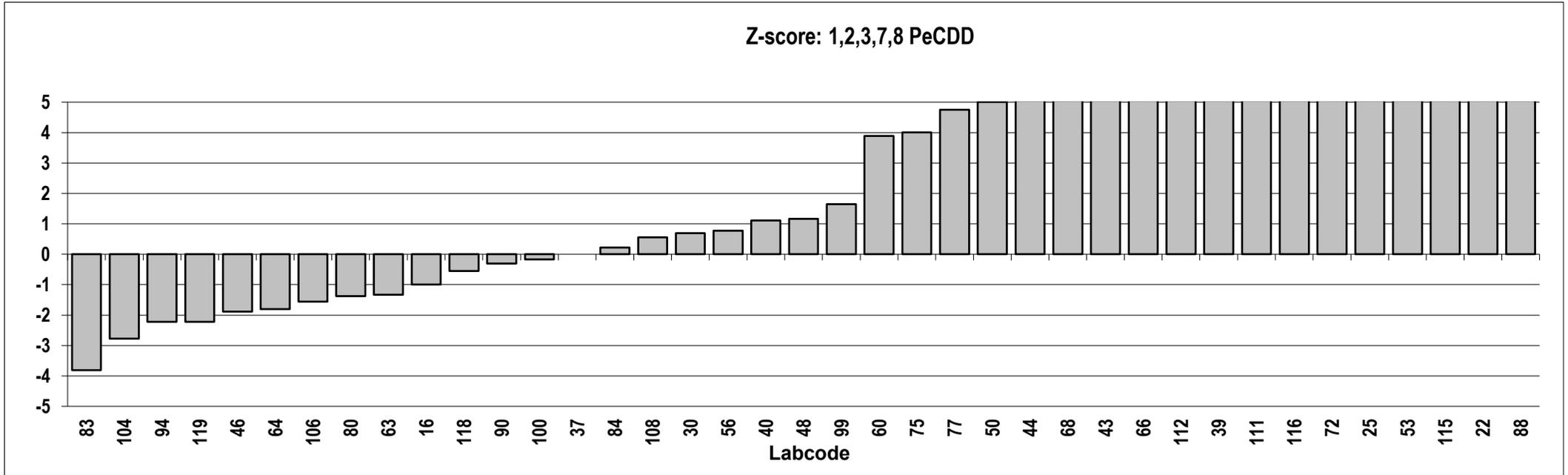
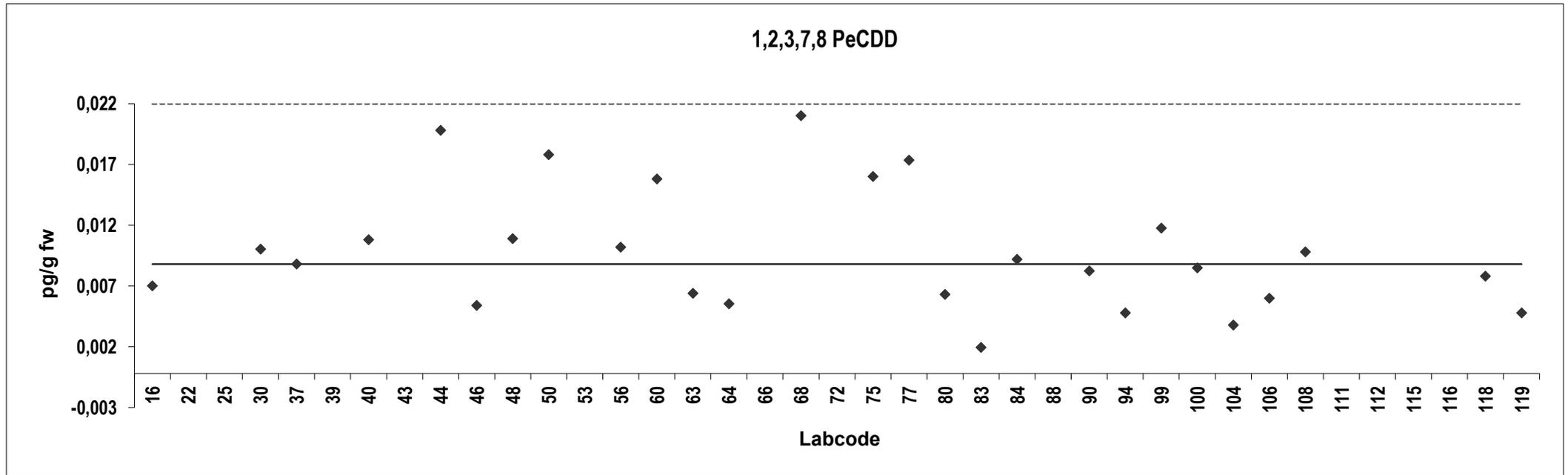


**Cream**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0072	-1,0	ND			
22	0,13	69	Outlier			
25	0,050	23	Outlier,ND			
30	0,010	0,69				
37	0,0090	0,00000				
39	0,040	17	Outlier			
40	0,011	1,1	ND			
43	0,026	9,4	Outlier,ND			
44	0,020	6,1	ND			
46	0,0056	-1,9				
48	0,011	1,2	ND			
50	0,018	5,0	ND			
53	0,080	39	Outlier,ND			
56	0,010	0,78				
60	0,016	3,9	ND			
63	0,0066	-1,3				
64	0,0058	-1,8				
66	0,031	12	Outlier			
68	0,021	6,8	ND			
72	0,048	22	Outlier,ND			
75	0,016	4,0	ND			
77	0,018	4,8				
80	0,0065	-1,4				
83	0,0021	-3,8				
84	0,0094	0,22				
88	0,15	78	Outlier,ND			
90	0,0084	-0,31				
94	0,0050	-2,2	ND			
99	0,012	1,6	ND			
100	0,0087	-0,17	ND			
104	0,0040	-2,8	ND			
106	0,0062	-1,6				
108	0,010	0,56	ND			
111	0,040	17	Outlier,ND			
112	0,032	13	Outlier			
115	0,11	56	Outlier,ND			
116	0,040	17	Outlier			
118	0,0080	-0,56	ND			
119	0,0050	-2,2	ND			

**Consensus statistics**

Consensus median, pg/g	0,0090
Median all values pg/g	0,011
Consensus mean, pg/g	0,010
Standard deviation, pg/g	0,0051
Relative standard deviation, %	50
No. of values reported	39
No. of values removed	12
No. of reported non-detects	22

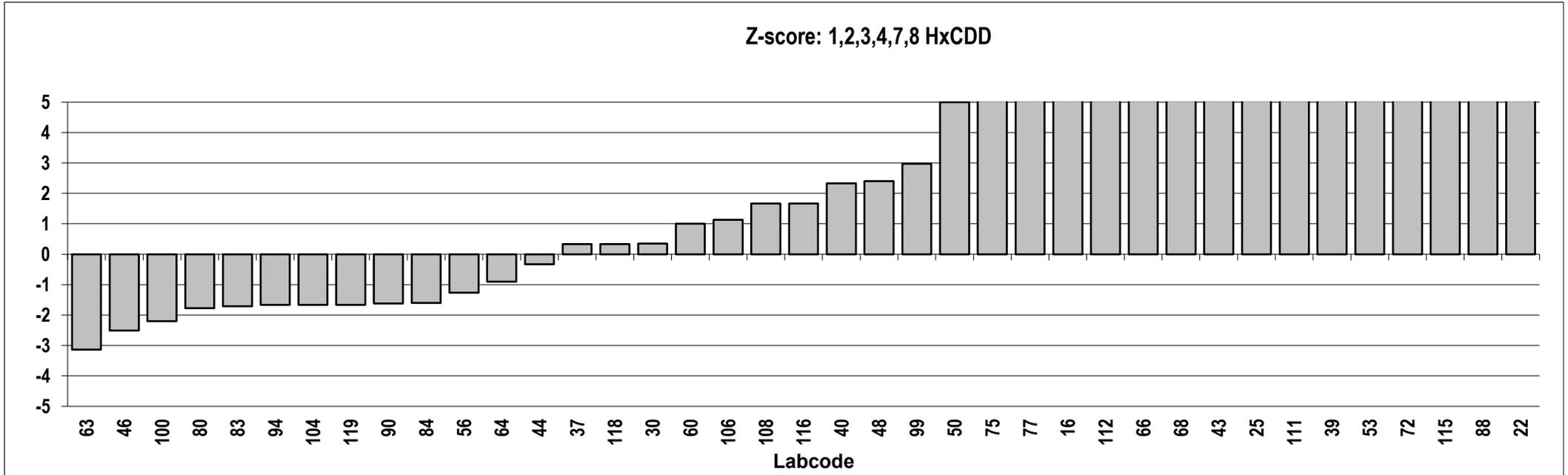
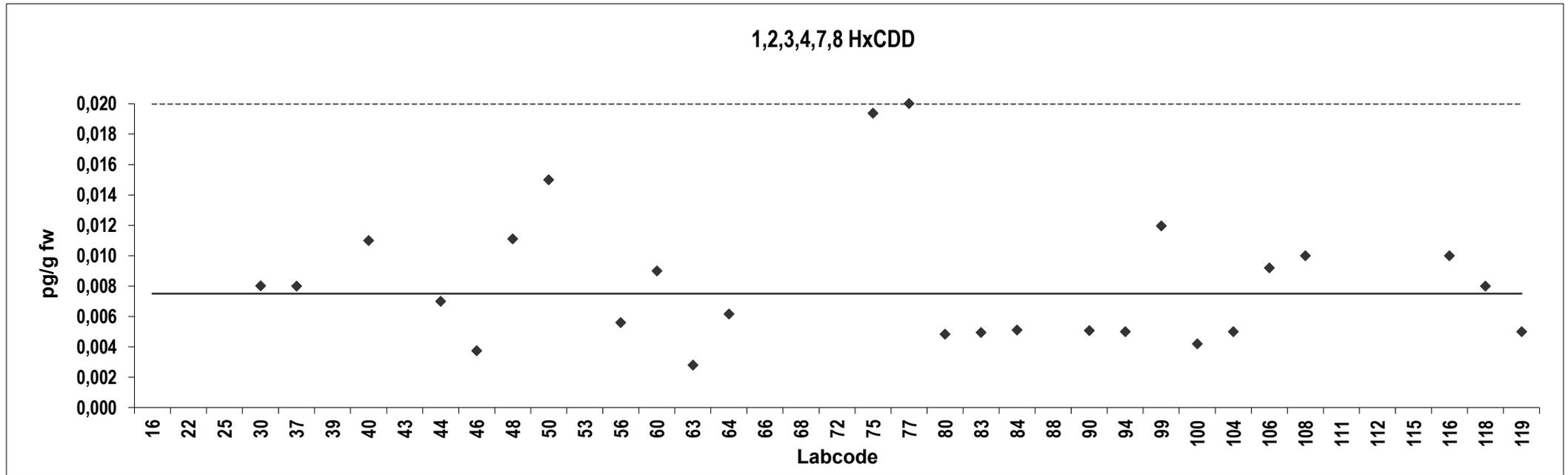


**Cream**  
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,021	8,8	Outlier			
22	0,21	138	Outlier			
25	0,050	28	Outlier,ND			
30	0,0080	0,35				
37	0,0080	0,33				
39	0,068	40	Outlier			
40	0,011	2,3				
43	0,035	18	Outlier,ND			
44	0,0070	-0,33	ND			
46	0,0037	-2,5				
48	0,011	2,4	ND			
50	0,015	5,0	ND			
53	0,080	48	Outlier,ND			
56	0,0056	-1,3				
60	0,0090	1,0	ND			
63	0,0028	-3,1	ND			
64	0,0062	-0,90				
66	0,028	14	Outlier			
68	0,035	18	Outlier,ND			
72	0,092	56	Outlier,ND			
75	0,019	7,9	ND			
77	0,020	8,3	ND			
80	0,0048	-1,8				
83	0,0049	-1,7				
84	0,0051	-1,6				
88	0,14	91	Outlier,ND			
90	0,0051	-1,6				
94	0,0050	-1,7	ND			
99	0,012	3,0	ND			
100	0,0042	-2,2	ND			
104	0,0050	-1,7	ND			
106	0,0092	1,1				
108	0,010	1,7	ND			
111	0,050	28	Outlier,ND			
112	0,027	13	Outlier			
115	0,11	70	Outlier,ND			
116	0,010	1,7				
118	0,0080	0,33	ND			
119	0,0050	-1,7	ND			

**Consensus statistics**

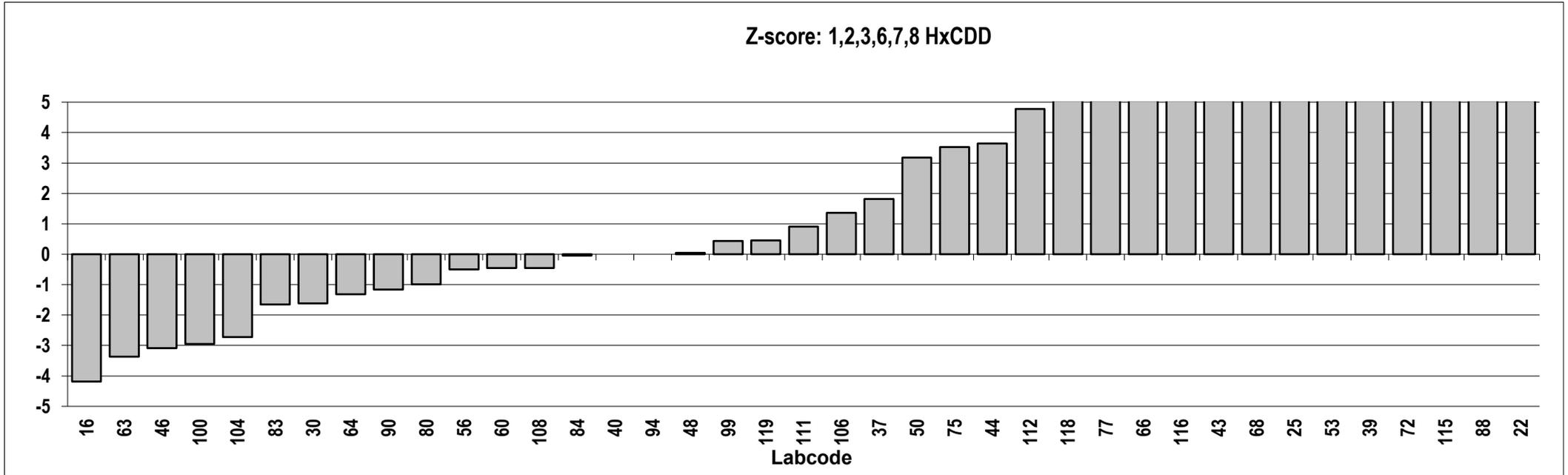
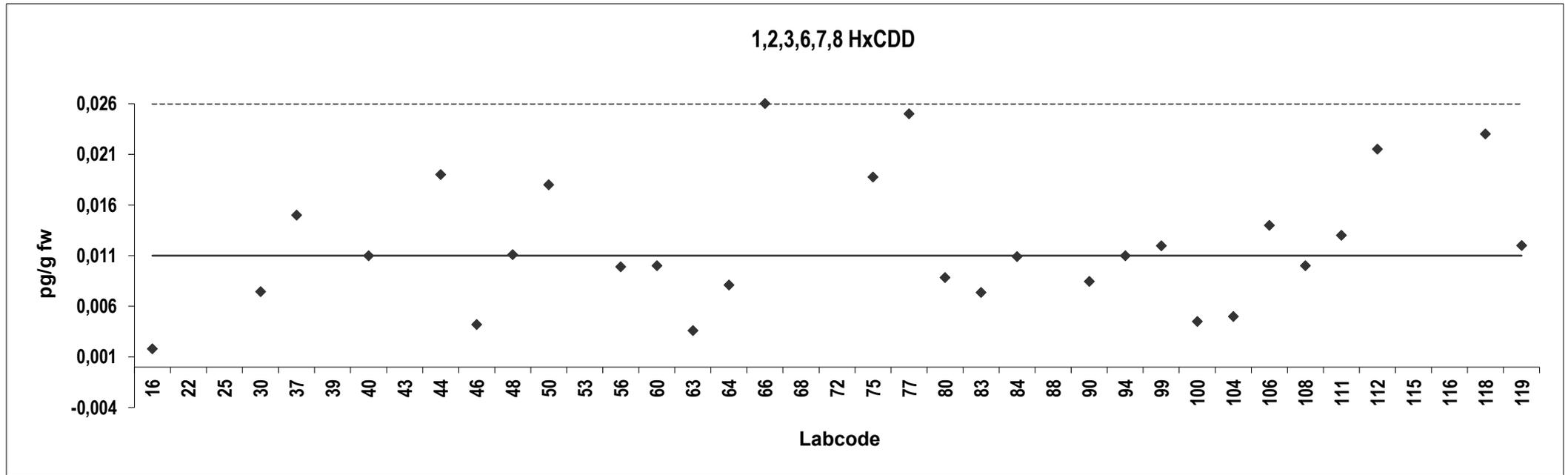
Consensus median, pg/g	0,0075
Median all values pg/g	0,010
Consensus mean, pg/g	0,0083
Standard deviation, pg/g	0,0045
Relative standard deviation, %	54
No. of values reported	39
No. of values removed	13
No. of reported non-detects	22



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0018	-4,2				
22	0,19	80	Outlier			
25	0,060	22	Outlier			
30	0,0074	-1,6				
37	0,015	1,8				
39	0,087	35	Outlier			
40	0,011	0,00000				
43	0,035	11	Outlier,ND			
44	0,019	3,6				
46	0,0042	-3,1				
48	0,011	0,045	ND			
50	0,018	3,2				
53	0,080	31	Outlier,ND			
56	0,0099	-0,50				
60	0,010	-0,45				
63	0,0036	-3,4				
64	0,0081	-1,3				
66	0,026	6,8				
68	0,038	12	Outlier,ND			
72	0,092	37	Outlier,ND			
75	0,019	3,5	ND			
77	0,025	6,4				
80	0,0088	-1,0				
83	0,0074	-1,7				
84	0,011	-0,045				
88	0,15	62	Outlier,ND			
90	0,0084	-1,2				
94	0,011	0,00000				
99	0,012	0,44	ND			
100	0,0045	-3,0	ND			
104	0,0050	-2,7	ND			
106	0,014	1,4				
108	0,010	-0,45				
111	0,013	0,91				
112	0,022	4,8				
115	0,099	40	Outlier,ND			
116	0,030	8,6	Outlier			
118	0,023	5,5				
119	0,012	0,45				

Consensus statistics	
Consensus median, pg/g	0,011
Median all values pg/g	0,013
Consensus mean, pg/g	0,012
Standard deviation, pg/g	0,0064
Relative standard deviation, %	53
No. of values reported	39
No. of values removed	10
No. of reported non-detects	11

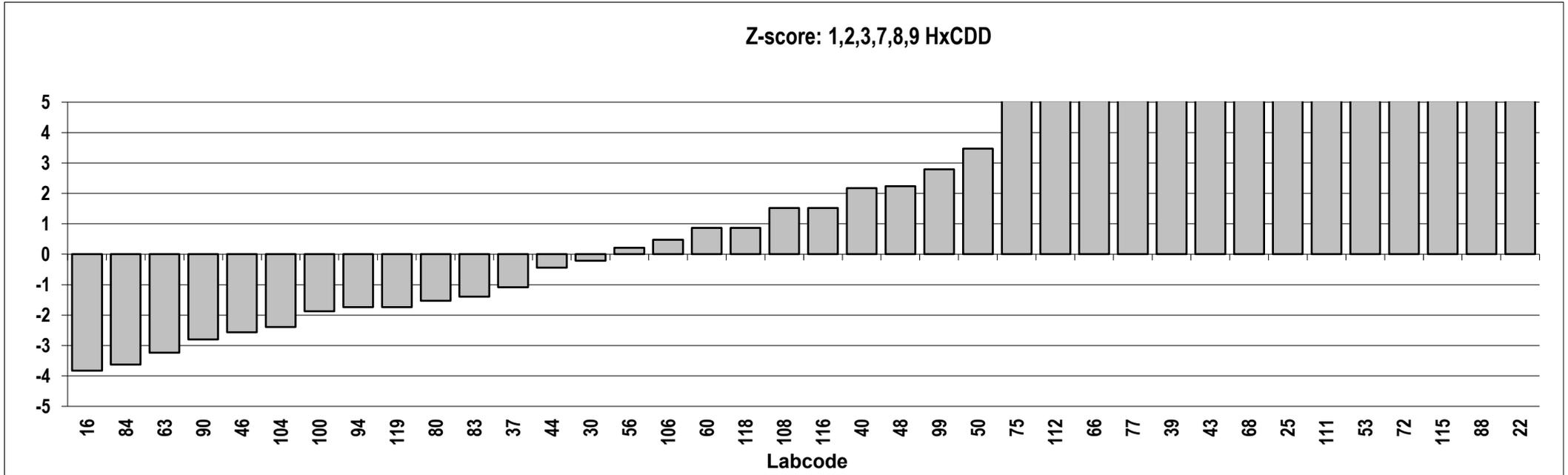
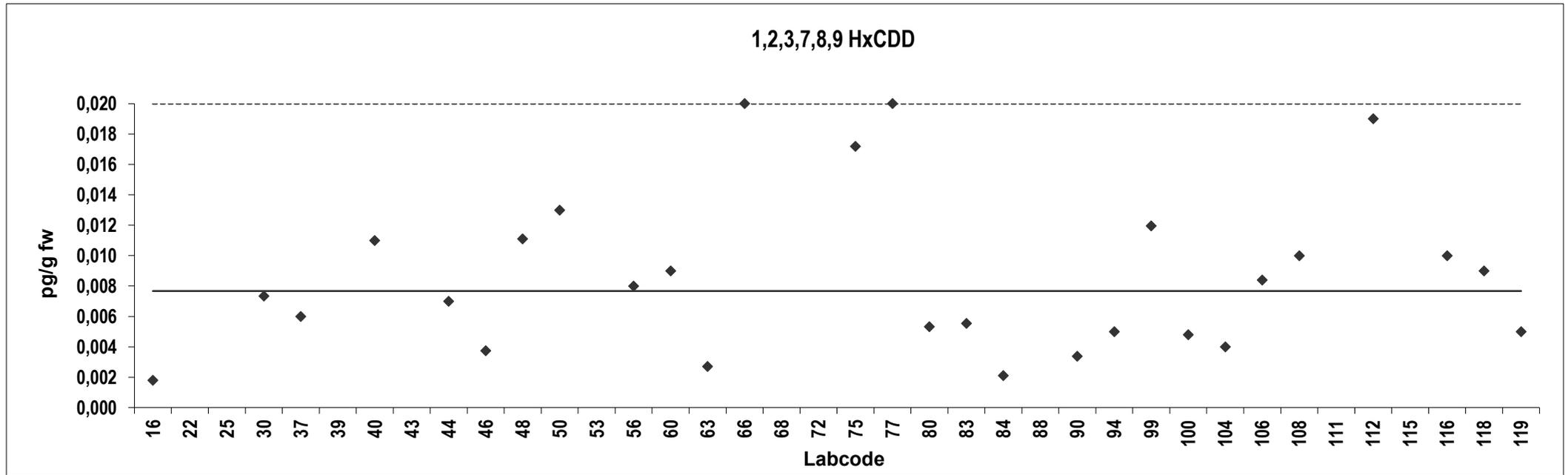


**Cream**  
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0018	-3,8				
22	0,17	104	Outlier			
25	0,050	28	Outlier,ND			
30	0,0073	-0,21				
37	0,0060	-1,1				
39	0,032	16	Outlier			
40	0,011	2,2	ND			
43	0,035	18	Outlier,ND			
44	0,0070	-0,44	ND			
46	0,0037	-2,6				
48	0,011	2,2	ND			
50	0,013	3,5	ND			
53	0,080	47	Outlier,ND			
56	0,0080	0,21				
60	0,0090	0,87	ND			
63	0,0027	-3,2	ND			
66	0,020	8,0				
68	0,039	20	Outlier,ND			
72	0,092	55	Outlier,ND			
75	0,017	6,2	ND			
77	0,020	8,0	ND			
80	0,0053	-1,5				
83	0,0055	-1,4				
84	0,0021	-3,6				
88	0,13	81	Outlier,ND			
90	0,0034	-2,8				
94	0,0050	-1,7	ND			
99	0,012	2,8	ND			
100	0,0048	-1,9	ND			
104	0,0040	-2,4	ND			
106	0,0084	0,47				
108	0,010	1,5	ND			
111	0,050	28	Outlier,ND			
112	0,019	7,4	ND			
115	0,10	63	Outlier,ND			
116	0,010	1,5				
118	0,0090	0,87				
119	0,0050	-1,7	ND			

**Consensus statistics**

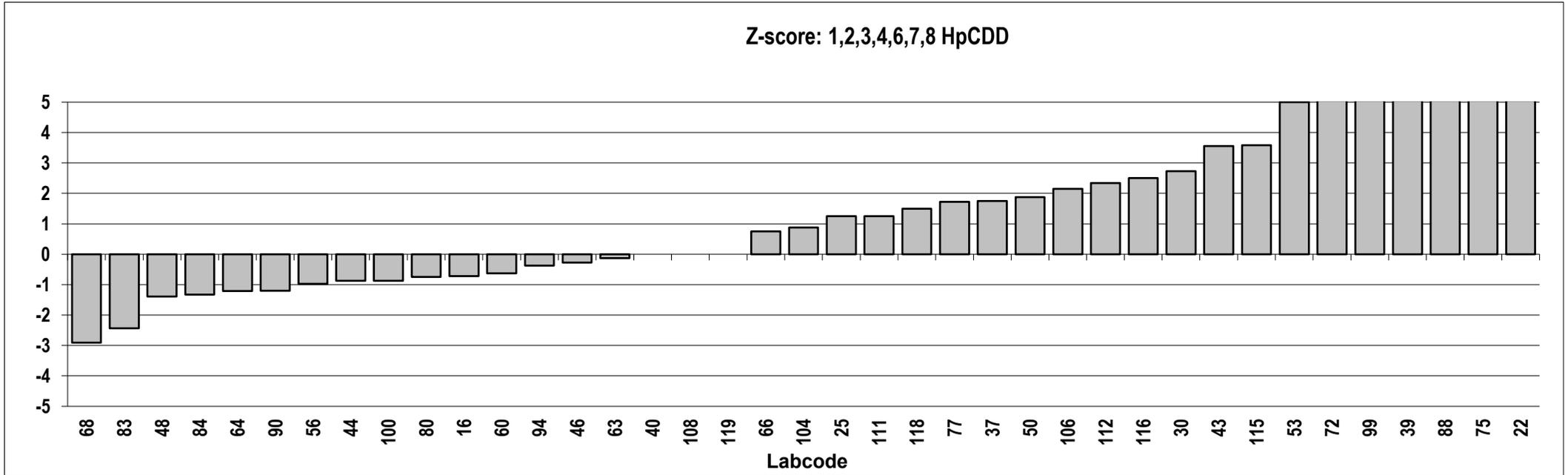
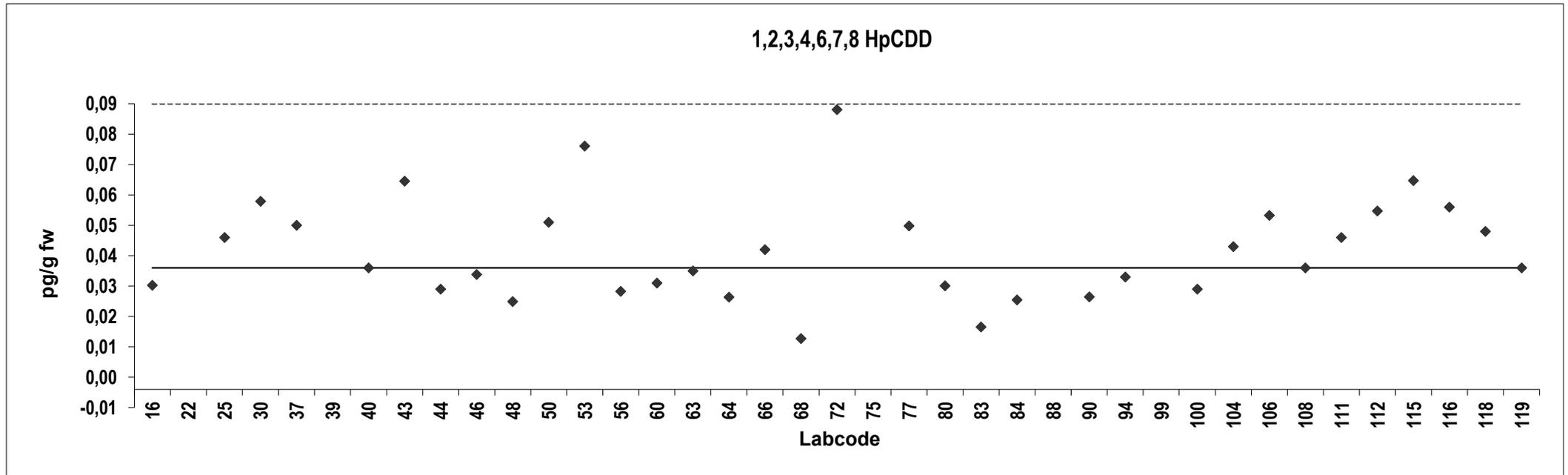
Consensus median, pg/g	0,0077
Median all values pg/g	0,010
Consensus mean, pg/g	0,0086
Standard deviation, pg/g	0,0053
Relative standard deviation, %	61
No. of values reported	38
No. of values removed	10
No. of reported non-detects	23



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,034	-0,72				
22	2,6	3,15	Outlier			
25	0,050	1,3	ND			
30	0,062	2,7				
37	0,054	1,8				
39	0,098	7,2	Outlier			
40	0,040	0,00000				
43	0,068	3,6				
44	0,033	-0,88				
46	0,038	-0,27				
48	0,029	-1,4				
50	0,055	1,9				
53	0,080	5,0	ND			
56	0,032	-0,98				
60	0,035	-0,63				
63	0,039	-0,13				
64	0,030	-1,2				
66	0,046	0,75				
68	0,017	-2,9	ND			
72	0,092	6,5	ND			
75	0,43	49	Outlier			
77	0,054	1,7				
80	0,034	-0,75				
83	0,021	-2,4				
84	0,029	-1,3				
88	0,20	19	Outlier,ND			
90	0,030	-1,2				
94	0,037	-0,38				
99	0,096	7,0	Outlier,ND			
100	0,033	-0,88				
104	0,047	0,88				
106	0,057	2,2				
108	0,040	0,00000				
111	0,050	1,3	ND			
112	0,059	2,3				
115	0,069	3,6	ND			
116	0,060	2,5				
118	0,052	1,5				
119	0,040	0,00000				

Consensus statistics	
Consensus median, pg/g	0,040
Median all values pg/g	0,047
Consensus mean, pg/g	0,045
Standard deviation, pg/g	0,017
Relative standard deviation, %	36
No. of values reported	39
No. of values removed	5
No. of reported non-detects	8

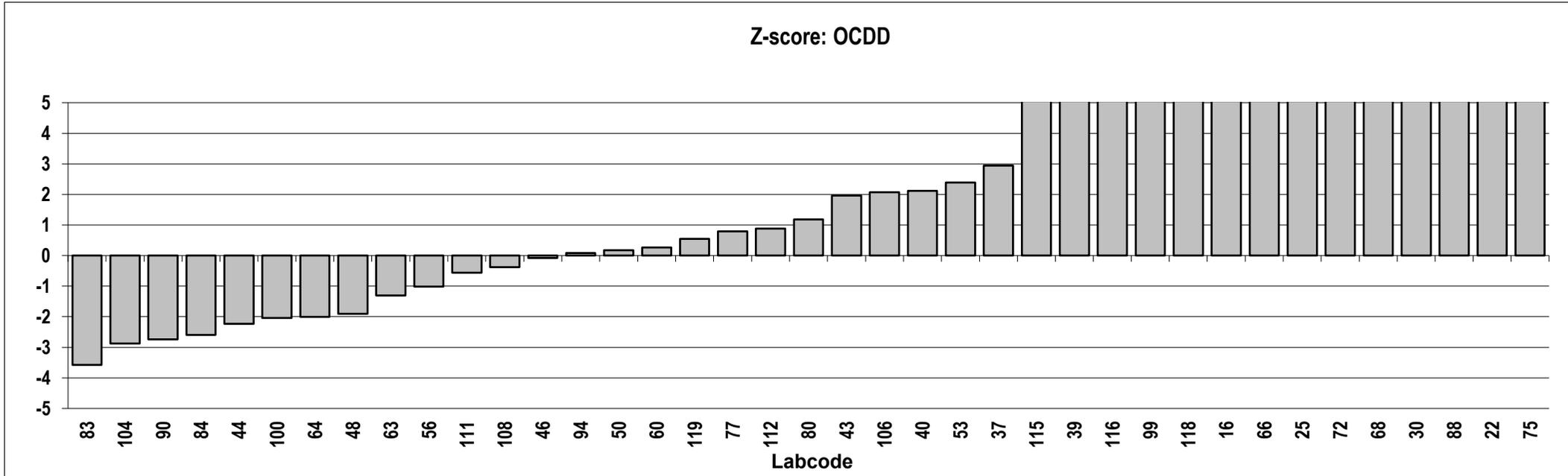
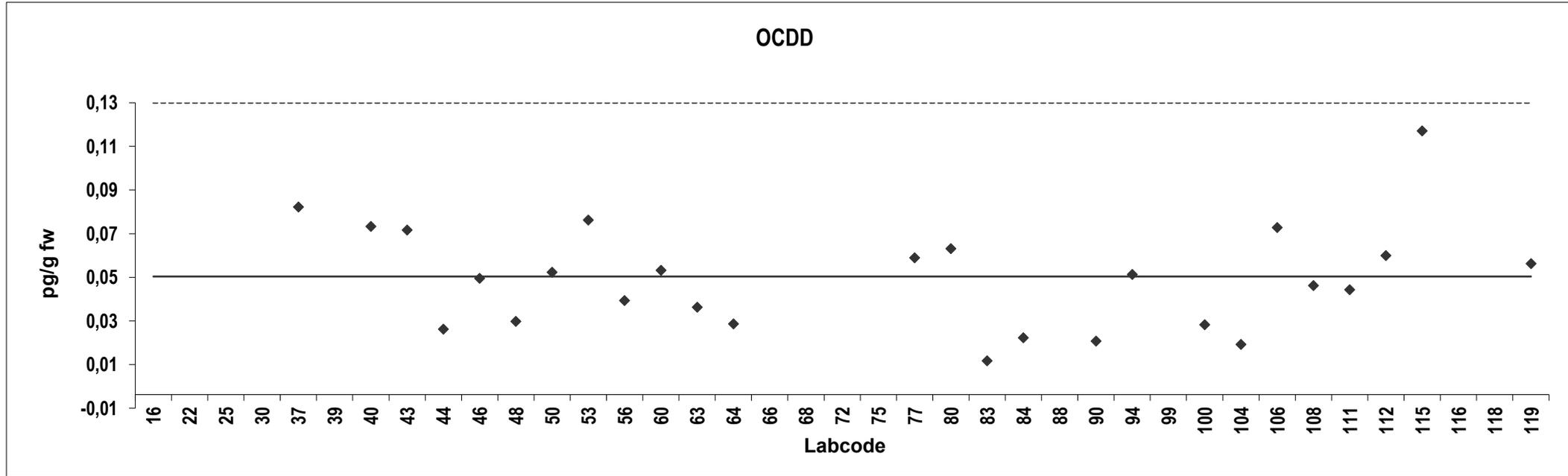


**Cream**  
**Congener: OCDD**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,20	13	Outlier			
22	2,1	191	Outlier			
25	0,20	13	Outlier,ND			
30	0,42	33	Outlier			
37	0,086	2,9				
39	0,13	7,4	Outlier			
40	0,077	2,1				
43	0,075	2,0				
44	0,030	-2,2				
46	0,053	-0,082				
48	0,034	-1,9				
50	0,056	0,17				
53	0,080	2,4	ND			
56	0,043	-1,0				
60	0,057	0,27				
63	0,040	-1,3				
64	0,032	-2,0				
66	0,20	13	Outlier			
68	0,35	27	Outlier			
72	0,23	16	Outlier,ND			
75	2,7	240	Outlier			
77	0,063	0,79				
80	0,067	1,2				
83	0,015	-3,6				
84	0,026	-2,6				
88	0,57	48	Outlier,ND			
90	0,024	-2,7				
94	0,055	0,082				
99	0,19	13	Outlier,ND			
100	0,032	-2,0	ND			
104	0,023	-2,9	ND			
106	0,077	2,1				
108	0,050	-0,38				
111	0,048	-0,56				
112	0,064	0,89				
115	0,12	6,2	ND			
116	0,17	11	Outlier			
118	0,19	13	Outlier			
119	0,060	0,54				

**Consensus statistics**

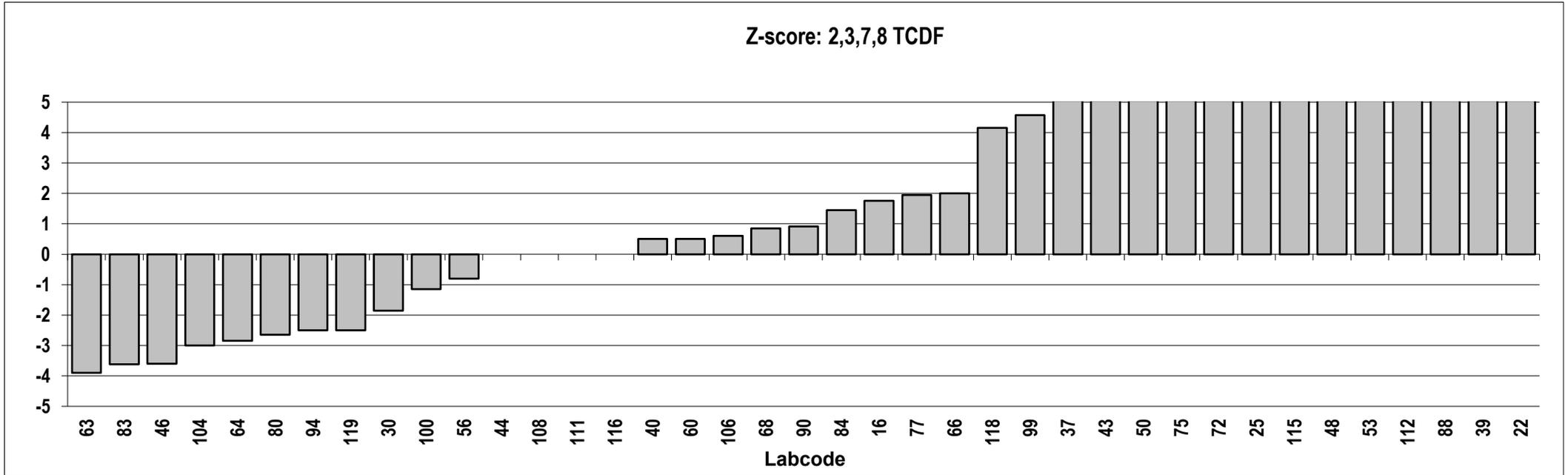
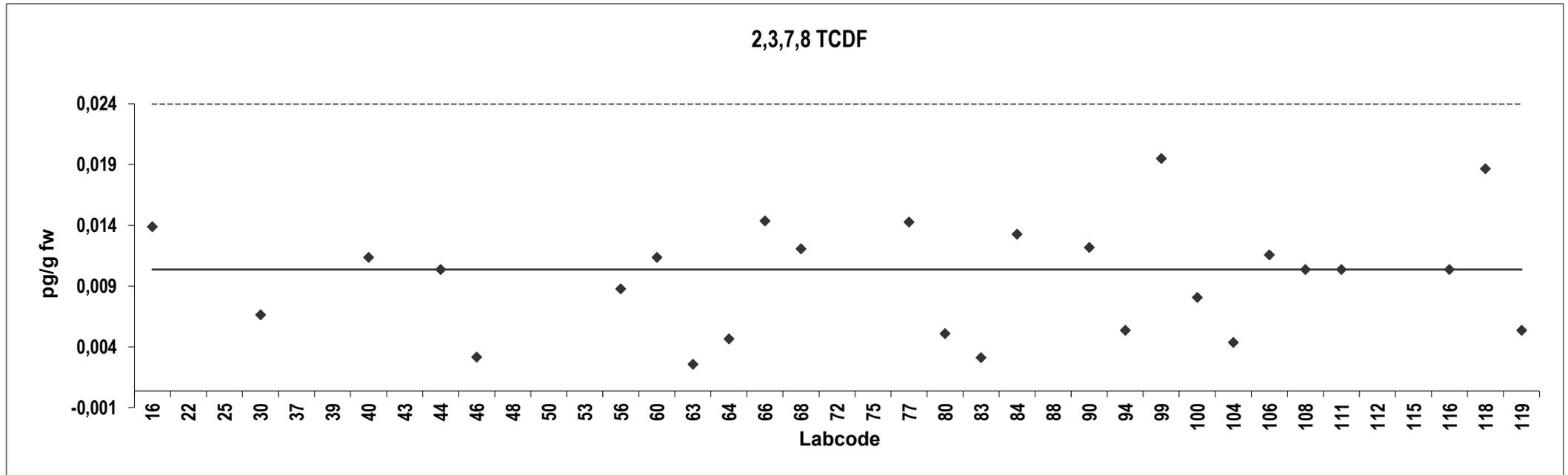
Consensus median, pg/g	0,054
Median all values pg/g	0,067
Consensus mean, pg/g	0,053
Standard deviation, pg/g	0,024
Relative standard deviation, %	45
No. of values reported	39
No. of values removed	13
No. of reported non-detects	8



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,014	1,8				
22	0,20	97	Outlier			
25	0,050	20	Outlier,ND			
30	0,0063	-1,9				
37	0,024	7,0	Outlier			
39	0,20	94	Outlier			
40	0,011	0,50				
43	0,026	8,0	Outlier,ND			
44	0,010	0,00000	ND			
46	0,0028	-3,6				
48	0,060	25	Outlier			
50	0,028	9,0	Outlier			
53	0,080	35	Outlier,ND			
56	0,0084	-0,80				
60	0,011	0,50	ND			
63	0,0022	-3,9				
64	0,0043	-2,9				
66	0,014	2,0				
68	0,012	0,85	ND			
72	0,048	19	Outlier,ND			
75	0,035	13	Outlier			
77	0,014	2,0				
80	0,0047	-2,6				
83	0,0028	-3,6				
84	0,013	1,5				
88	0,12	56	Outlier,ND			
90	0,012	0,91				
94	0,0050	-2,5	ND			
99	0,019	4,6	ND			
100	0,0077	-1,2	ND			
104	0,0040	-3,0	ND			
106	0,011	0,60				
108	0,010	0,00000	ND			
111	0,010	0,00000				
112	0,087	39	Outlier			
115	0,051	20	Outlier,ND			
116	0,010	0,00000				
118	0,018	4,2				
119	0,0050	-2,5	ND			

Consensus statistics	
Consensus median, pg/g	0,010
Median all values pg/g	0,012
Consensus mean, pg/g	0,0093
Standard deviation, pg/g	0,0046
Relative standard deviation, %	50
No. of values reported	39
No. of values removed	13
No. of reported non-detects	15

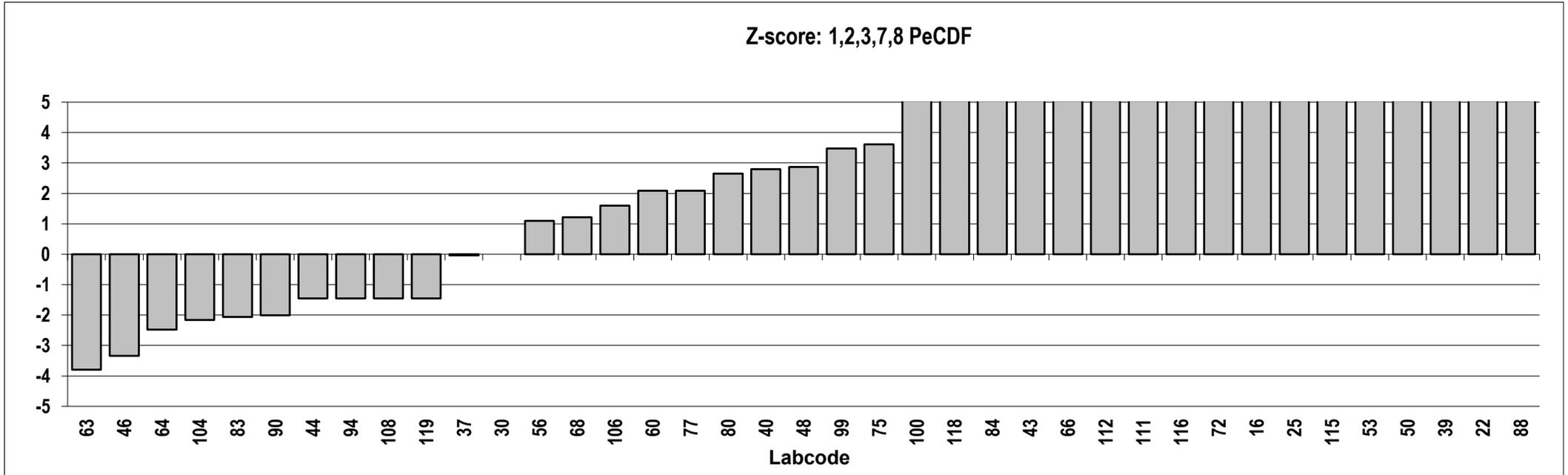
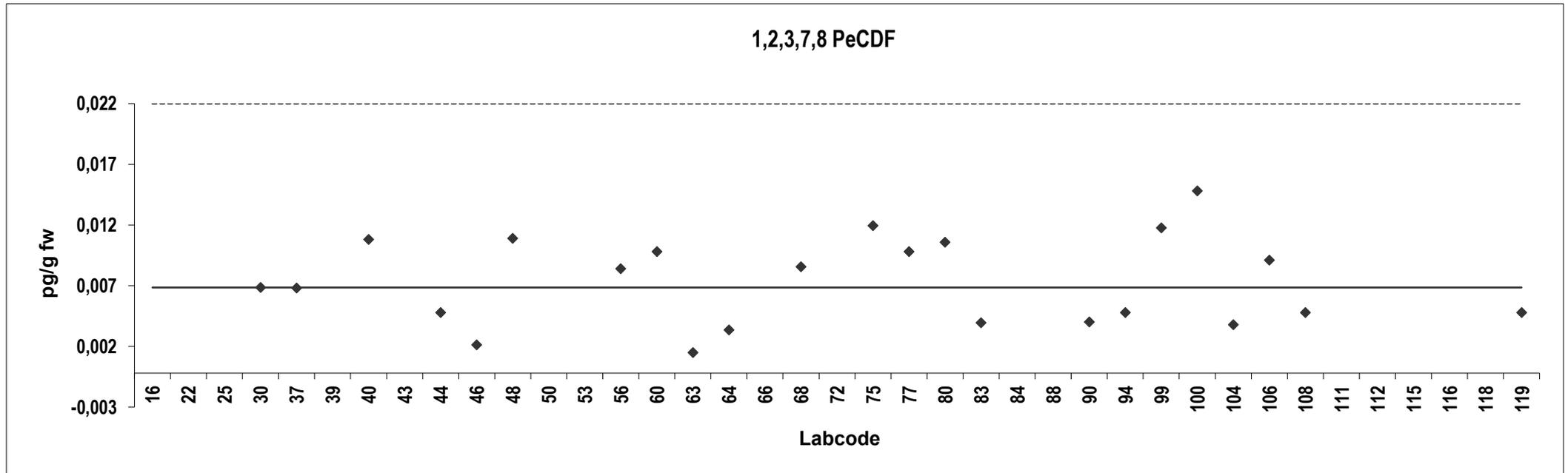


**Cream**  
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,050	30	Outlier			
22	0,100	66	Outlier			
25	0,050	30	Outlier,ND			
30	0,0071	0,00000				
37	0,0070	-0,038				
39	0,098	65	Outlier			
40	0,011	2,8	ND			
43	0,026	13	Outlier,ND			
44	0,0050	-1,5	ND			
46	0,0023	-3,3				
48	0,011	2,9	ND			
50	0,091	60	Outlier			
53	0,080	52	Outlier,ND			
56	0,0086	1,1				
60	0,010	2,1	ND			
63	0,0017	-3,8				
64	0,0036	-2,5				
66	0,033	18	Outlier			
68	0,0088	1,2	ND			
72	0,048	29	Outlier,ND			
75	0,012	3,6	ND			
77	0,010	2,1	ND			
80	0,011	2,6				
83	0,0041	-2,1				
84	0,024	12	Outlier			
88	0,15	100	Outlier,ND			
90	0,0042	-2,0				
94	0,0050	-1,5	ND			
99	0,012	3,5	ND			
100	0,015	5,6	ND			
104	0,0040	-2,2	ND			
106	0,0093	1,6				
108	0,0050	-1,5	ND			
111	0,040	23	Outlier,ND			
112	0,040	23	Outlier			
115	0,050	31	Outlier,ND			
116	0,040	23	Outlier			
118	0,023	11	Outlier			
119	0,0050	-1,5	ND			

**Consensus statistics**

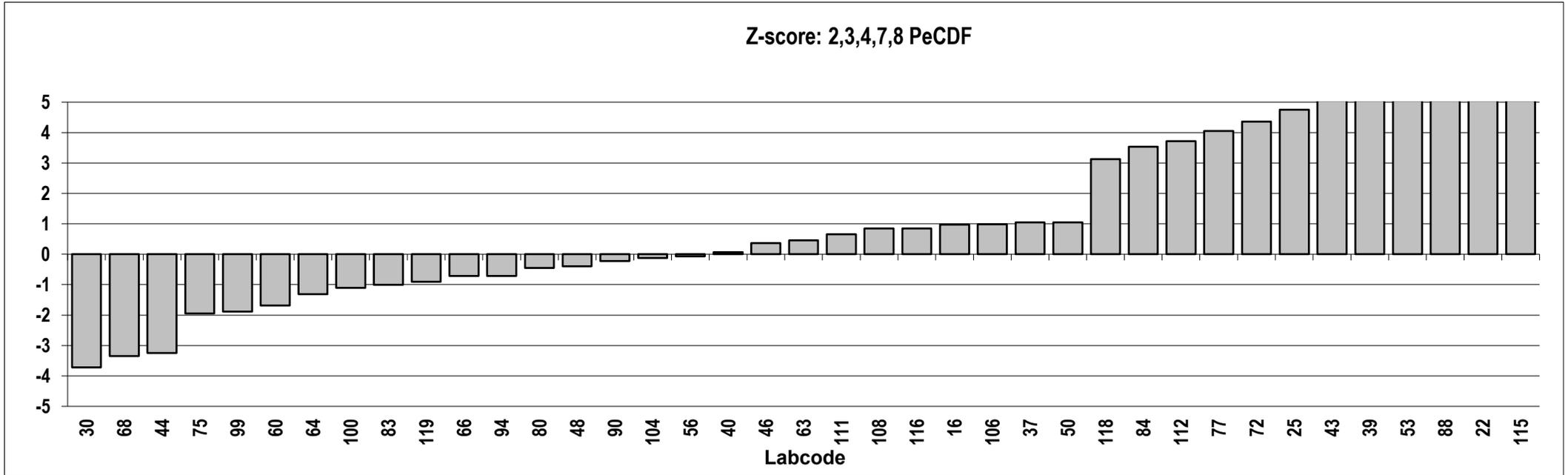
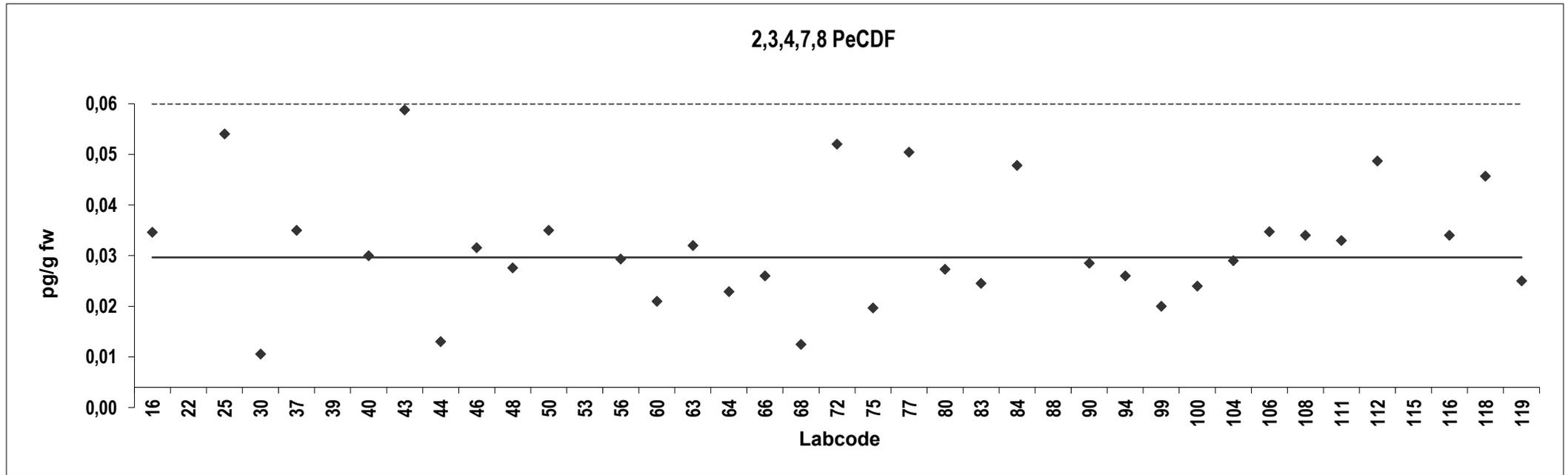
Consensus median, pg/g	0,0071
Median all values pg/g	0,011
Consensus mean, pg/g	0,0075
Standard deviation, pg/g	0,0036
Relative standard deviation, %	48
No. of values reported	39
No. of values removed	16
No. of reported non-detects	20



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,031	0,97				
22	0,25	43	Outlier			
25	0,050	4,7	ND			
30	0,0066	-3,7				
37	0,031	1,0				
39	0,077	10	Outlier			
40	0,026	0,068				
43	0,055	5,7				
44	0,0090	-3,2	ND			
46	0,028	0,37				
48	0,024	-0,40				
50	0,031	1,0				
53	0,080	11	Outlier,ND			
56	0,025	-0,068				
60	0,017	-1,7				
63	0,028	0,46				
64	0,019	-1,3				
66	0,022	-0,71				
68	0,0085	-3,3	ND			
72	0,048	4,4	ND			
75	0,016	-1,9				
77	0,046	4,1				
80	0,023	-0,45				
83	0,021	-1,0				
84	0,044	3,5				
88	0,15	23	Outlier,ND			
90	0,024	-0,23				
94	0,022	-0,71				
99	0,016	-1,9	ND			
100	0,020	-1,1				
104	0,025	-0,13				
106	0,031	0,98				
108	0,030	0,85				
111	0,029	0,65				
112	0,045	3,7				
115	0,43	78	Outlier,ND			
116	0,030	0,85				
118	0,042	3,1				
119	0,021	-0,91				

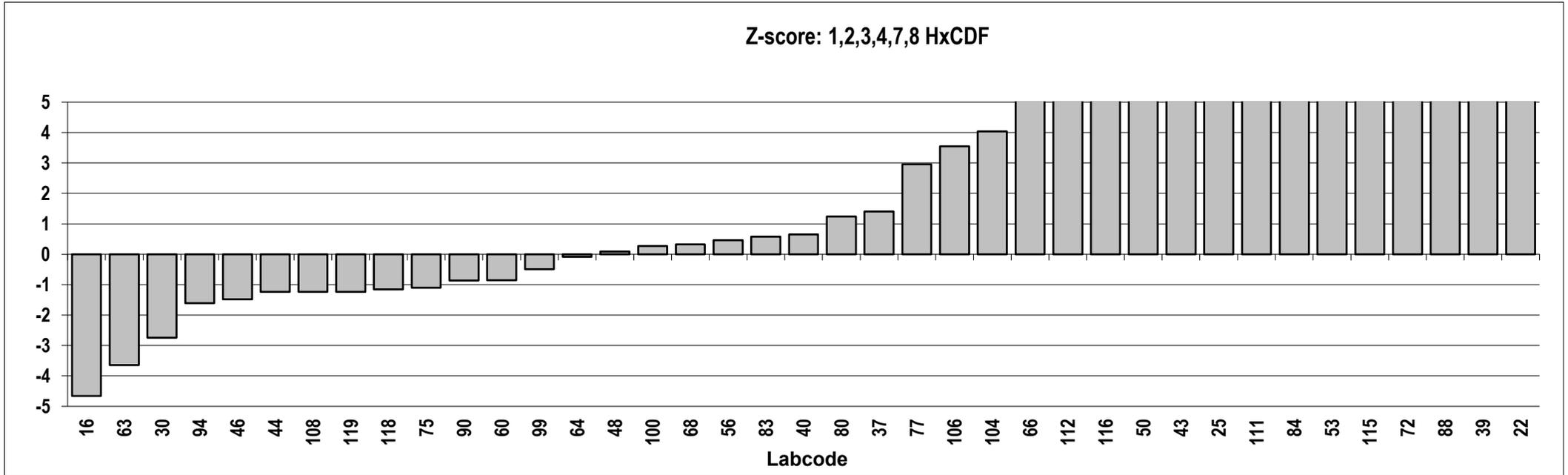
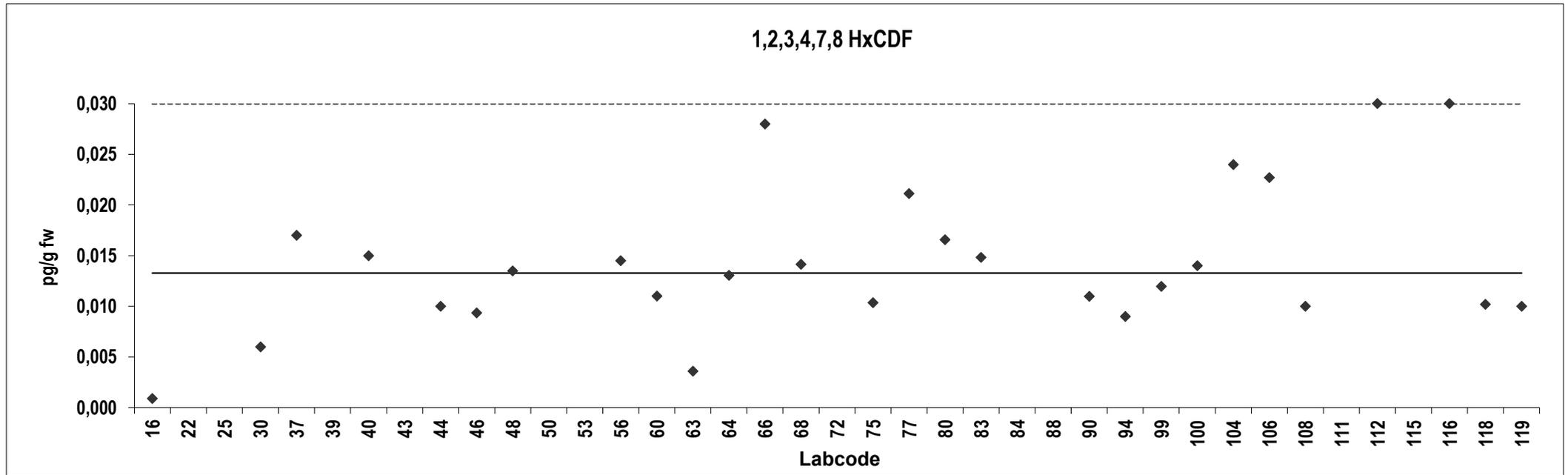
Consensus statistics	
Consensus median, pg/g	0,026
Median all values pg/g	0,028
Consensus mean, pg/g	0,028
Standard deviation, pg/g	0,012
Relative standard deviation, %	43
No. of values reported	39
No. of values removed	5
No. of reported non-detects	8



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00090	-4,7	ND			
22	0,19	66	Outlier			
25	0,050	14	Outlier,ND			
30	0,0060	-2,7				
37	0,017	1,4				
39	0,16	56	Outlier			
40	0,015	0,65				
43	0,035	8,2	Outlier,ND			
44	0,010	-1,2				
46	0,0093	-1,5				
48	0,014	0,085				
50	0,032	7,1	Outlier			
53	0,080	25	Outlier,ND			
56	0,015	0,46				
60	0,011	-0,86				
63	0,0036	-3,6				
64	0,013	-0,085				
66	0,028	5,5				
68	0,014	0,33	ND			
72	0,092	30	Outlier,ND			
75	0,010	-1,1	ND			
77	0,021	3,0				
80	0,017	1,2				
83	0,015	0,58				
84	0,073	22	Outlier			
88	0,14	46	Outlier,ND			
90	0,011	-0,87				
94	0,0090	-1,6				
99	0,012	-0,50	ND			
100	0,014	0,27	ND			
104	0,024	4,0	ND			
106	0,023	3,5				
108	0,010	-1,2				
111	0,050	14	Outlier,ND			
112	0,030	6,3				
115	0,089	28	Outlier,ND			
116	0,030	6,3				
118	0,010	-1,2				
119	0,010	-1,2				

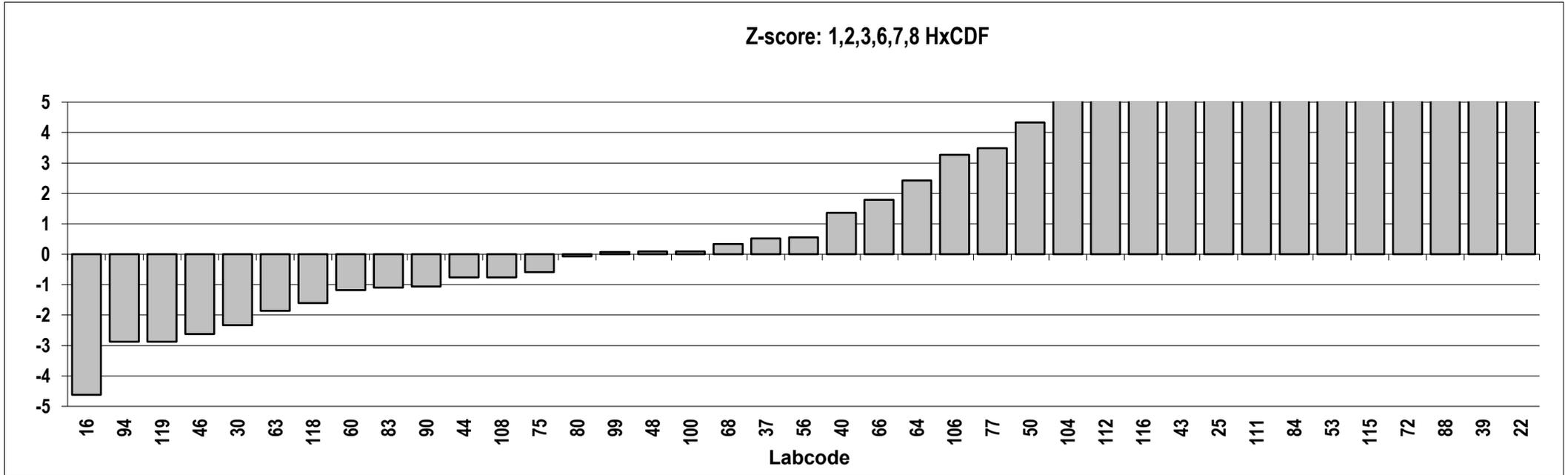
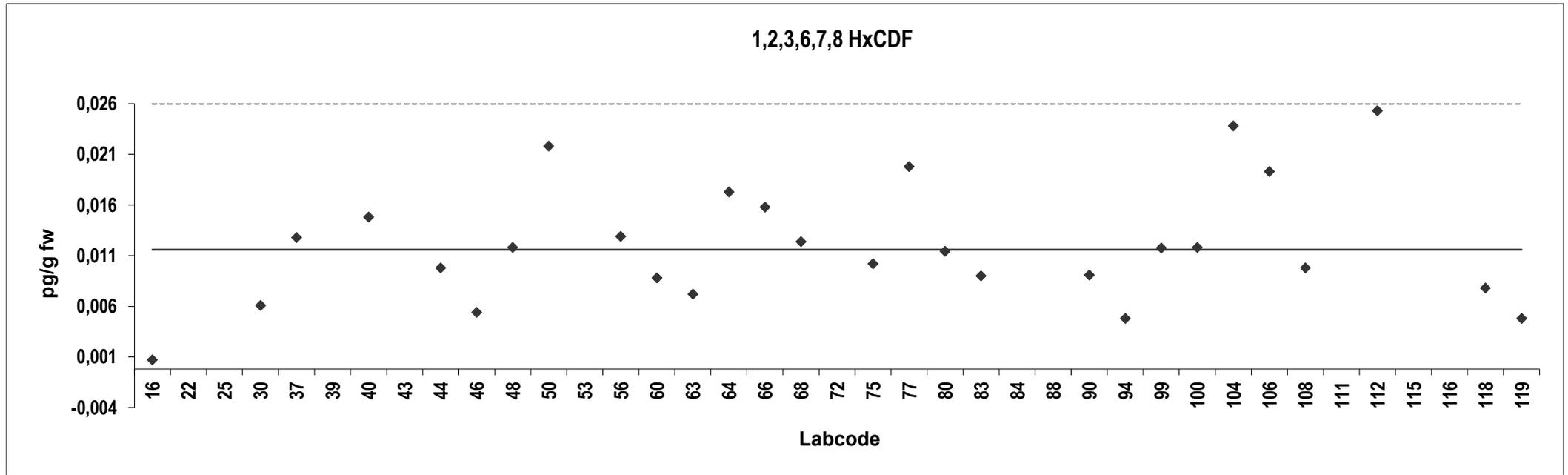
Consensus statistics	
Consensus median, pg/g	0,013
Median all values pg/g	0,015
Consensus mean, pg/g	0,014
Standard deviation, pg/g	0,0073
Relative standard deviation, %	51
No. of values reported	39
No. of values removed	11
No. of reported non-detects	13



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00090	-4,6	ND			
22	0,18	70	Outlier			
25	0,050	16	Outlier,ND			
30	0,0063	-2,3				
37	0,013	0,51				
39	0,14	56	Outlier			
40	0,015	1,4				
43	0,035	9,8	Outlier,ND			
44	0,010	-0,76				
46	0,0056	-2,6				
48	0,012	0,091				
50	0,022	4,3				
53	0,080	29	Outlier,ND			
56	0,013	0,56				
60	0,0090	-1,2				
63	0,0074	-1,9				
64	0,018	2,4				
66	0,016	1,8				
68	0,013	0,33	ND			
72	0,092	34	Outlier,ND			
75	0,010	-0,59	ND			
77	0,020	3,5	ND			
80	0,012	-0,073				
83	0,0092	-1,1				
84	0,060	20	Outlier			
88	0,13	48	Outlier,ND			
90	0,0093	-1,1				
94	0,0050	-2,9	ND			
99	0,012	0,073	ND			
100	0,012	0,091	ND			
104	0,024	5,2	ND			
106	0,020	3,3				
108	0,010	-0,76				
111	0,050	16	Outlier,ND			
112	0,026	5,8				
115	0,089	33	Outlier,ND			
116	0,030	7,7	Outlier			
118	0,0080	-1,6				
119	0,0050	-2,9	ND			

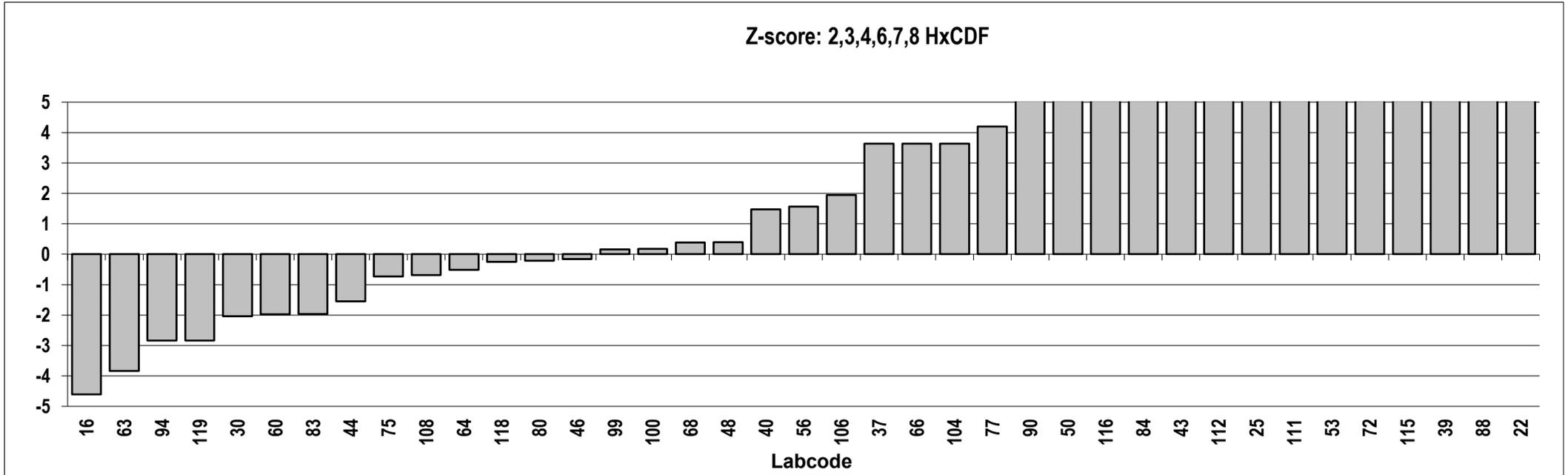
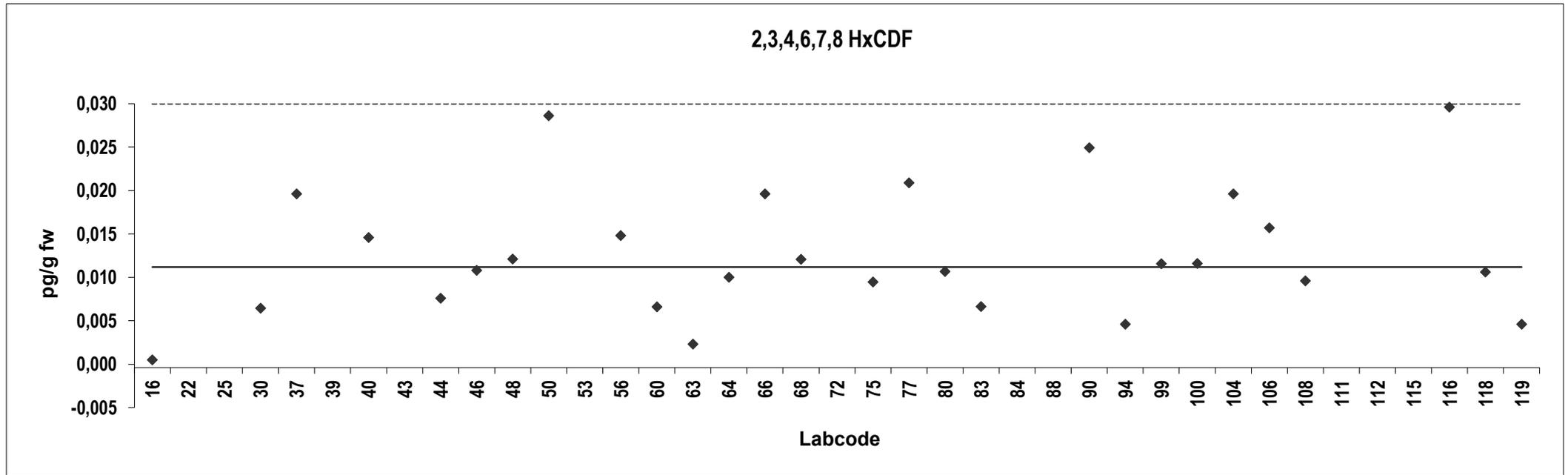
Consensus statistics	
Consensus median, pg/g	0,012
Median all values pg/g	0,013
Consensus mean, pg/g	0,012
Standard deviation, pg/g	0,0060
Relative standard deviation, %	49
No. of values reported	39
No. of values removed	11
No. of reported non-detects	16



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00090	-4,6	ND			
22	0,18	73	Outlier			
25	0,050	17	Outlier,ND			
30	0,0069	-2,0				
37	0,020	3,6				
39	0,13	53	Outlier			
40	0,015	1,5				
43	0,035	10	Outlier,ND			
44	0,0080	-1,5	ND			
46	0,011	-0,16				
48	0,013	0,40				
50	0,029	7,5				
53	0,080	30	Outlier,ND			
56	0,015	1,6				
60	0,0070	-2,0	ND			
63	0,0027	-3,8				
64	0,010	-0,51				
66	0,020	3,6				
68	0,012	0,38	ND			
72	0,092	35	Outlier,ND			
75	0,0099	-0,73	ND			
77	0,021	4,2				
80	0,011	-0,22				
83	0,0070	-2,0				
84	0,032	8,9	Outlier			
88	0,14	54	Outlier,ND			
90	0,025	5,9				
94	0,0050	-2,8	ND			
99	0,012	0,16	ND			
100	0,012	0,18	ND			
104	0,020	3,6	ND			
106	0,016	2,0				
108	0,010	-0,68				
111	0,050	17	Outlier,ND			
112	0,048	16	Outlier			
115	0,097	37	Outlier,ND			
116	0,030	8,0				
118	0,011	-0,25				
119	0,0050	-2,8	ND			

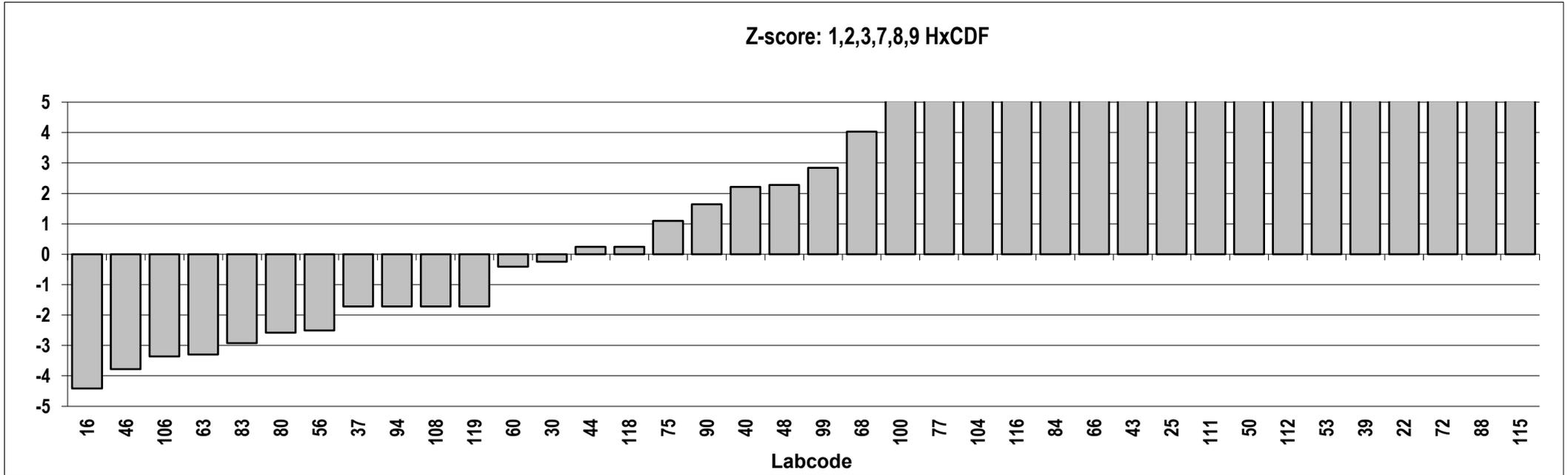
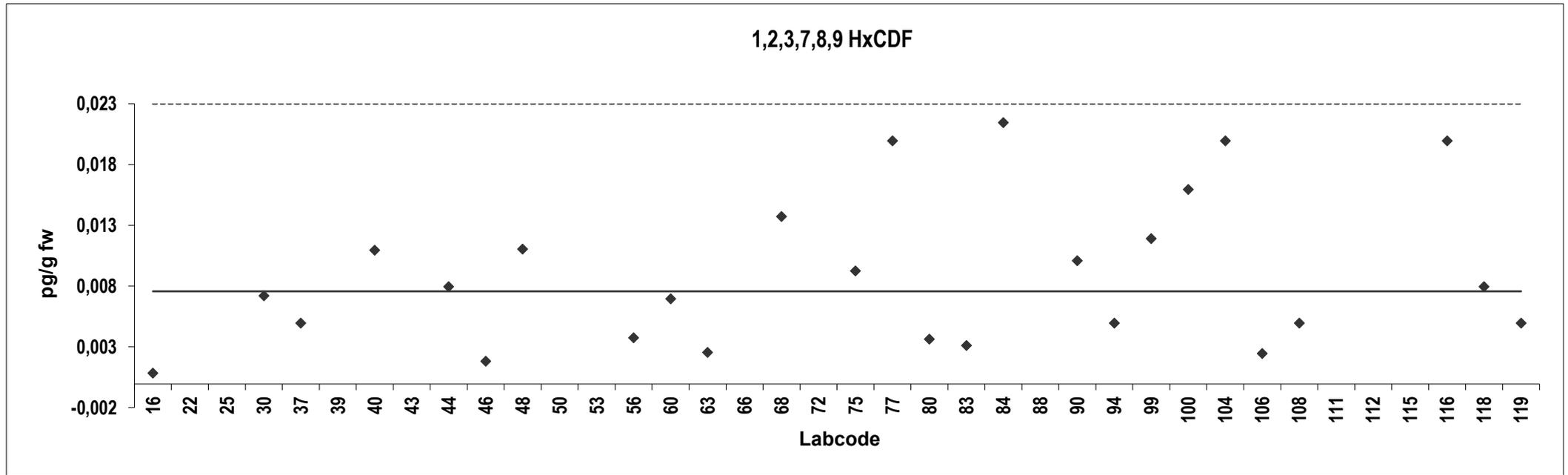
Consensus statistics	
Consensus median, pg/g	0,012
Median all values pg/g	0,015
Consensus mean, pg/g	0,013
Standard deviation, pg/g	0,0074
Relative standard deviation, %	57
No. of values reported	39
No. of values removed	11
No. of reported non-detects	17



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00090	-4,4	ND			
22	0,088	53	Outlier			
25	0,050	28	Outlier,ND			
30	0,0072	-0,25				
37	0,0050	-1,7				
39	0,081	48	Outlier			
40	0,011	2,2	ND			
43	0,035	18	Outlier,ND			
44	0,0080	0,25	ND			
46	0,0019	-3,8	ND			
48	0,011	2,3	ND			
50	0,053	30	Outlier			
53	0,080	47	Outlier,ND			
56	0,0038	-2,5	ND			
60	0,0070	-0,41	ND			
63	0,0026	-3,3	ND			
66	0,024	11	Outlier			
68	0,014	4,0	ND			
72	0,092	55	Outlier,ND			
75	0,0093	1,1				
77	0,020	8,1	ND			
80	0,0037	-2,6				
83	0,0032	-2,9				
84	0,022	9,1				
88	0,14	86	Outlier,ND			
90	0,010	1,6				
94	0,0050	-1,7	ND			
99	0,012	2,8	ND			
100	0,016	5,5	ND			
104	0,020	8,1	ND			
106	0,0025	-3,4				
108	0,0050	-1,7	ND			
111	0,050	28	Outlier,ND			
112	0,070	41	Outlier			
115	0,15	96	Outlier,ND			
116	0,020	8,1				
118	0,0080	0,25	ND			
119	0,0050	-1,7	ND			

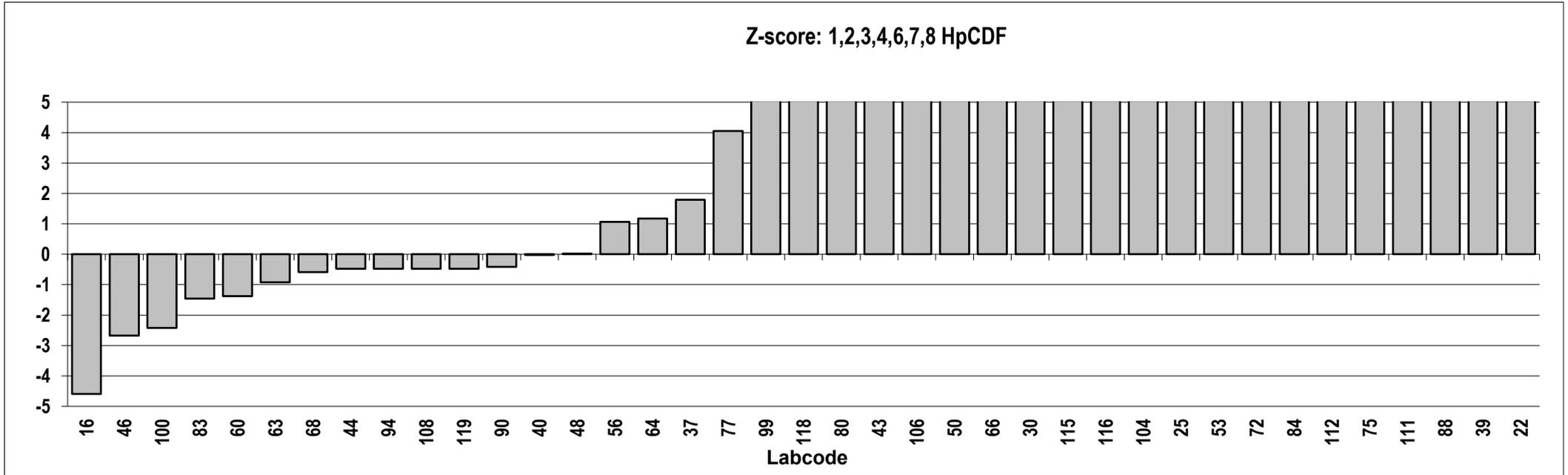
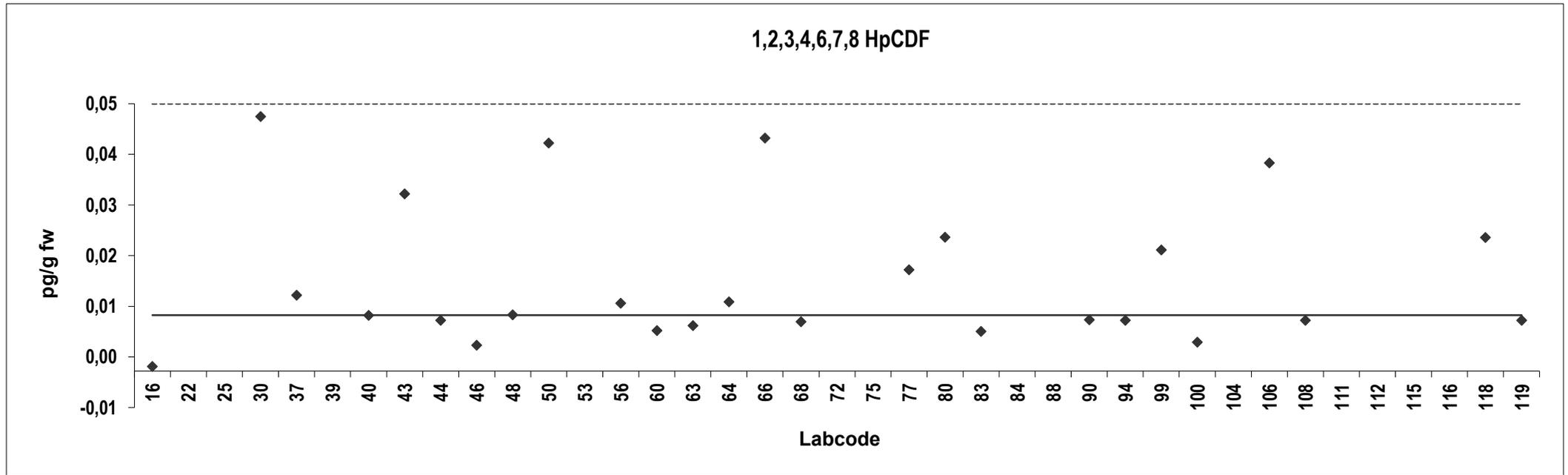
Consensus statistics	
Consensus median, pg/g	0,0076
Median all values pg/g	0,012
Consensus mean, pg/g	0,0090
Standard deviation, pg/g	0,0062
Relative standard deviation, %	69
No. of values reported	38
No. of values removed	12
No. of reported non-detects	24



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00090	-4,6	ND			
22	0,51	227	Outlier			
25	0,080	31	Outlier			
30	0,050	18				
37	0,015	1,8				
39	0,22	96	Outlier			
40	0,011	-0,023				
43	0,035	11	ND			
44	0,010	-0,48				
46	0,0051	-2,7				
48	0,011	0,023	ND			
50	0,045	15				
53	0,080	31	Outlier,ND			
56	0,013	1,1				
60	0,0080	-1,4				
63	0,0090	-0,93				
64	0,014	1,2				
66	0,046	16				
68	0,0098	-0,59	ND			
72	0,092	37	Outlier,ND			
75	0,10	41	Outlier			
77	0,020	4,0	ND			
80	0,026	7,0				
83	0,0078	-1,5				
84	0,098	39	Outlier			
88	0,19	82	Outlier,ND			
90	0,010	-0,42				
94	0,010	-0,48	ND			
99	0,024	5,8	ND			
100	0,0057	-2,4				
104	0,077	30	Outlier			
106	0,041	14				
108	0,010	-0,48	ND			
111	0,15	63	Outlier,ND			
112	0,098	39	Outlier			
115	0,065	25	Outlier,ND			
116	0,070	27	Outlier			
118	0,026	6,9				
119	0,010	-0,48	ND			

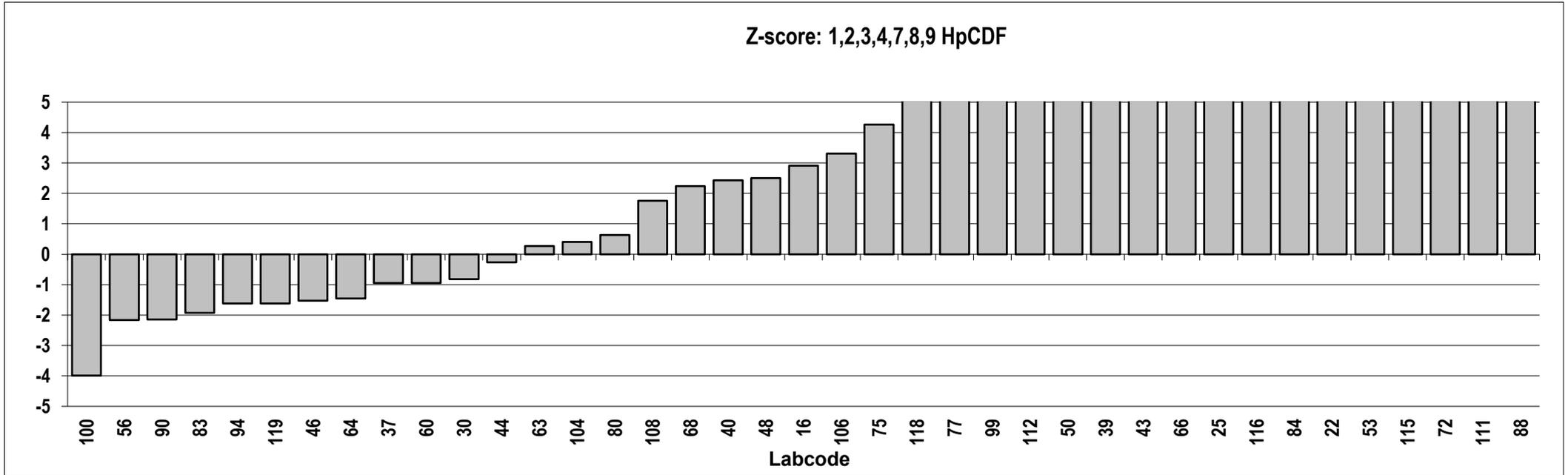
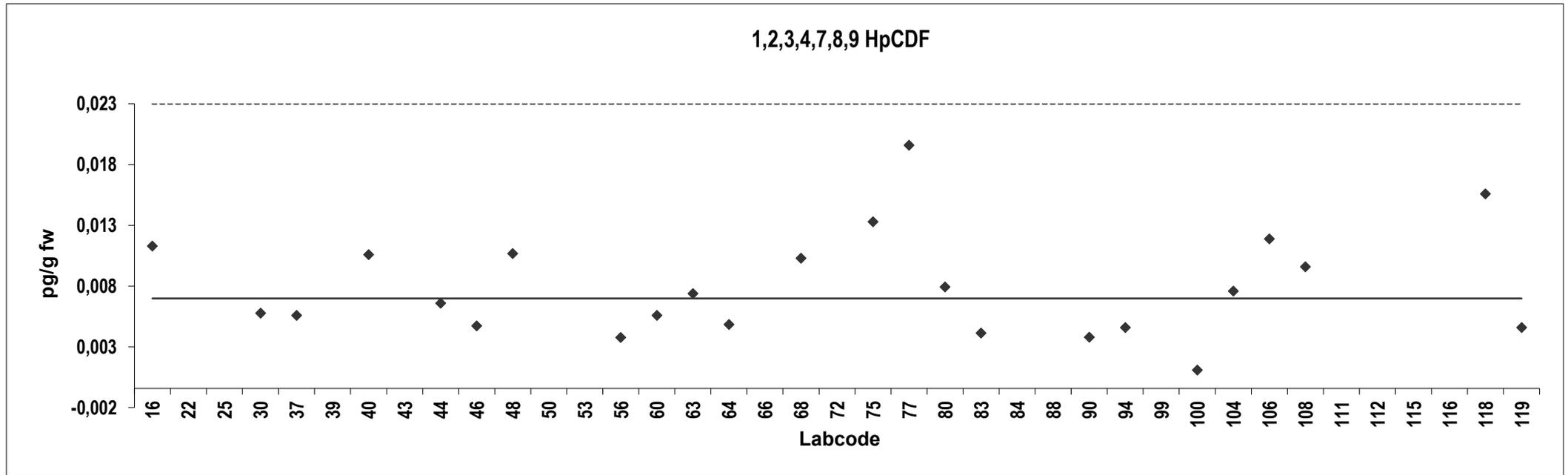
Consensus statistics	
Consensus median, pg/g	0,011
Median all values pg/g	0,026
Consensus mean, pg/g	0,018
Standard deviation, pg/g	0,014
Relative standard deviation, %	77
No. of values reported	39
No. of values removed	13
No. of reported non-detects	14



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,012	2,9				
22	0,071	43	Outlier			
25	0,050	29	Outlier,ND			
30	0,0062	-0,82				
37	0,0060	-0,95				
39	0,030	15	Outlier			
40	0,011	2,4	ND			
43	0,035	19	Outlier,ND			
44	0,0070	-0,27	ND			
46	0,0051	-1,5				
48	0,011	2,5	ND			
50	0,029	15	Outlier			
53	0,080	49	Outlier,ND			
56	0,0042	-2,2				
60	0,0060	-0,95	ND			
63	0,0078	0,27				
64	0,0053	-1,5				
66	0,045	25	Outlier			
68	0,011	2,2	ND			
72	0,092	57	Outlier,ND			
75	0,014	4,3				
77	0,020	8,5	ND			
80	0,0083	0,64				
83	0,0045	-1,9				
84	0,059	35	Outlier			
88	0,22	143	Outlier,ND			
90	0,0042	-2,1				
94	0,0050	-1,6	ND			
99	0,024	11	Outlier,ND			
100	0,0015	-4,0	ND			
104	0,0080	0,41	ND			
106	0,012	3,3				
108	0,010	1,8	ND			
111	0,15	96	Outlier,ND			
112	0,025	12	Outlier,ND			
115	0,087	54	Outlier,ND			
116	0,050	29	Outlier			
118	0,016	5,8	ND			
119	0,0050	-1,6	ND			

Consensus statistics	
Consensus median, pg/g	0,0074
Median all values pg/g	0,012
Consensus mean, pg/g	0,0084
Standard deviation, pg/g	0,0043
Relative standard deviation, %	52
No. of values reported	39
No. of values removed	15
No. of reported non-detects	21

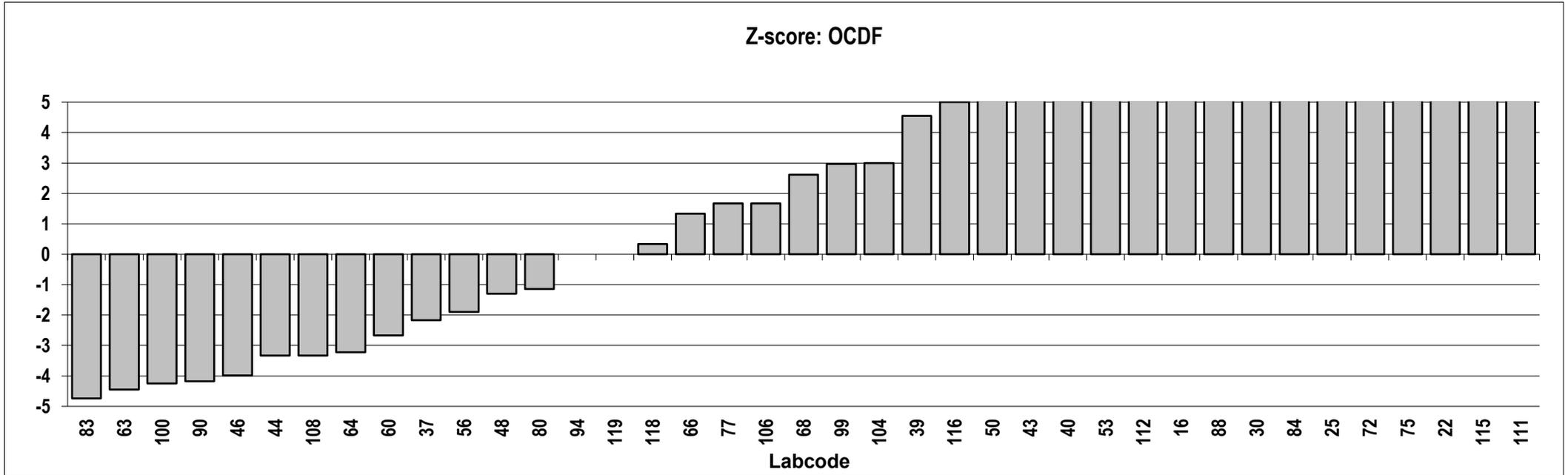
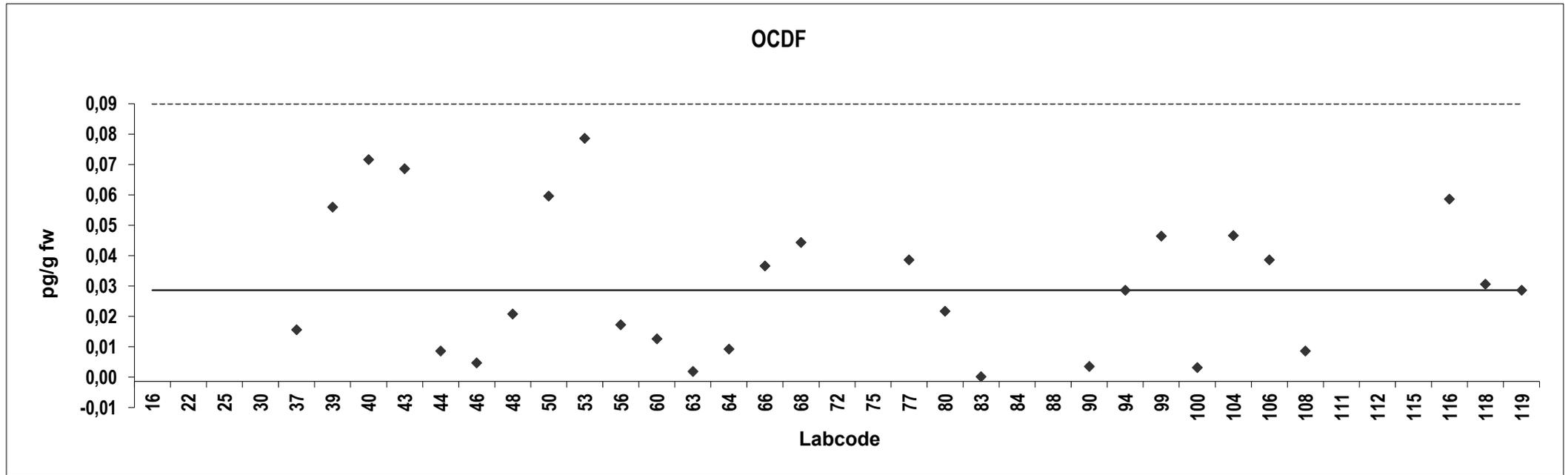


**Cream**  
**Congener: OCDF**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,14	19	Outlier			
22	0,45	70	Outlier			
25	0,20	28	Outlier,ND			
30	0,15	20	Outlier			
37	0,017	-2,2				
39	0,057	4,5				
40	0,073	7,2	ND			
43	0,070	6,7	ND			
44	0,010	-3,3	ND			
46	0,0061	-4,0				
48	0,022	-1,3	ND			
50	0,061	5,2				
53	0,080	8,3	ND			
56	0,019	-1,9				
60	0,014	-2,7	ND			
63	0,0033	-4,5				
64	0,011	-3,2				
66	0,038	1,3				
68	0,046	2,6	ND			
72	0,23	33	Outlier,ND			
75	0,30	44	Outlier			
77	0,040	1,7	ND			
80	0,023	-1,1				
83	0,0016	-4,7				
84	0,20	28	Outlier			
88	0,15	19	Outlier,ND			
90	0,0049	-4,2	ND			
94	0,030	0,00000	ND			
99	0,048	3,0	ND			
100	0,0045	-4,3	ND			
104	0,048	3,0				
106	0,040	1,7				
108	0,010	-3,3	ND			
111	2,0	328	Outlier,ND			
112	0,11	13	Outlier			
115	0,45	71	Outlier,ND			
116	0,060	5,0				
118	0,032	0,33	ND			
119	0,030	0,00000	ND			

**Consensus statistics**

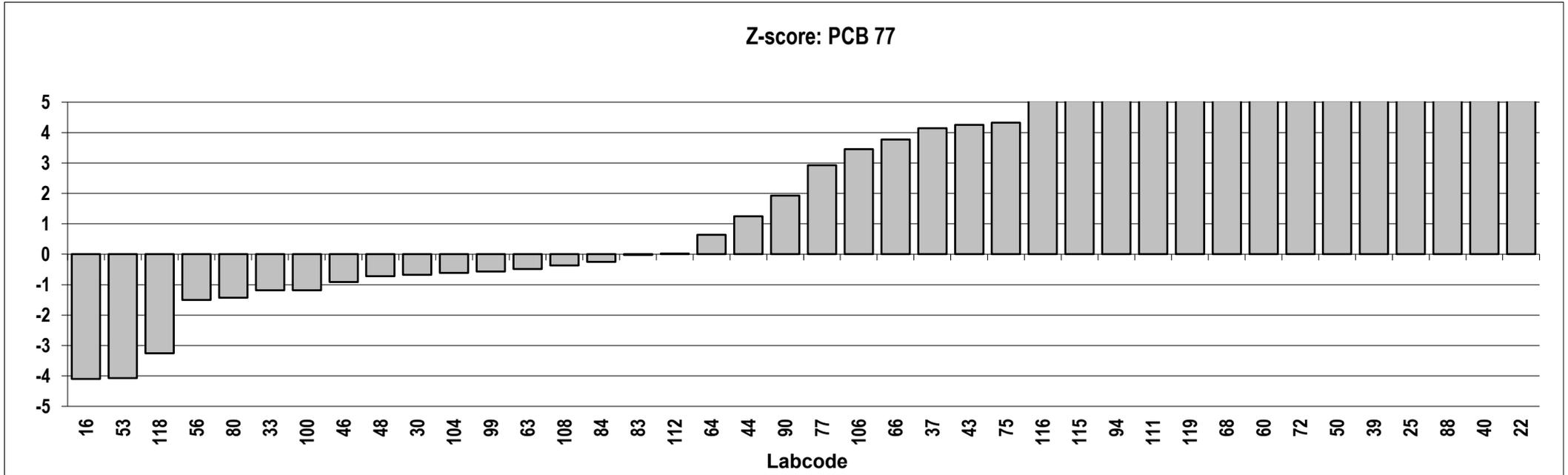
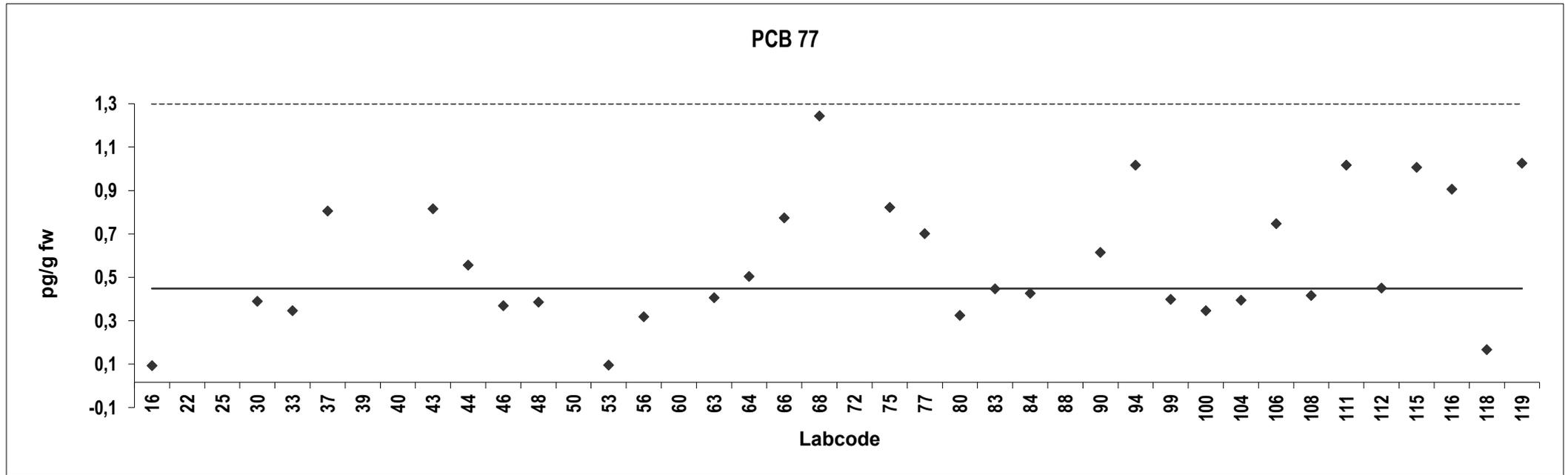
Consensus median, pg/g	0,030
Median all values pg/g	0,046
Consensus mean, pg/g	0,032
Standard deviation, pg/g	0,023
Relative standard deviation, %	73
No. of values reported	39
No. of values removed	11
No. of reported non-detects	20



**Cream**  
**Congener: PCB 77**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,077	-4,1				
22	3,1	31	Outlier			
25	2,0	18	Outlier,ND			
30	0,37	-0,67				
33	0,33	-1,2				
37	0,79	4,1				
39	1,7	15	Outlier			
40	3,0	30	Outlier			
43	0,80	4,3				
44	0,54	1,2				
46	0,35	-0,91				
48	0,37	-0,72				
50	1,6	14	Outlier			
53	0,080	-4,1	ND			
56	0,30	-1,5				
60	1,4	11	Outlier			
63	0,39	-0,49				
64	0,49	0,64				
66	0,76	3,8				
68	1,2	9,2				
72	1,5	12	Outlier,ND			
75	0,81	4,3				
77	0,69	2,9				
80	0,31	-1,4				
83	0,43	-0,021				
84	0,41	-0,26				
88	2,4	23	Outlier,ND			
90	0,60	1,9				
94	1,0	6,6				
99	0,38	-0,57	ND			
100	0,33	-1,2				
104	0,38	-0,62				
106	0,73	3,5				
108	0,40	-0,37				
111	1,0	6,6	ND			
112	0,43	0,021				
115	0,99	6,5				
116	0,89	5,3				
118	0,15	-3,3				
119	1,0	6,7				

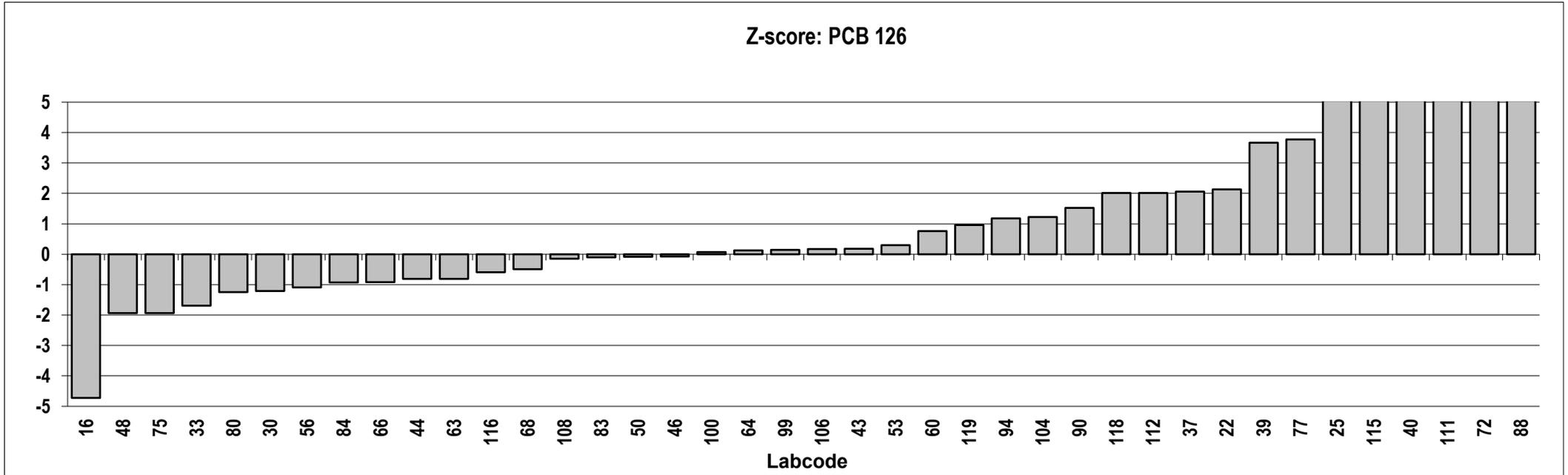
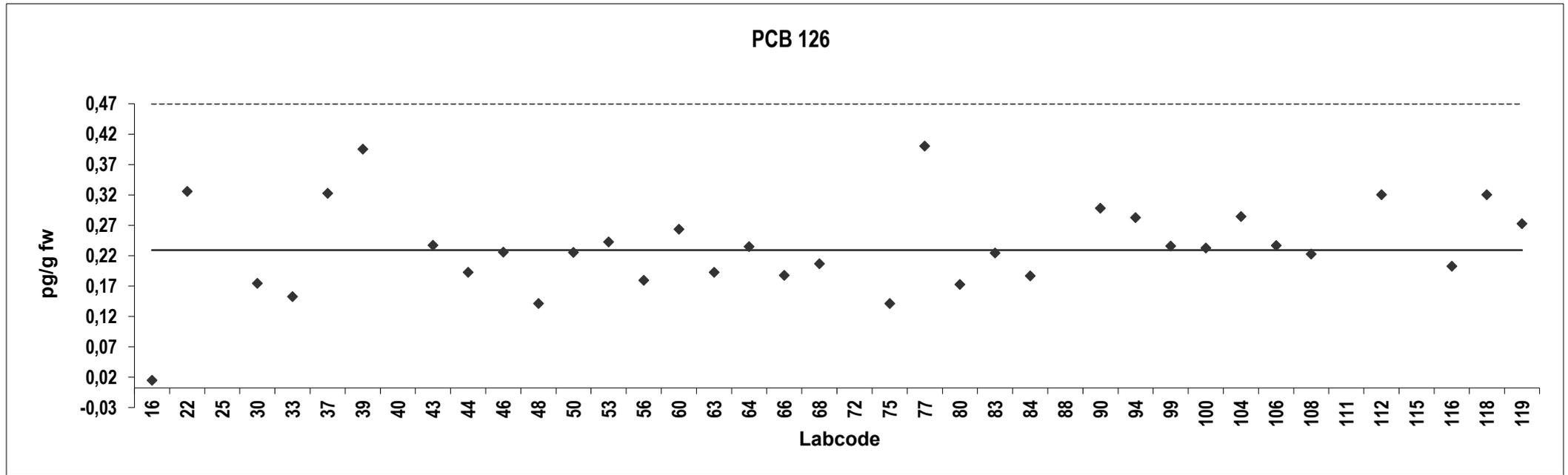
Consensus statistics	
Consensus median, pg/g	0,43
Median all values pg/g	0,64
Consensus mean, pg/g	0,56
Standard deviation, pg/g	0,30
Relative standard deviation, %	53
No. of values reported	40
No. of values removed	8
No. of reported non-detects	6



**Cream**  
**Congener: PCB 126**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,013	-4,7	ND			
22	0,32	2,1				
25	0,50	6,0	Outlier,ND			
30	0,17	-1,2				
33	0,15	-1,7				
37	0,32	2,1				
39	0,39	3,7				
40	0,66	9,6	Outlier			
43	0,23	0,18				
44	0,19	-0,81				
46	0,22	-0,074				
48	0,14	-1,9	ND			
50	0,22	-0,080	ND			
53	0,24	0,29				
56	0,18	-1,1				
60	0,26	0,76				
63	0,19	-0,81				
64	0,23	0,13				
66	0,19	-0,92				
68	0,20	-0,49	ND			
72	1,5	28	Outlier,ND			
75	0,14	-1,9				
77	0,40	3,8				
80	0,17	-1,2				
83	0,22	-0,11				
84	0,18	-0,93				
88	2,2	44	Outlier,ND			
90	0,30	1,5				
94	0,28	1,2				
99	0,23	0,15				
100	0,23	0,074				
104	0,28	1,2				
106	0,23	0,17				
108	0,22	-0,15				
111	1,0	17	Outlier,ND			
112	0,32	2,0				
115	0,51	6,3	Outlier			
116	0,20	-0,59				
118	0,32	2,0				
119	0,27	1,0				

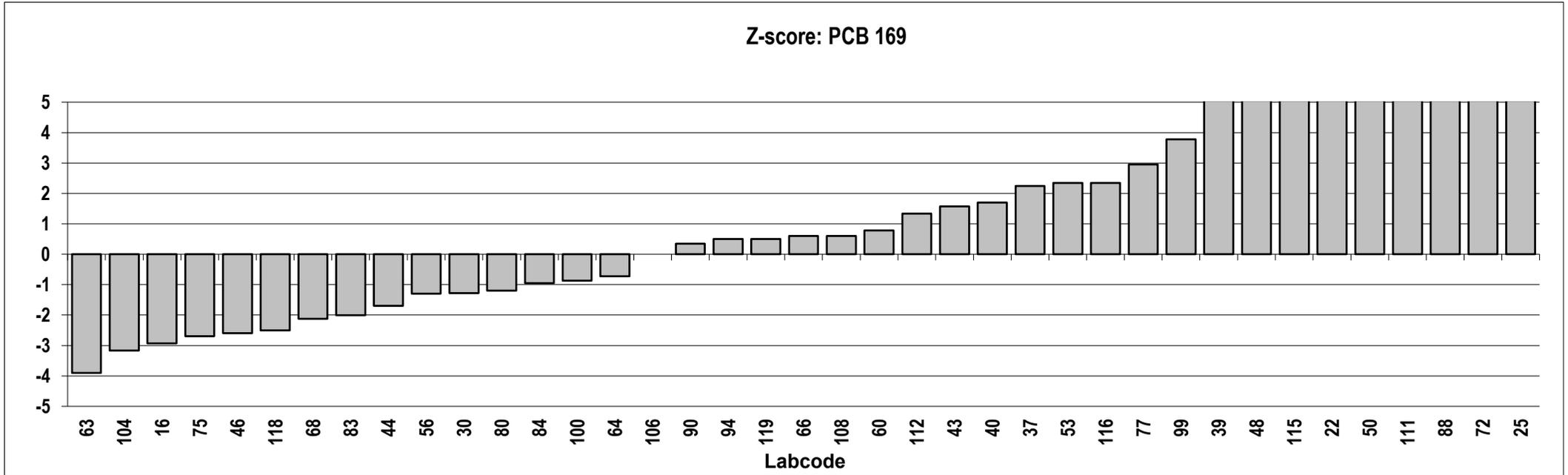
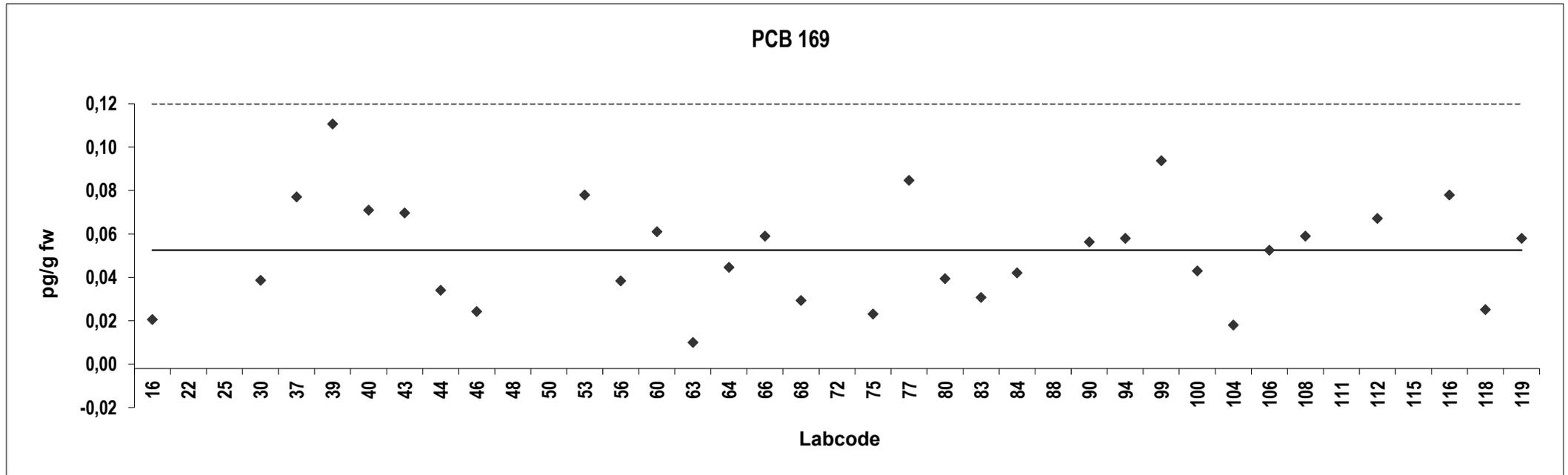
Consensus statistics	
Consensus median, pg/g	0,23
Median all values pg/g	0,23
Consensus mean, pg/g	0,23
Standard deviation, pg/g	0,076
Relative standard deviation, %	33
No. of values reported	40
No. of values removed	6
No. of reported non-detects	8



**Cream**  
**Congener: PCB 169**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,023	-2,9	ND			
22	0,27	20	Outlier			
25	2,0	178	Outlier,ND			
30	0,041	-1,3				
37	0,079	2,2				
39	0,11	5,3				
40	0,073	1,7	ND			
43	0,072	1,6				
44	0,036	-1,7				
46	0,026	-2,6				
48	0,14	7,7	Outlier,ND			
50	0,42	34	Outlier,ND			
53	0,080	2,3	ND			
56	0,040	-1,3				
60	0,063	0,78				
63	0,012	-3,9				
64	0,047	-0,73				
66	0,061	0,60				
68	0,031	-2,1	ND			
72	1,5	133	Outlier,ND			
75	0,025	-2,7				
77	0,087	3,0				
80	0,041	-1,2				
83	0,033	-2,0				
84	0,044	-0,95				
88	1,5	132	Outlier,ND			
90	0,058	0,34				
94	0,060	0,50				
99	0,096	3,8	ND			
100	0,045	-0,87				
104	0,020	-3,2	ND			
106	0,055	0,00000				
108	0,061	0,60				
111	1,0	87	Outlier,ND			
112	0,069	1,3				
115	0,16	9,7	Outlier			
116	0,080	2,3				
118	0,027	-2,5				
119	0,060	0,50				

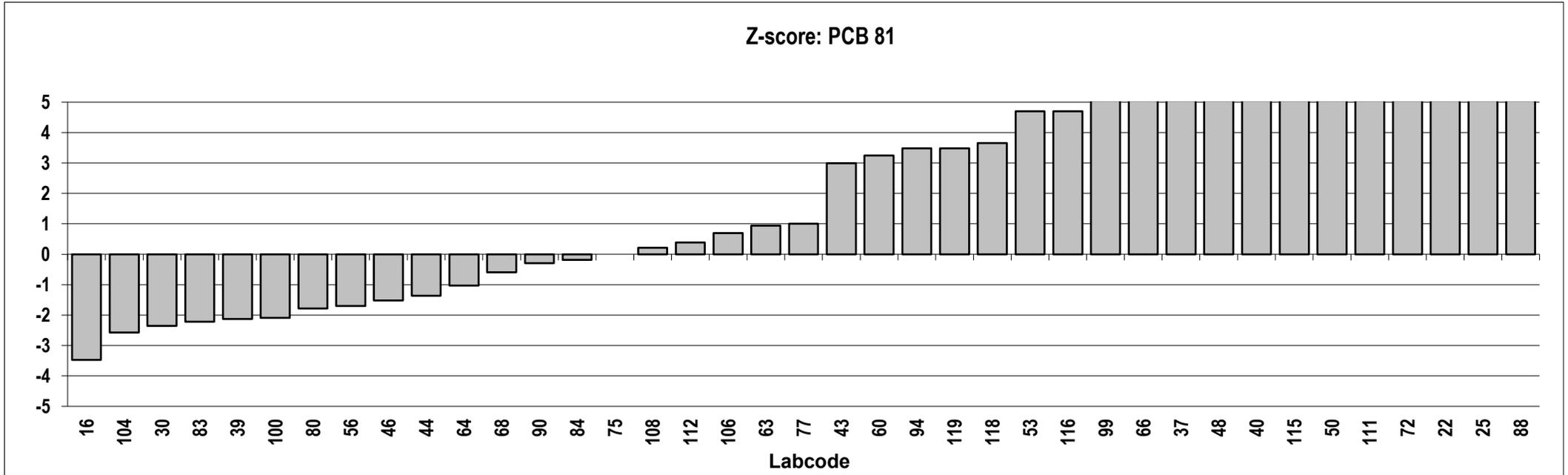
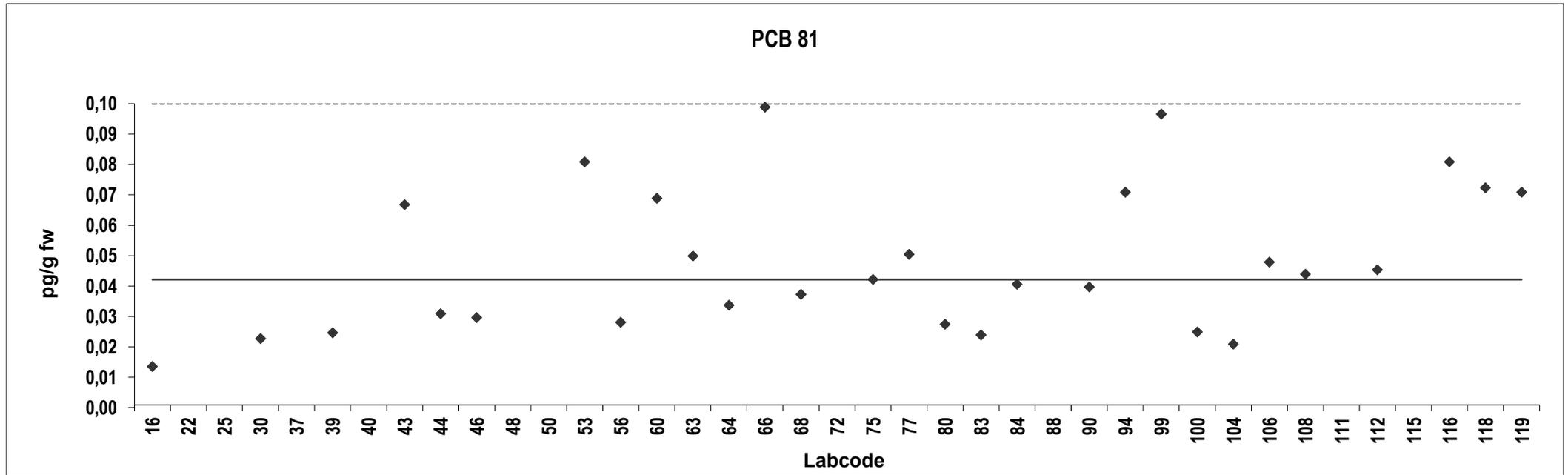
Consensus statistics	
Consensus median, pg/g	0,055
Median all values pg/g	0,061
Consensus mean, pg/g	0,053
Standard deviation, pg/g	0,024
Relative standard deviation, %	45
No. of values reported	39
No. of values removed	8
No. of reported non-detects	12



**Cream**  
**Congener: PCB 81**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,013	-3,5	ND			
22	1,8	218	Outlier			
25	2,0	237	Outlier,ND			
30	0,022	-2,4				
37	0,12	9,5	Outlier			
39	0,024	-2,1				
40	0,14	12	Outlier			
43	0,066	3,0				
44	0,030	-1,4				
46	0,029	-1,5				
48	0,14	12	Outlier,ND			
50	0,24	24	Outlier,ND			
53	0,080	4,7	ND			
56	0,027	-1,7				
60	0,068	3,2				
63	0,049	0,94				
64	0,033	-1,0				
66	0,098	6,9				
68	0,036	-0,59	ND			
72	1,5	177	Outlier,ND			
75	0,041	0,00000				
77	0,050	1,0				
80	0,027	-1,8				
83	0,023	-2,2				
84	0,040	-0,19	ND			
88	2,3	279	Outlier,ND			
90	0,039	-0,29				
94	0,070	3,5				
99	0,096	6,6	ND			
100	0,024	-2,1				
104	0,020	-2,6	ND			
106	0,047	0,70				
108	0,043	0,21				
111	1,0	116	Outlier,ND			
112	0,044	0,38				
115	0,18	17	Outlier			
116	0,080	4,7				
118	0,071	3,7				
119	0,070	3,5				

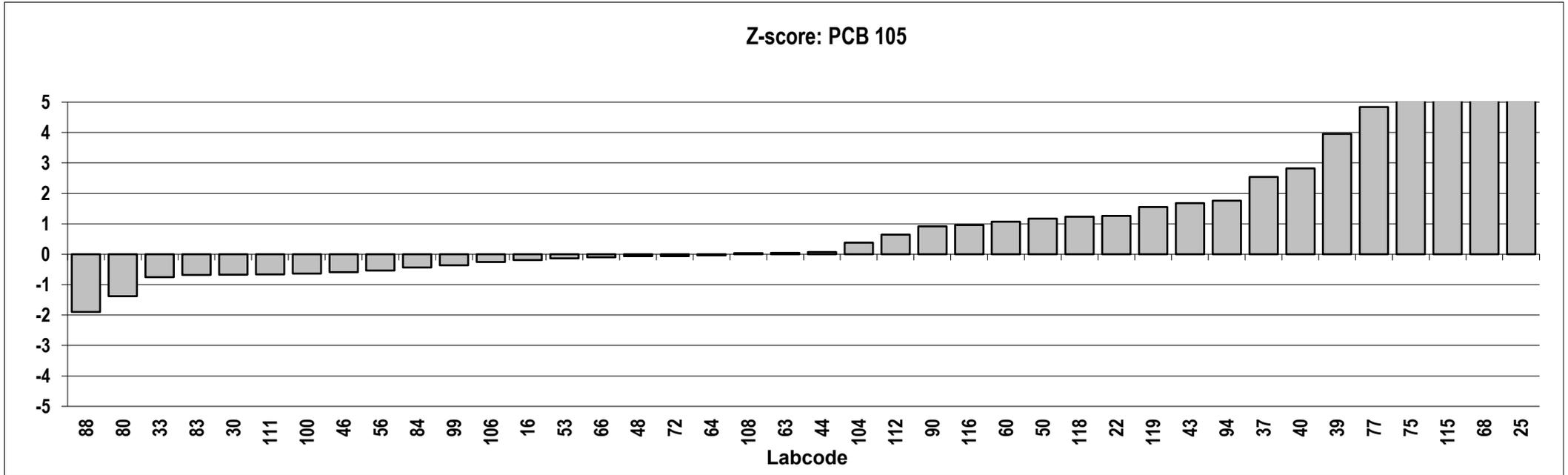
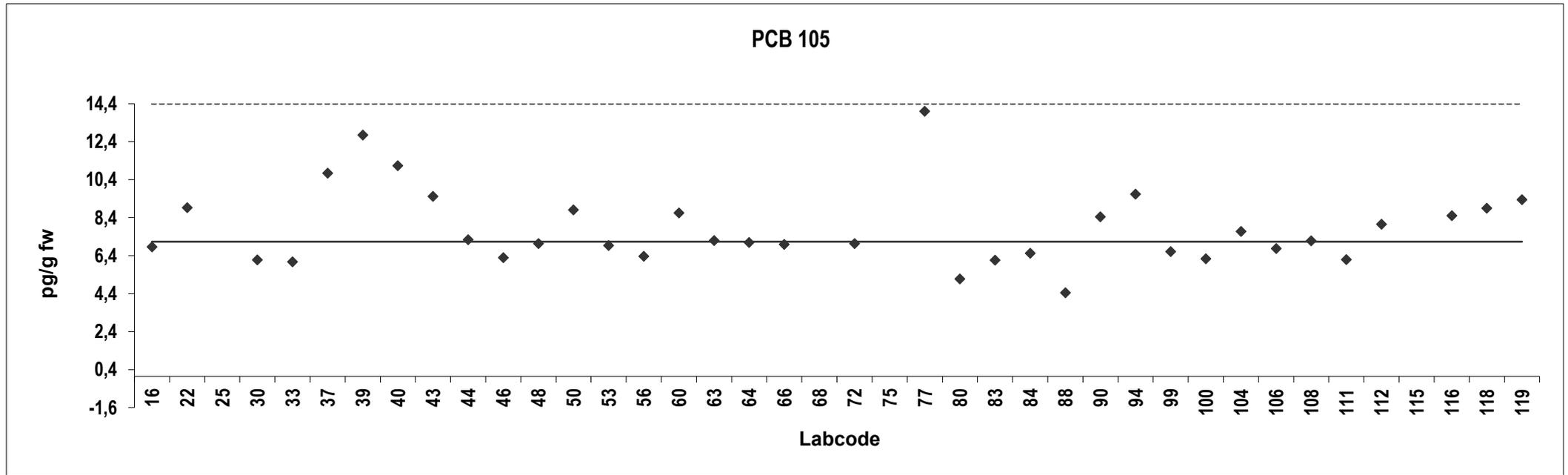
Consensus statistics	
Consensus median, pg/g	0,041
Median all values pg/g	0,050
Consensus mean, pg/g	0,047
Standard deviation, pg/g	0,024
Relative standard deviation, %	51
No. of values reported	39
No. of values removed	10
No. of reported non-detects	12



**Cream**  
**Congener: PCB 105**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	6,8	-0,19				
22	8,9	1,3				
25	26	13	Outlier			
30	6,1	-0,68				
33	6,0	-0,75				
37	11	2,5				
39	13	4,0				
40	11	2,8				
43	9,5	1,7				
44	7,2	0,073				
46	6,3	-0,59				
48	7,0	-0,068				
50	8,8	1,2				
53	6,9	-0,14				
56	6,3	-0,54				
60	8,6	1,1				
63	7,2	0,045				
64	7,0	-0,035				
66	7,0	-0,10				
68	20	8,9	Outlier			
72	7,0	-0,068				
75	18	7,6	Outlier,ND			
77	14	4,8				
80	5,1	-1,4				
83	6,1	-0,68				
84	6,5	-0,44				
88	4,4	-1,9				
90	8,4	0,92				
94	9,6	1,8				
99	6,6	-0,37				
100	6,2	-0,64	ND			
104	7,6	0,38				
106	6,7	-0,26				
108	7,1	0,035				
111	6,2	-0,66				
112	8,0	0,64				
115	19	8,7	Outlier			
116	8,5	0,96				
118	8,9	1,2				
119	9,3	1,6				

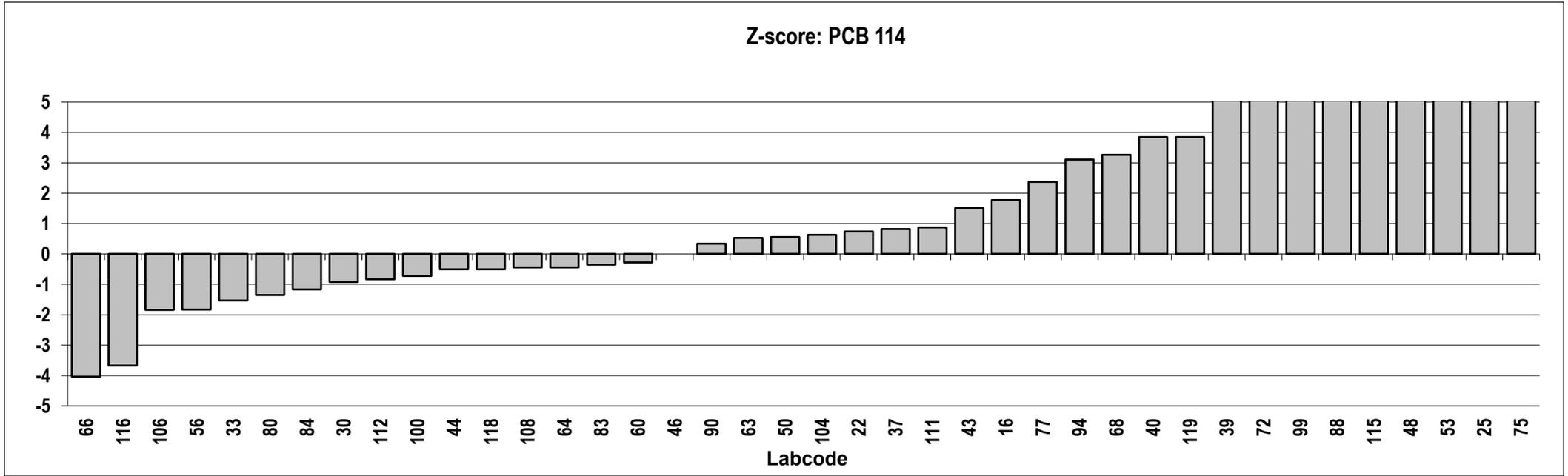
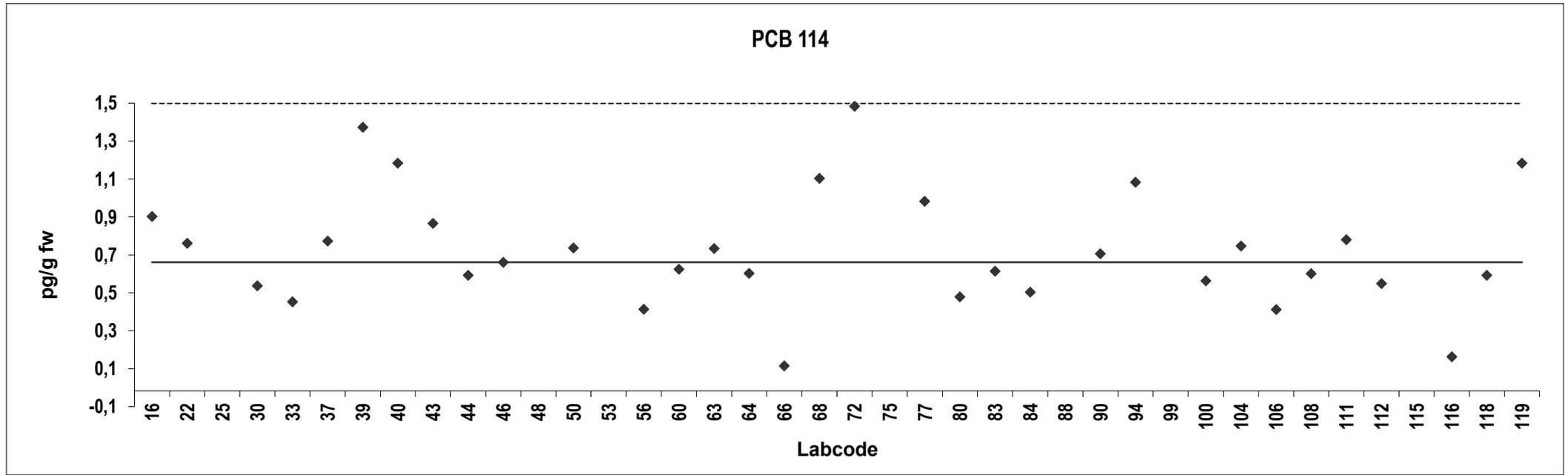
Consensus statistics	
Consensus median, pg/g	7,1
Median all values pg/g	7,2
Consensus mean, pg/g	7,8
Standard deviation, pg/g	2,0
Relative standard deviation, %	26
No. of values reported	40
No. of values removed	4
No. of reported non-detects	2



**Cream**  
**Congener: PCB 114**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,92	1,8				
22	0,78	0,74				
25	10	69	Outlier,ND			
30	0,55	-0,92				
33	0,47	-1,5				
37	0,79	0,82				
39	1,4	5,2				
40	1,2	3,8				
43	0,88	1,5				
44	0,61	-0,50				
46	0,68	0,00000				
48	2,8	15	Outlier,ND			
50	0,75	0,56				
53	3,1	18	Outlier,ND			
56	0,43	-1,8				
60	0,64	-0,27				
63	0,75	0,53				
64	0,62	-0,44				
66	0,13	-4,0				
68	1,1	3,3				
72	1,5	6,1	ND			
75	11	72	Outlier,ND			
77	1,0	2,4	ND			
80	0,50	-1,3				
83	0,63	-0,35				
84	0,52	-1,2				
88	2,1	10	Outlier,ND			
90	0,72	0,33				
94	1,1	3,1				
99	1,9	9,1	Outlier,ND			
100	0,58	-0,72	ND			
104	0,76	0,62				
106	0,43	-1,8				
108	0,62	-0,45				
111	0,80	0,88				
112	0,57	-0,83				
115	2,5	14	Outlier			
116	0,18	-3,7				
118	0,61	-0,50				
119	1,2	3,8				

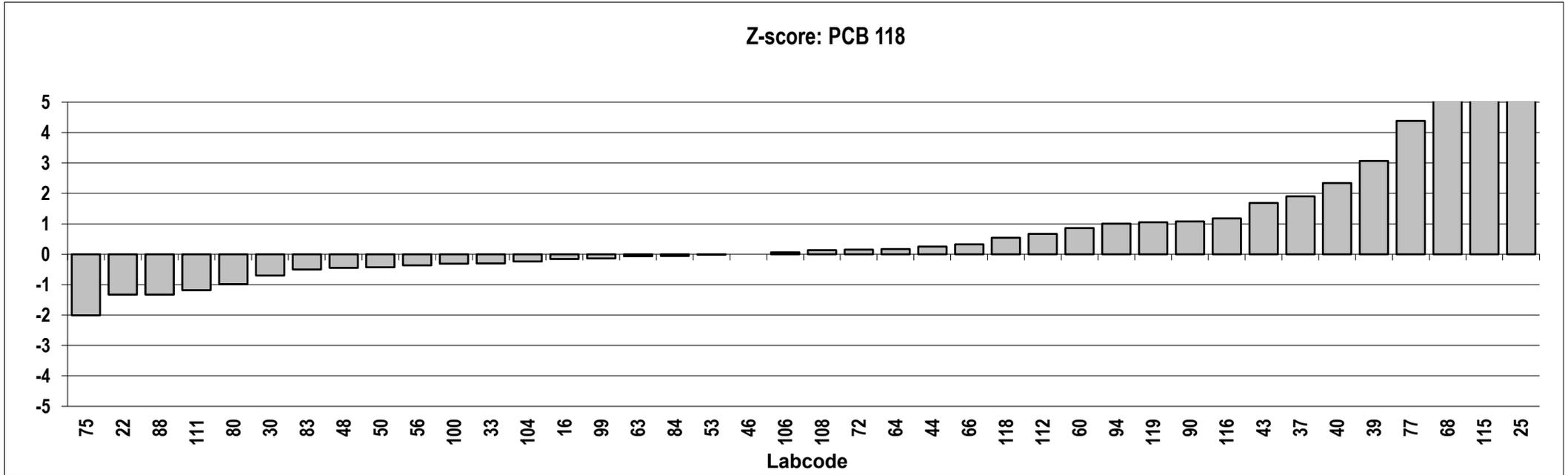
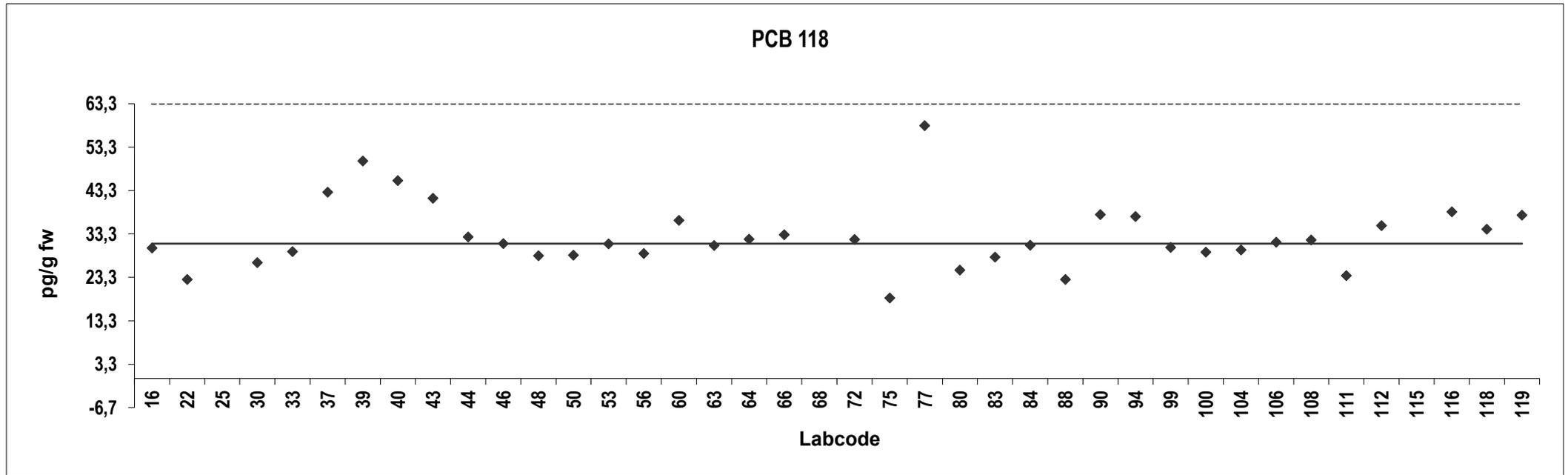
Consensus statistics	
Consensus median, pg/g	0,68
Median all values pg/g	0,76
Consensus mean, pg/g	0,74
Standard deviation, pg/g	0,31
Relative standard deviation, %	42
No. of values reported	40
No. of values removed	7
No. of reported non-detects	9



**Cream**  
**Congener: PCB 118**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	30	-0,16				
22	23	-1,3				
25	106	12	Outlier			
30	27	-0,70				
33	29	-0,30				
37	43	1,9				
39	50	3,1				
40	46	2,3				
43	42	1,7				
44	33	0,25				
46	31	0,00000				
48	28	-0,44				
50	28	-0,43				
53	31	-0,010				
56	29	-0,36				
60	36	0,86				
63	31	-0,066				
64	32	0,17				
66	33	0,33				
68	79	7,7	Outlier			
72	32	0,15				
75	19	-2,0				
77	58	4,4				
80	25	-0,98				
83	28	-0,50				
84	31	-0,057				
88	23	-1,3				
90	38	1,1				
94	37	1,0				
99	30	-0,14				
100	29	-0,32				
104	30	-0,23				
106	31	0,057				
108	32	0,13				
111	24	-1,2				
112	35	0,67				
115	86	8,9	Outlier			
116	38	1,2				
118	34	0,54				
119	38	1,1				

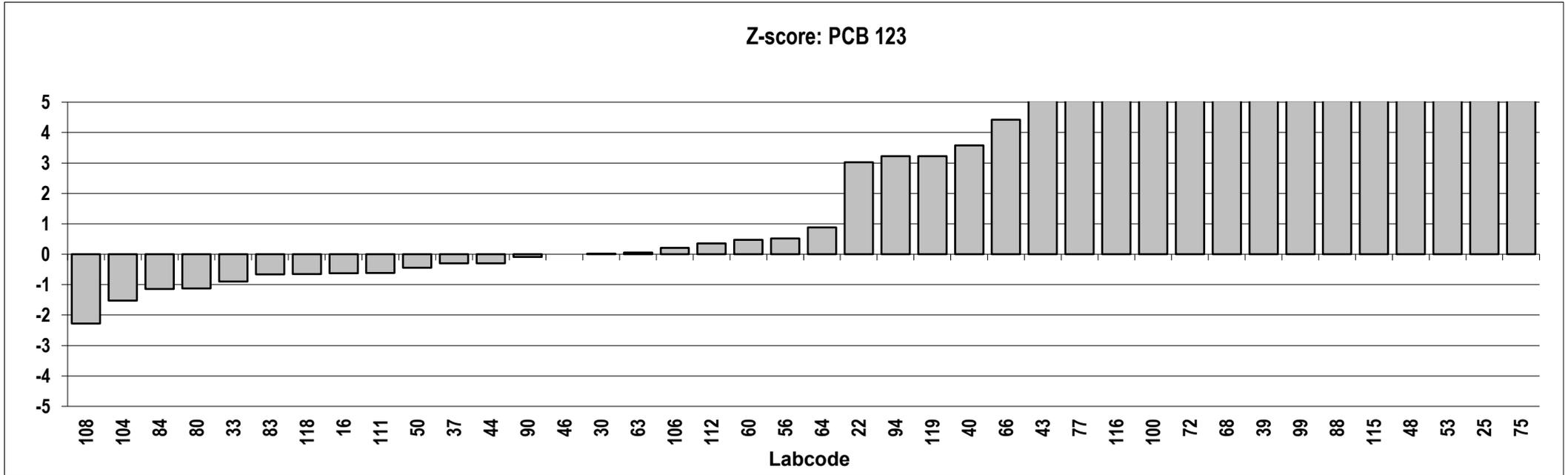
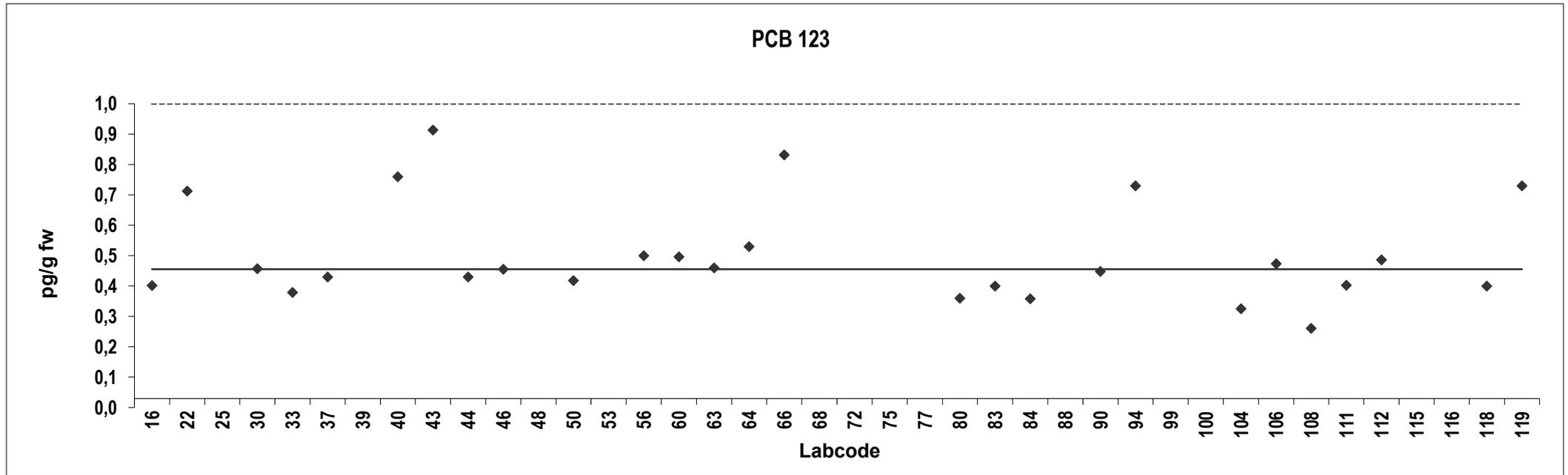
Consensus statistics	
Consensus median, pg/g	31
Median all values pg/g	32
Consensus mean, pg/g	33
Standard deviation, pg/g	7,7
Relative standard deviation, %	24
No. of values reported	40
No. of values removed	3
No. of reported non-detects	0



**Cream**  
**Congener: PCB 123**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,37	-0,63				
22	0,68	3,0				
25	10	112	Outlier,ND			
30	0,43	0,016				
33	0,35	-0,90				
37	0,40	-0,30				
39	1,7	15	Outlier			
40	0,73	3,6	ND			
43	0,88	5,4				
44	0,40	-0,30				
46	0,43	0,00000				
48	2,8	28	Outlier,ND			
50	0,39	-0,44				
53	3,1	31	Outlier,ND			
56	0,47	0,52				
60	0,47	0,47				
63	0,43	0,051				
64	0,50	0,88				
66	0,80	4,4				
68	1,6	14	Outlier			
72	1,5	13	Outlier,ND			
75	13	145	Outlier,ND			
77	1,0	6,7	Outlier,ND			
80	0,33	-1,1				
83	0,37	-0,66				
84	0,33	-1,1				
88	2,2	20	Outlier,ND			
90	0,42	-0,091				
94	0,70	3,2				
99	1,9	17	Outlier,ND			
100	1,2	9,0	Outlier,ND			
104	0,30	-1,5				
106	0,44	0,21				
108	0,23	-2,3				
111	0,37	-0,62				
112	0,46	0,36				
115	2,4	23	Outlier			
116	1,1	7,3	Outlier			
118	0,37	-0,65				
119	0,70	3,2				

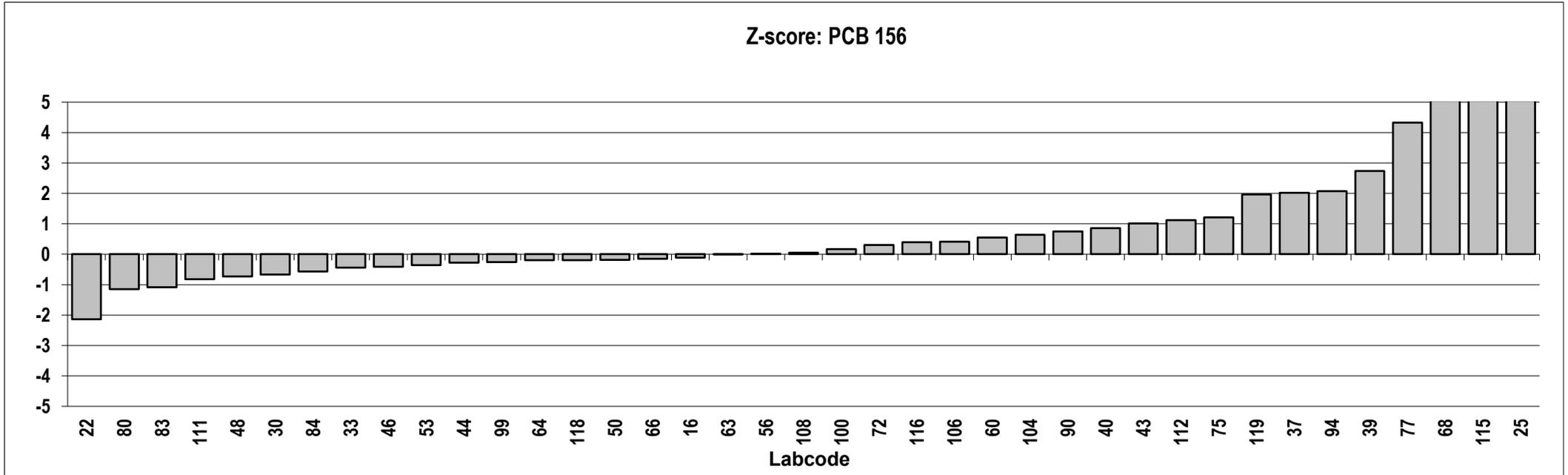
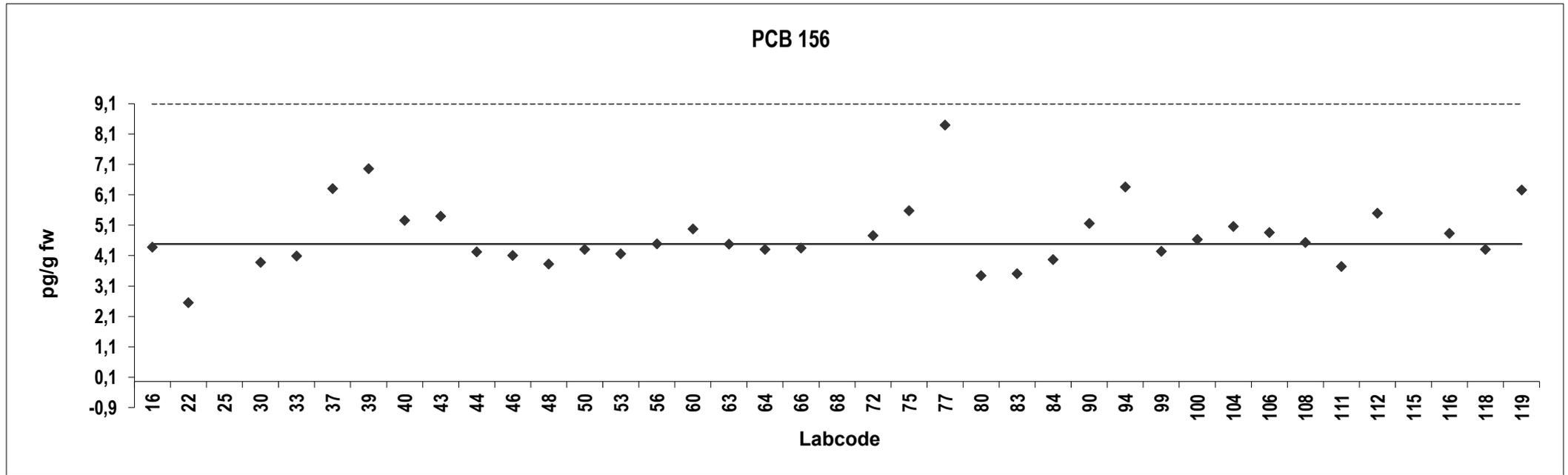
Consensus statistics	
Consensus median, pg/g	0,43
Median all values pg/g	0,49
Consensus mean, pg/g	0,47
Standard deviation, pg/g	0,16
Relative standard deviation, %	35
No. of values reported	40
No. of values removed	13
No. of reported non-detects	10



**Cream**  
**Congener: PCB 156**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	4,4	-0,12				
22	2,6	-2,1				
25	16	13	Outlier			
30	3,9	-0,67				
33	4,1	-0,44				
37	6,4	2,0				
39	7,0	2,7				
40	5,3	0,86				
43	5,4	1,0				
44	4,3	-0,28				
46	4,1	-0,42				
48	3,9	-0,73				
50	4,4	-0,19				
53	4,2	-0,36				
56	4,5	0,0055				
60	5,0	0,55				
63	4,5	-0,0055				
64	4,3	-0,20				
66	4,4	-0,15				
68	13	9,1	Outlier			
72	4,8	0,30				
75	5,6	1,2	ND			
77	8,4	4,3				
80	3,5	-1,1				
83	3,5	-1,1				
84	4,0	-0,57				
90	5,2	0,75				
94	6,4	2,1				
99	4,3	-0,26				
100	4,7	0,17				
104	5,1	0,64				
106	4,9	0,41				
108	4,6	0,051				
111	3,8	-0,82				
112	5,5	1,1				
115	13	9,1	Outlier			
116	4,9	0,39				
118	4,4	-0,19				
119	6,3	2,0				

Consensus statistics	
Consensus median, pg/g	4,5
Median all values pg/g	4,6
Consensus mean, pg/g	4,8
Standard deviation, pg/g	1,1
Relative standard deviation, %	23
No. of values reported	39
No. of values removed	3
No. of reported non-detects	1

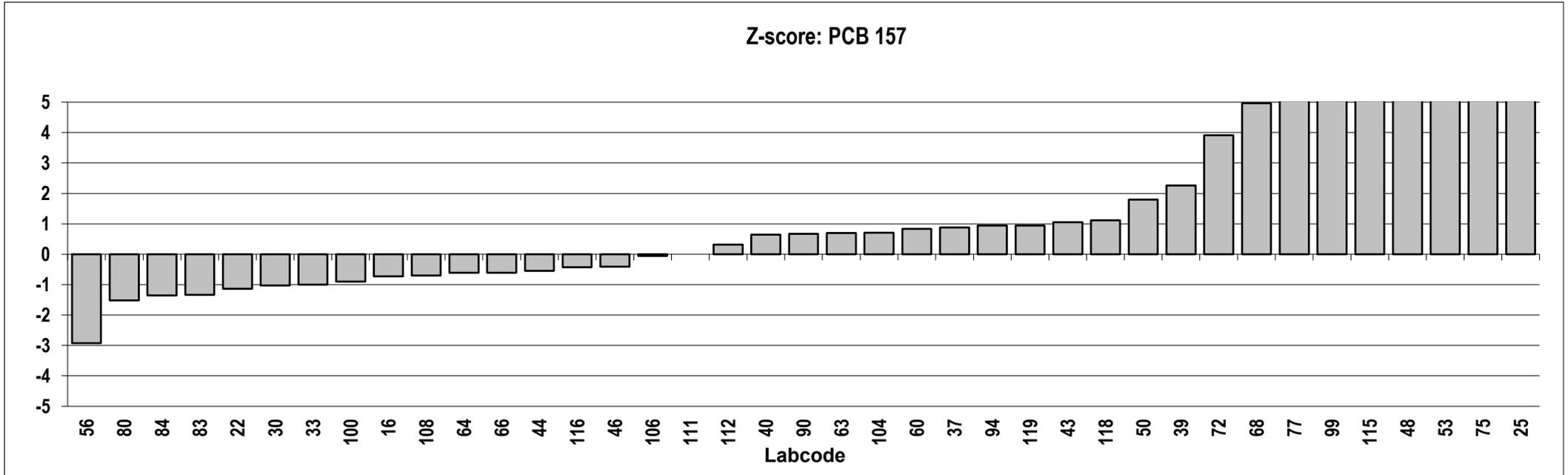
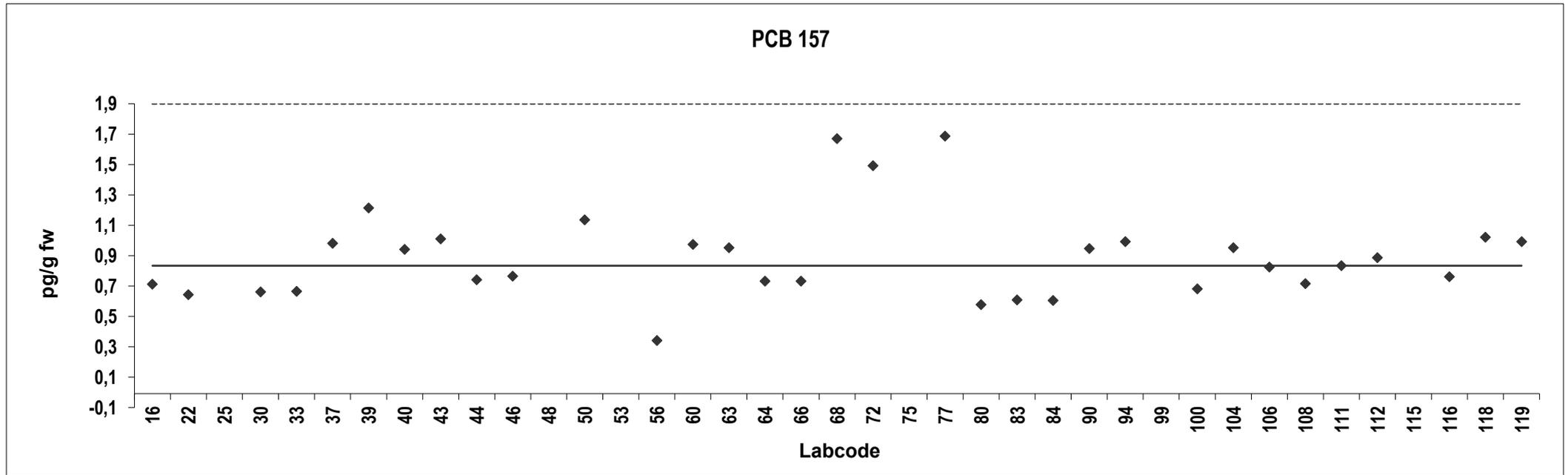


**Cream**  
**Congener: PCB 157**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,72	-0,73				
22	0,65	-1,1				
25	10	54	Outlier,ND			
30	0,67	-1,0				
33	0,67	-1,0				
37	0,99	0,88				
39	1,2	2,3				
40	0,95	0,64				
43	1,0	1,1				
44	0,75	-0,55				
46	0,77	-0,41				
48	2,8	11	Outlier,ND			
50	1,1	1,8				
53	3,1	13	Outlier,ND			
56	0,35	-2,9				
60	0,98	0,84				
63	0,96	0,70				
64	0,74	-0,61				
66	0,74	-0,61				
68	1,7	5,0				
72	1,5	3,9	ND			
75	6,4	33	Outlier,ND			
77	1,7	5,1				
80	0,59	-1,5				
83	0,62	-1,3				
84	0,61	-1,4				
90	0,95	0,67				
94	1,0	0,94				
99	1,9	6,4	Outlier,ND			
100	0,69	-0,90				
104	0,96	0,71				
106	0,83	-0,058				
108	0,72	-0,70				
111	0,84	0,00000				
112	0,90	0,31				
115	2,1	7,5	Outlier			
116	0,77	-0,43				
118	1,0	1,1				
119	1,0	0,94				

**Consensus statistics**

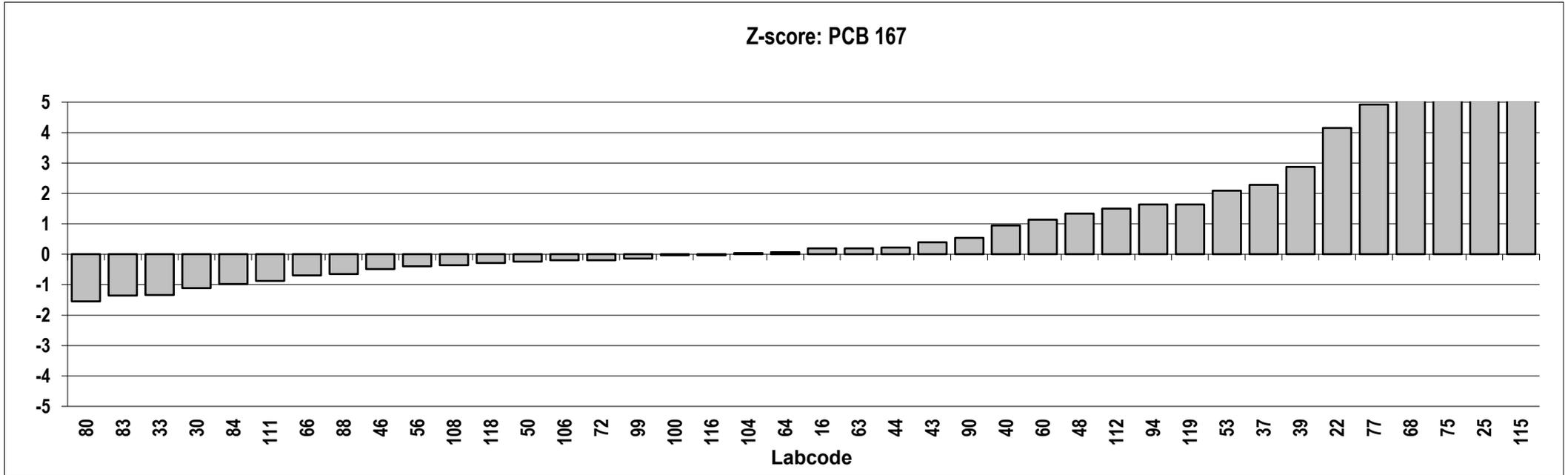
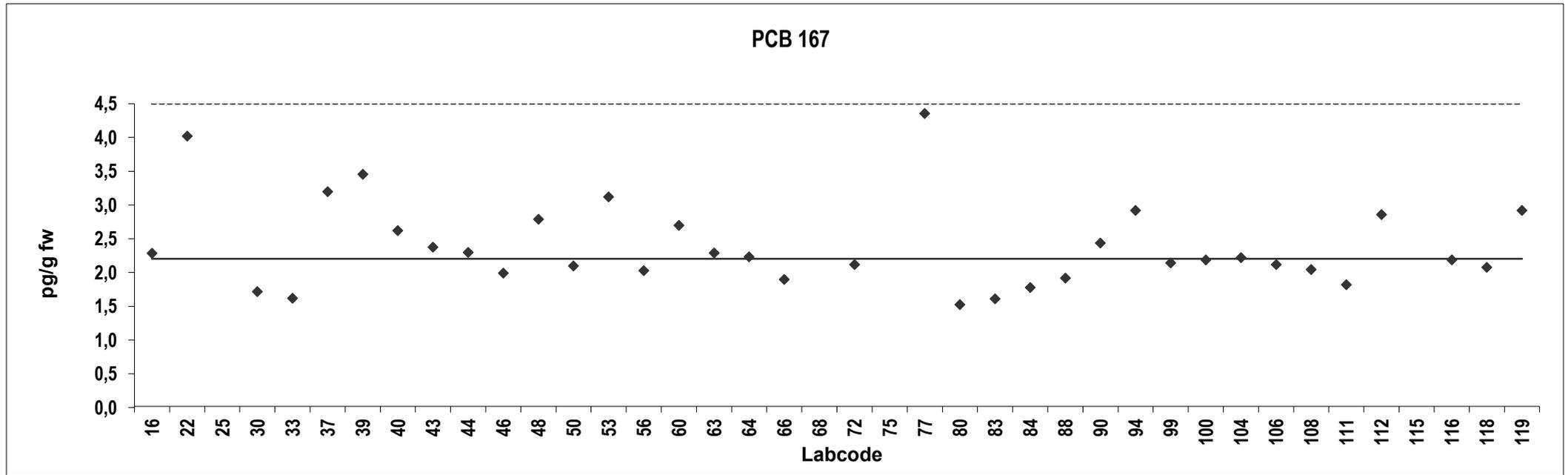
Consensus median, pg/g	0,84
Median all values pg/g	0,95
Consensus mean, pg/g	0,90
Standard deviation, pg/g	0,30
Relative standard deviation, %	33
No. of values reported	39
No. of values removed	6
No. of reported non-detects	6



**Cream**  
**Congener: PCB 167**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	2,3	0,19				
22	4,0	4,2				
25	10	18	Outlier,ND			
30	1,7	-1,1				
33	1,6	-1,3				
37	3,2	2,3				
39	3,4	2,9				
40	2,6	0,95				
43	2,4	0,39				
44	2,3	0,22				
46	2,0	-0,49				
48	2,8	1,3	ND			
50	2,1	-0,24				
53	3,1	2,1	ND			
56	2,0	-0,40				
60	2,7	1,1				
63	2,3	0,19				
64	2,2	0,064				
66	1,9	-0,70				
68	6,4	9,6	Outlier			
72	2,1	-0,19				
75	7,3	12	Outlier,ND			
77	4,3	4,9				
80	1,5	-1,6				
83	1,6	-1,4				
84	1,8	-0,98				
88	1,9	-0,65				
90	2,4	0,54				
94	2,9	1,6				
99	2,1	-0,14				
100	2,2	-0,034				
104	2,2	0,034				
106	2,1	-0,20				
108	2,0	-0,36				
111	1,8	-0,88				
112	2,8	1,5				
115	12	23	Outlier			
116	2,2	-0,034				
118	2,1	-0,29				
119	2,9	1,6				

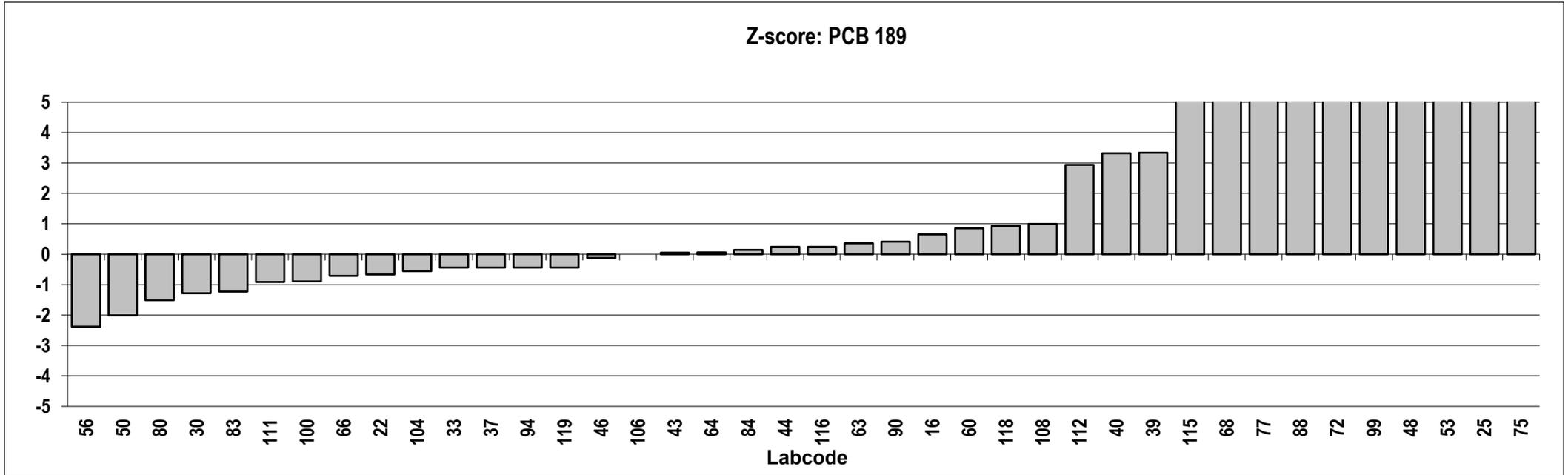
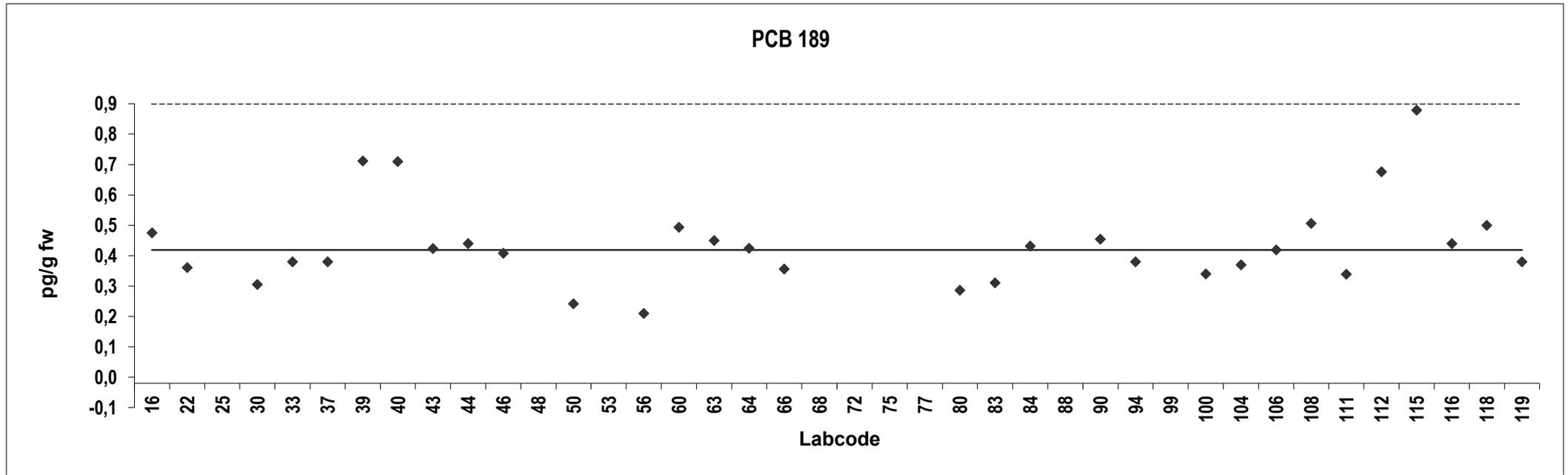
Consensus statistics	
Consensus median, pg/g	2,2
Median all values pg/g	2,2
Consensus mean, pg/g	2,4
Standard deviation, pg/g	0,64
Relative standard deviation, %	27
No. of values reported	40
No. of values removed	4
No. of reported non-detects	4



**Cream**  
**Congener: PCB 189**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,50	0,65				
22	0,38	-0,66				
25	10	109	Outlier,ND			
30	0,33	-1,3				
33	0,40	-0,44				
37	0,40	-0,44				
39	0,73	3,3				
40	0,73	3,3	ND			
43	0,44	0,050				
44	0,46	0,24				
46	0,43	-0,12				
48	2,8	27	Outlier,ND			
50	0,26	-2,01	ND			
53	3,1	30	Outlier,ND			
56	0,23	-2,4	ND			
60	0,51	0,85				
63	0,47	0,36				
64	0,44	0,062				
66	0,38	-0,71				
68	1,0	6,5	Outlier			
72	1,5	12	Outlier,ND			
75	22	244	Outlier,ND			
77	1,0	6,5	Outlier			
80	0,31	-1,5				
83	0,33	-1,2				
84	0,45	0,14				
88	1,2	8,6	Outlier,ND			
90	0,47	0,41				
94	0,40	-0,44				
99	1,9	17	Outlier,ND			
100	0,36	-0,90				
104	0,39	-0,55				
106	0,44	0,00000				
108	0,53	1,0				
111	0,36	-0,91				
112	0,70	2,9				
115	0,90	5,2	ND			
116	0,46	0,24				
118	0,52	0,93				
119	0,40	-0,44				

Consensus statistics	
Consensus median, pg/g	0,44
Median all values pg/g	0,46
Consensus mean, pg/g	0,45
Standard deviation, pg/g	0,14
Relative standard deviation, %	31
No. of values reported	40
No. of values removed	9
No. of reported non-detects	11

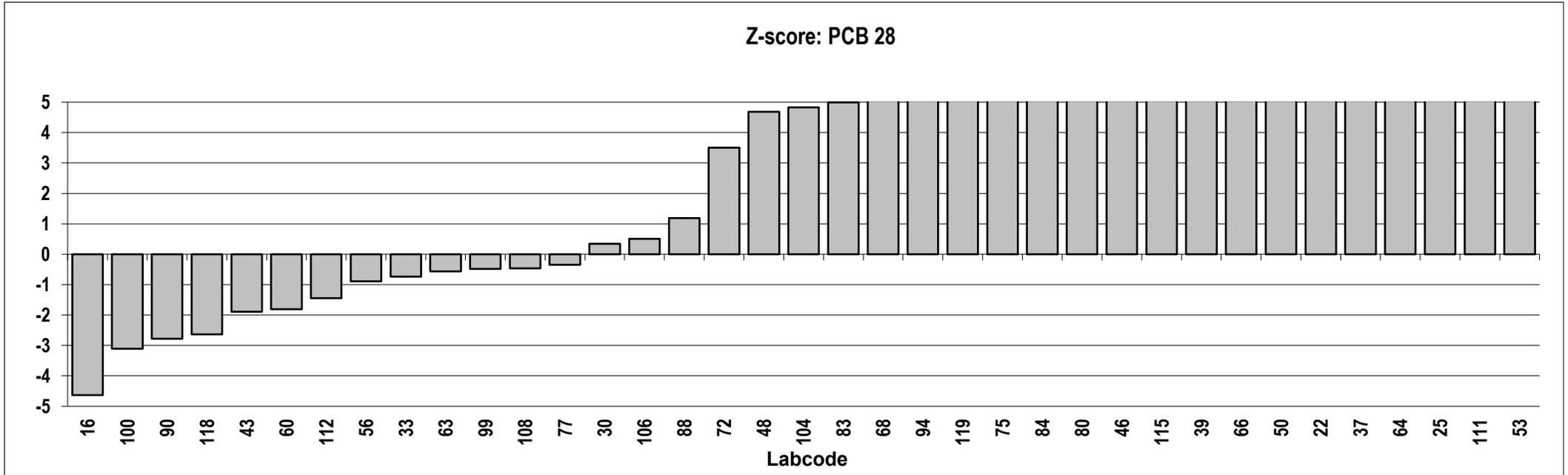
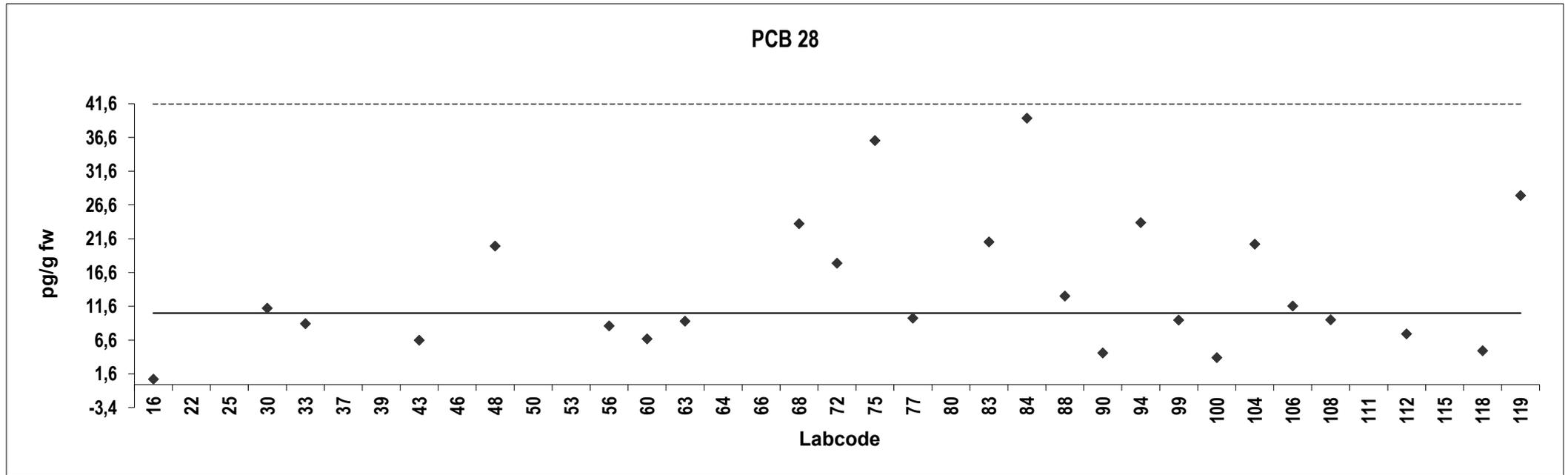


**Cream**  
**Congener: PCB 28**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,79	-4,6				
22	65	26	Outlier			
25	100	42	Outlier,ND			
30	11	0,35				
33	9,0	-0,74				
37	87	36	Outlier			
39	50	19	Outlier			
43	6,6	-1,9				
46	45	16	Outlier			
48	21	4,7				
50	55	21	Outlier			
53	190	85	Outlier,ND			
56	8,7	-0,89				
60	6,8	-1,8				
63	9,4	-0,57				
64	95	40	Outlier			
66	52	19	Outlier			
68	24	6,2				
72	18	3,5	ND			
75	36	12				
77	9,8	-0,35				
80	45	16	Outlier			
83	21	5,0				
84	39	14				
88	13	1,2				
90	4,7	-2,8				
94	24	6,3				
99	9,6	-0,48	ND			
100	4,0	-3,1				
104	21	4,8				
106	12	0,50				
108	9,6	-0,46				
111	100	42	Outlier,ND			
112	7,5	-1,4				
115	50	19	Outlier			
118	5,0	-2,6	ND			
119	28	8,2				

**Consensus statistics**

Consensus median, pg/g	11
Median all values pg/g	21
Consensus mean, pg/g	14
Standard deviation, pg/g	10
Relative standard deviation, %	70
No. of values reported	37
No. of values removed	12
No. of reported non-detects	6

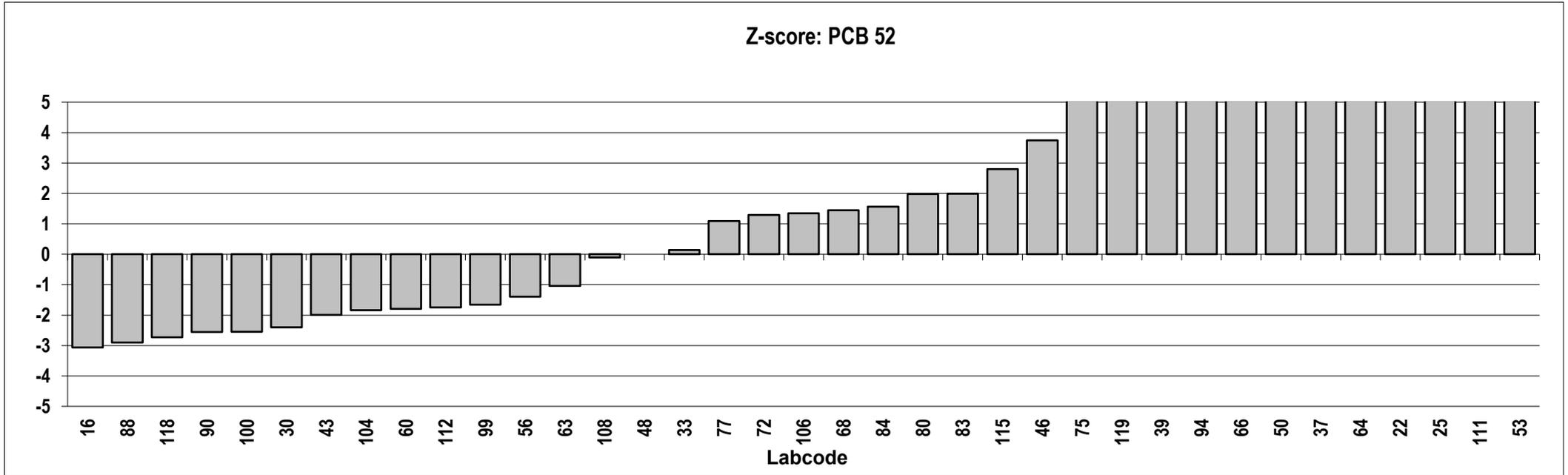
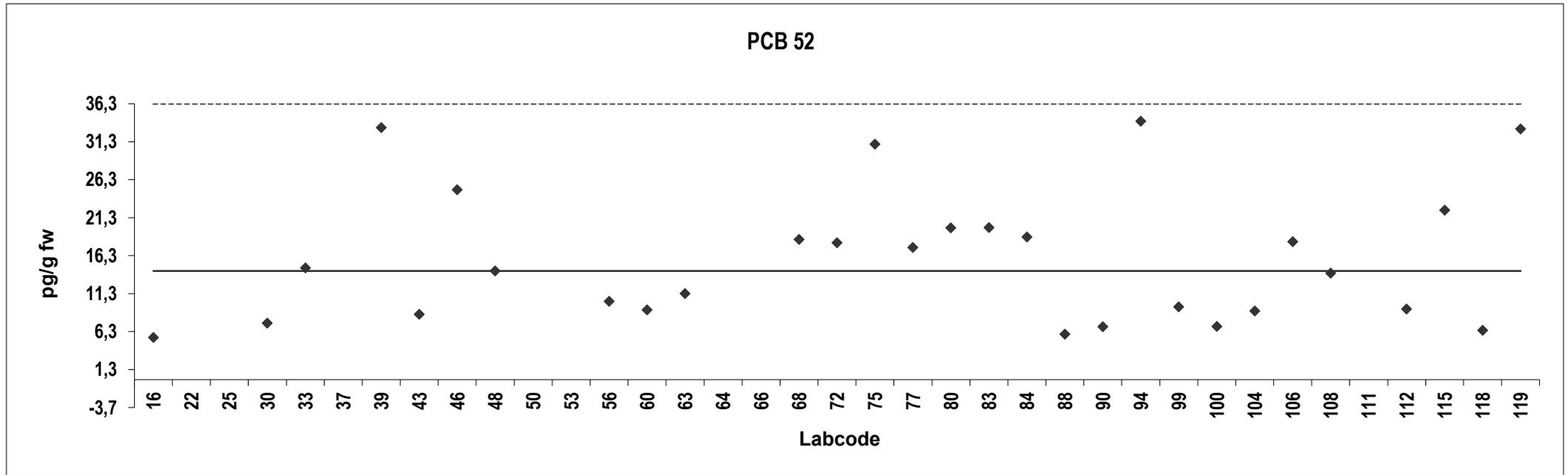


**Cream**  
**Congener: PCB 52**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	5,5	-3,1				
22	61	16	Outlier			
25	100	30	Outlier,ND			
30	7,4	-2,4				
33	15	0,14				
37	50	12	Outlier			
39	33	6,6				
43	8,6	-2,0				
46	25	3,7				
48	14	0,00000				
50	42	9,8	Outlier			
53	190	61	Outlier,ND			
56	10	-1,4				
60	9,2	-1,8				
63	11	-1,0				
64	52	13	Outlier			
66	38	8,3	Outlier			
68	18	1,4				
72	18	1,3	ND			
75	31	5,8				
77	17	1,1				
80	20	2,0				
83	20	2,0				
84	19	1,6				
88	6,0	-2,9				
90	7,0	-2,6				
94	34	6,9				
99	9,6	-1,7	ND			
100	7,0	-2,6				
104	9,0	-1,8				
106	18	1,3				
108	14	-0,10				
111	100	30	Outlier,ND			
112	9,3	-1,7				
115	22	2,8				
118	6,5	-2,7				
119	33	6,5				

**Consensus statistics**

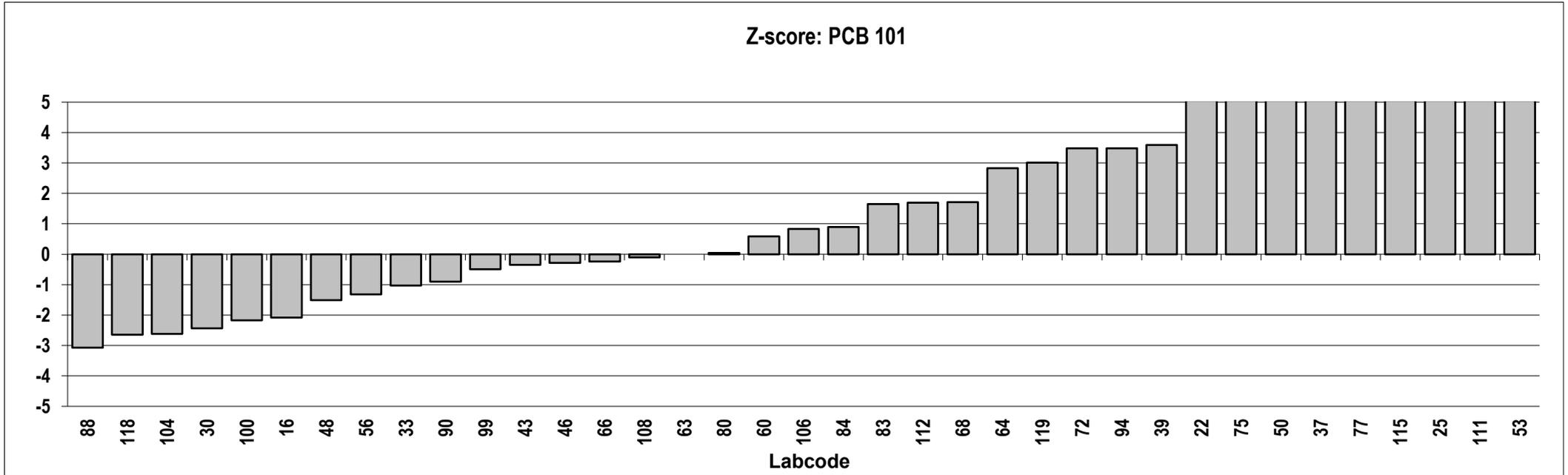
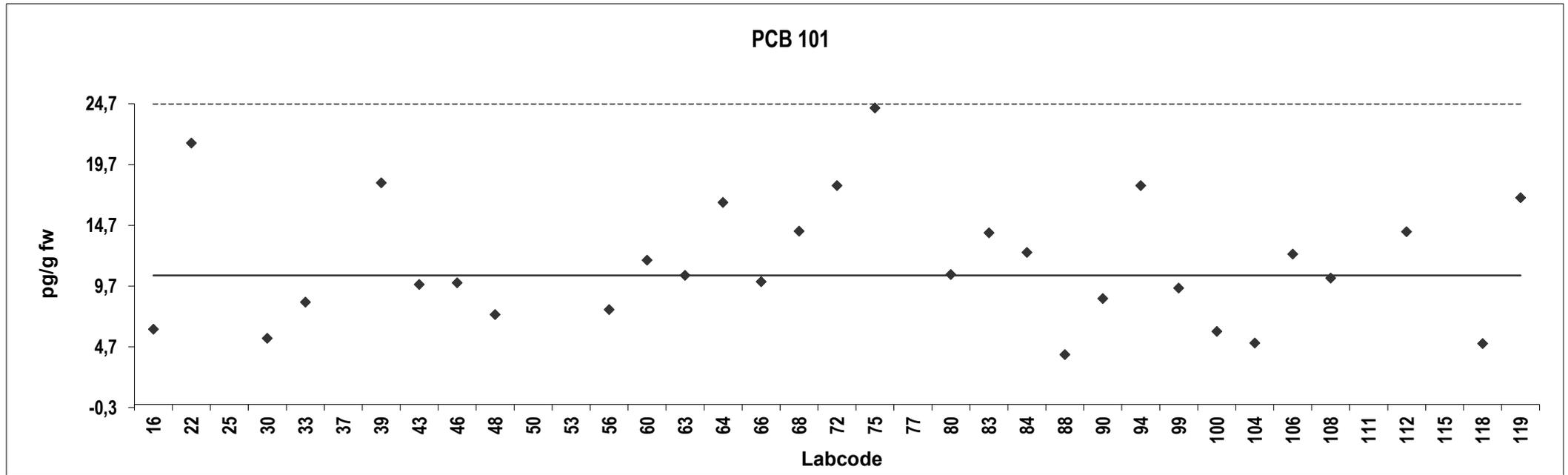
Consensus median, pg/g	14
Median all values pg/g	18
Consensus mean, pg/g	16
Standard deviation, pg/g	8,7
Relative standard deviation, %	55
No. of values reported	37
No. of values removed	8
No. of reported non-detects	5



**Cream**  
**Congener: PCB 101**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	6,2	-2,1				
22	21	5,1				
25	100	42	Outlier,ND			
30	5,4	-2,4				
33	8,4	-1,0				
37	32	10	Outlier			
39	18	3,6				
43	9,9	-0,35				
46	10	-0,29				
48	7,4	-1,5				
50	28	8,3	Outlier			
53	190	85	Outlier,ND			
56	7,8	-1,3				
60	12	0,59				
63	11	0,00000				
64	17	2,8				
66	10	-0,24				
68	14	1,7				
72	18	3,5	ND			
75	24	6,5				
77	33	10	Outlier			
80	11	0,038				
83	14	1,7				
84	13	0,89				
88	4,1	-3,1				
90	8,7	-0,90				
94	18	3,5				
99	9,6	-0,49	ND			
100	6,0	-2,2				
104	5,1	-2,6				
106	12	0,83				
108	10	-0,10				
111	100	42	Outlier,ND			
112	14	1,7				
115	43	15	Outlier			
118	5,0	-2,6	ND			
119	17	3,0				

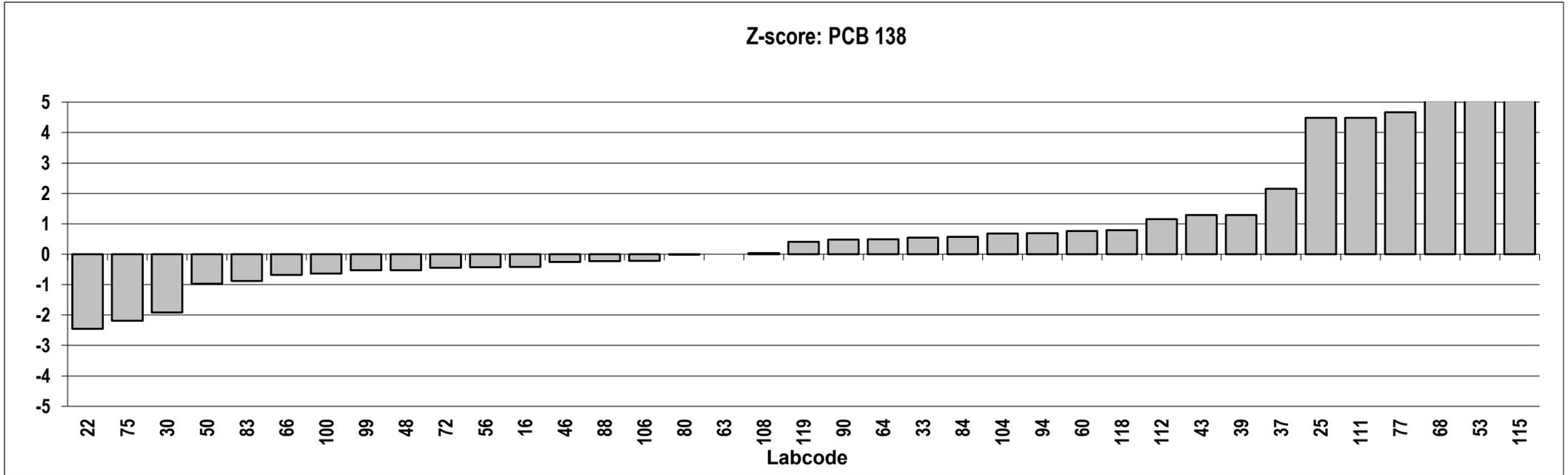
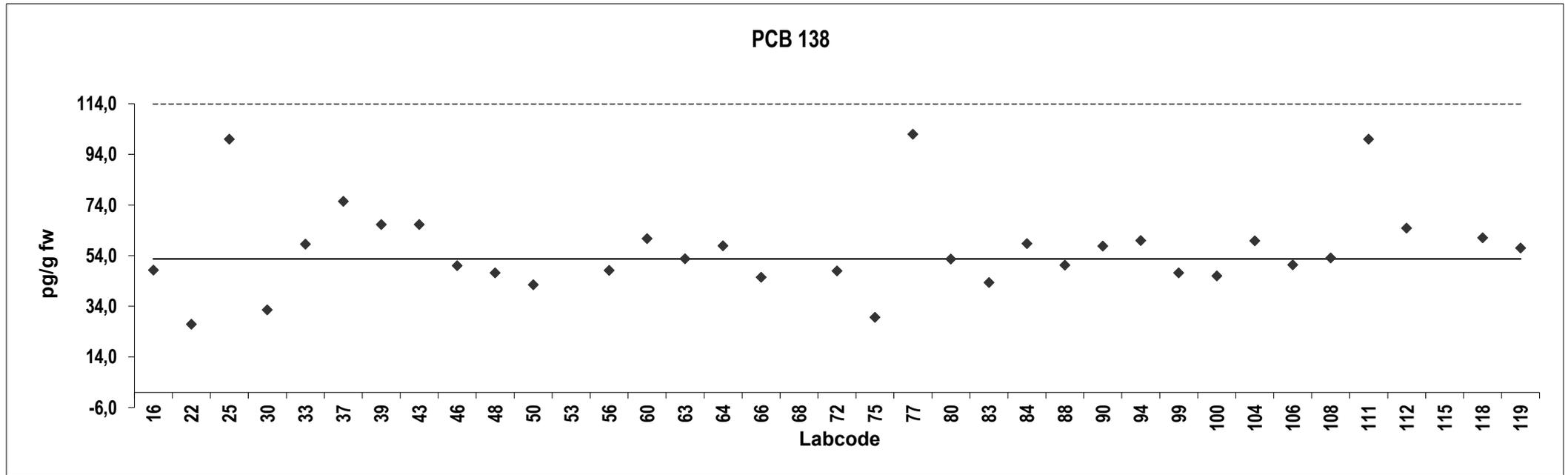
Consensus statistics	
Consensus median, pg/g	11
Median all values pg/g	12
Consensus mean, pg/g	12
Standard deviation, pg/g	5,2
Relative standard deviation, %	44
No. of values reported	37
No. of values removed	7
No. of reported non-detects	6



**Cream**  
**Congener: PCB 138**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	48	-0,42				
22	27	-2,4				
25	100	4,5				
30	33	-1,9				
33	59	0,55				
37	75	2,2				
39	66	1,3				
43	66	1,3				
46	50	-0,26				
48	47	-0,52				
50	43	-0,97				
53	190	13	Outlier,ND			
56	48	-0,43				
60	61	0,76				
63	53	0,00000				
64	58	0,49				
66	46	-0,68				
68	132	7,5	Outlier			
72	48	-0,45				
75	30	-2,2				
77	102	4,7				
80	53	-0,011				
83	43	-0,88				
84	59	0,58				
88	50	-0,23				
90	58	0,48				
94	60	0,69				
99	47	-0,53				
100	46	-0,64				
104	60	0,68				
106	50	-0,22				
108	53	0,036				
111	100	4,5	ND			
112	65	1,2				
115	194	13	Outlier			
118	61	0,79				
119	57	0,41				

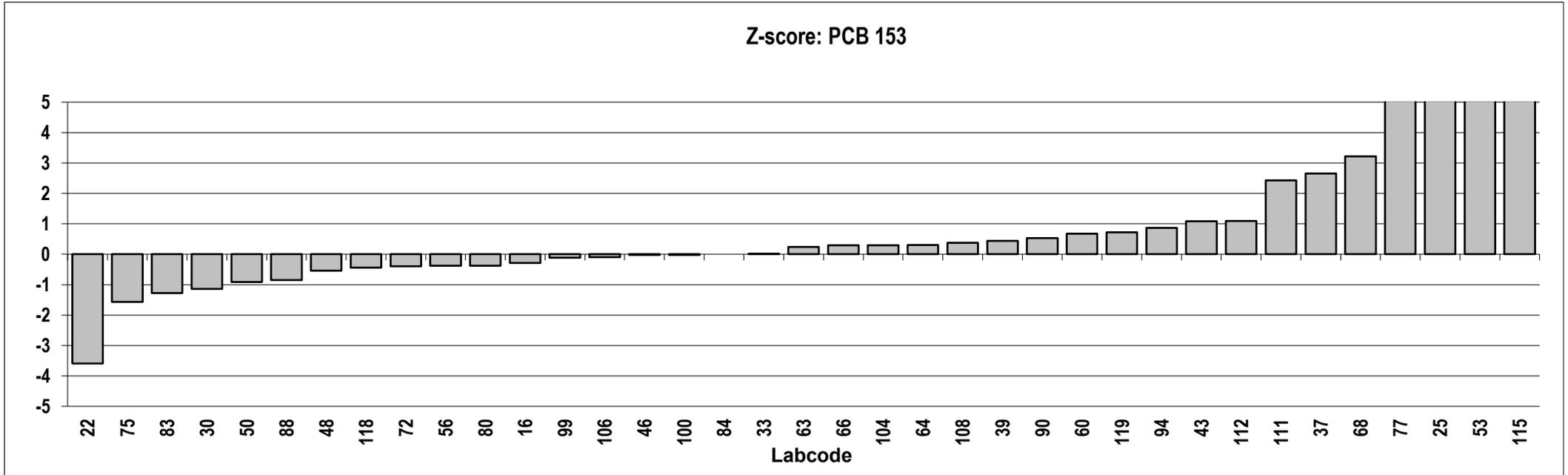
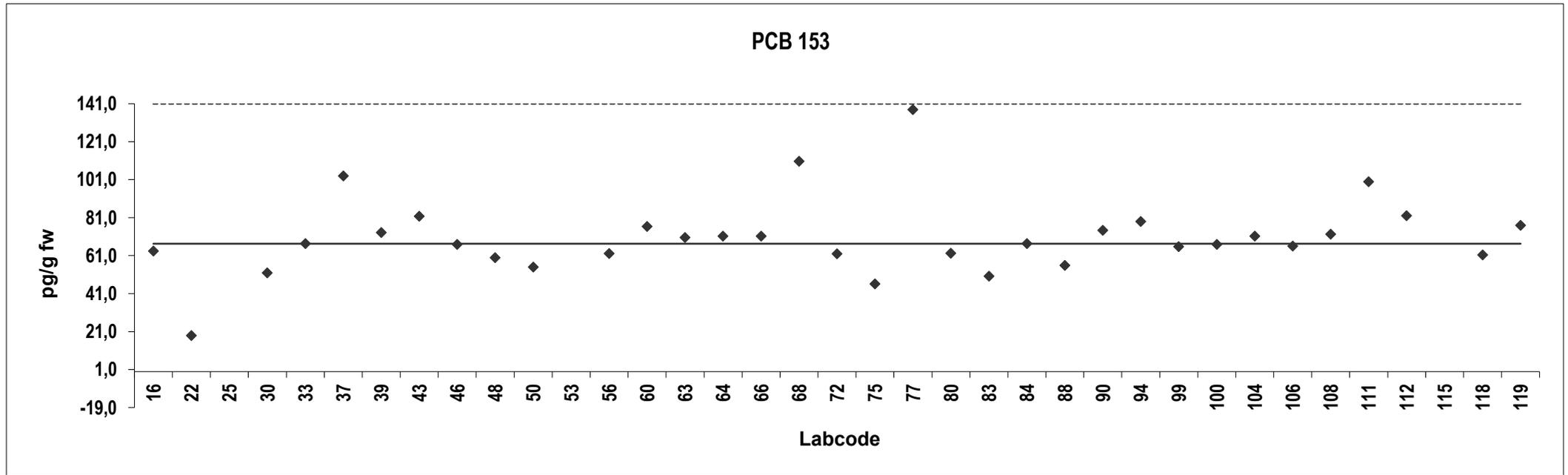
Consensus statistics	
Consensus median, pg/g	53
Median all values pg/g	57
Consensus mean, pg/g	56
Standard deviation, pg/g	17
Relative standard deviation, %	31
No. of values reported	37
No. of values removed	3
No. of reported non-detects	2



**Cream**  
**Congener: PCB 153**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	63	-0,29				
22	19	-3,6				
25	150	6,1	Outlier			
30	52	-1,1				
33	67	0,0064				
37	103	2,7				
39	73	0,44				
43	82	1,1				
46	67	-0,023				
48	60	-0,54				
50	55	-0,91				
53	190	9,1	Outlier,ND			
56	62	-0,38				
60	76	0,68				
63	71	0,24				
64	71	0,30				
66	71	0,30				
68	111	3,2				
72	62	-0,39				
75	46	-1,6				
77	138	5,2				
80	62	-0,38				
83	50	-1,3				
84	67	0,00000				
88	56	-0,85				
90	74	0,53				
94	79	0,87				
99	66	-0,11				
100	67	-0,023				
104	71	0,30				
106	66	-0,095				
108	72	0,38				
111	100	2,4	ND			
112	82	1,1				
115	248	13	Outlier			
118	61	-0,44				
119	77	0,72				

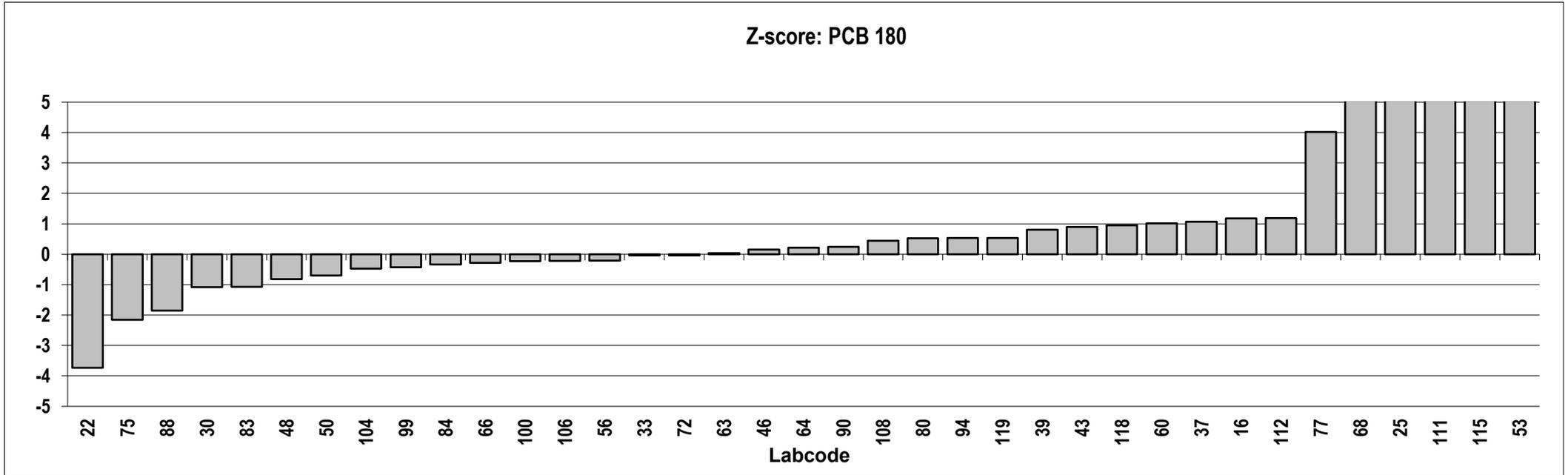
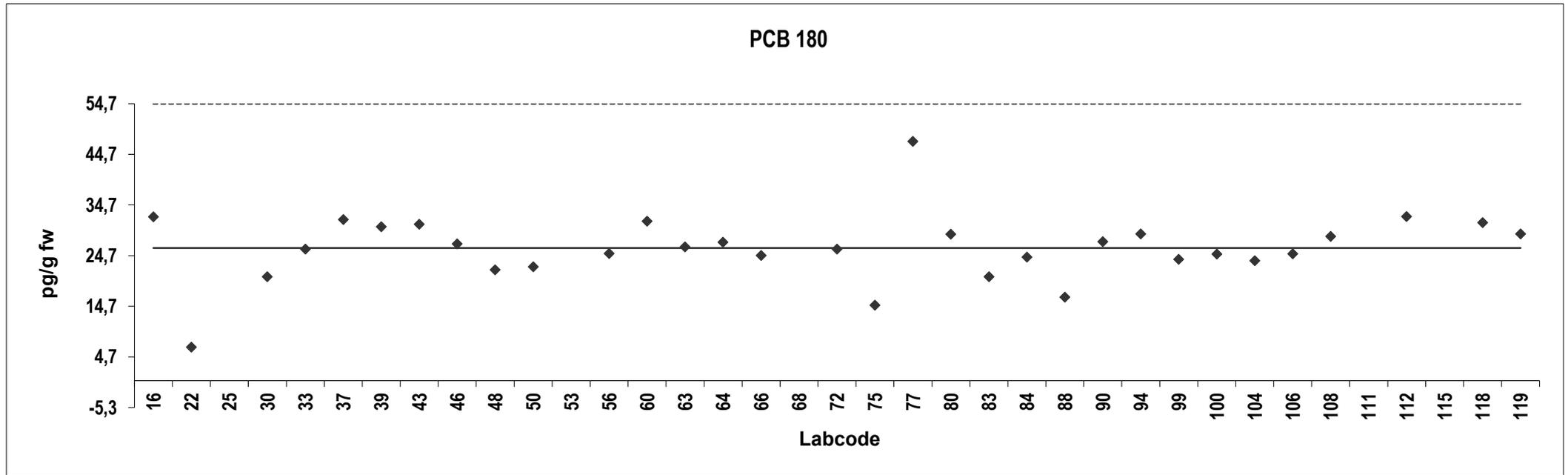
Consensus statistics	
Consensus median, pg/g	67
Median all values pg/g	71
Consensus mean, pg/g	71
Standard deviation, pg/g	20
Relative standard deviation, %	29
No. of values reported	37
No. of values removed	3
No. of reported non-detects	2



**Cream**  
**Congener: PCB 180**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	32	1,2				
22	6,6	-3,7				
25	100	14	Outlier,ND			
30	21	-1,1				
33	26	-0,037				
37	32	1,1				
39	30	0,80				
43	31	0,90				
46	27	0,15				
48	22	-0,82				
50	23	-0,71				
53	190	31	Outlier,ND			
56	25	-0,21				
60	32	1,0				
63	26	0,037				
64	27	0,22				
66	25	-0,29				
68	57	5,9	Outlier			
72	26	-0,037				
75	15	-2,2				
77	47	4,0				
80	29	0,52				
83	21	-1,1				
84	24	-0,34				
88	17	-1,9				
90	27	0,24				
94	29	0,54				
99	24	-0,43				
100	25	-0,23				
104	24	-0,48				
106	25	-0,22				
108	29	0,44				
111	100	14	Outlier,ND			
112	32	1,2				
115	127	19	Outlier			
118	31	0,96				
119	29	0,54				

Consensus statistics	
Consensus median, pg/g	26
Median all values pg/g	27
Consensus mean, pg/g	26
Standard deviation, pg/g	6,7
Relative standard deviation, %	26
No. of values reported	37
No. of values removed	5
No. of reported non-detects	3

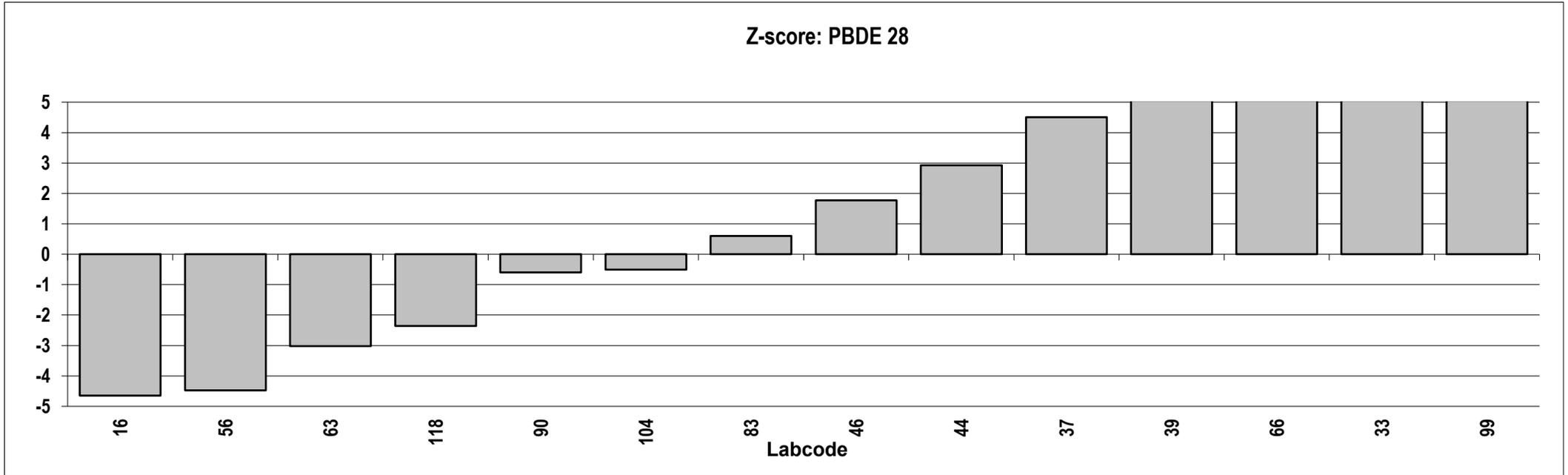
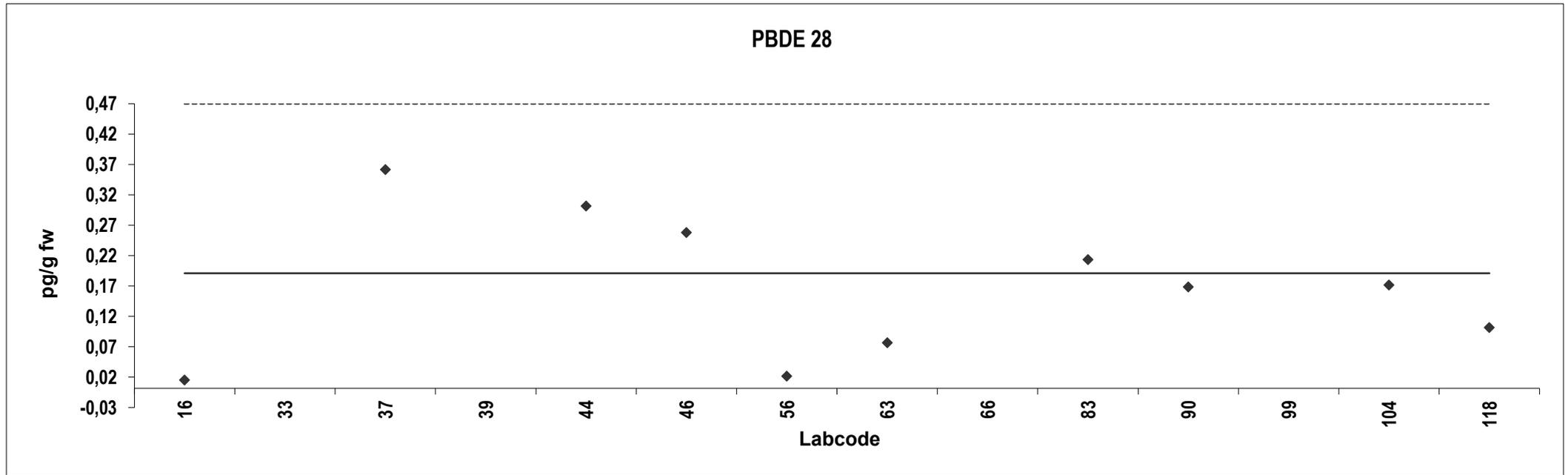


**Cream**  
**Congener: PBDE 28**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,014	-4,6	ND			
33	1,9	45	Outlier,ND			
37	0,36	4,5				
39	0,81	16	Outlier			
44	0,30	2,9	ND			
46	0,26	1,8				
56	0,020	-4,5				
63	0,075	-3,0				
66	1,1	23	Outlier			
83	0,21	0,60				
90	0,17	-0,60				
99	2,4	58	Outlier,ND			
104	0,17	-0,51	ND			
118	0,10	-2,4	ND			

**Consensus statistics**

Consensus median, pg/g	0,19
Median all values pg/g	0,23
Consensus mean, pg/g	0,17
Standard deviation, pg/g	0,12
Relative standard deviation, %	70
No. of values reported	14
No. of values removed	4
No. of reported non-detects	6

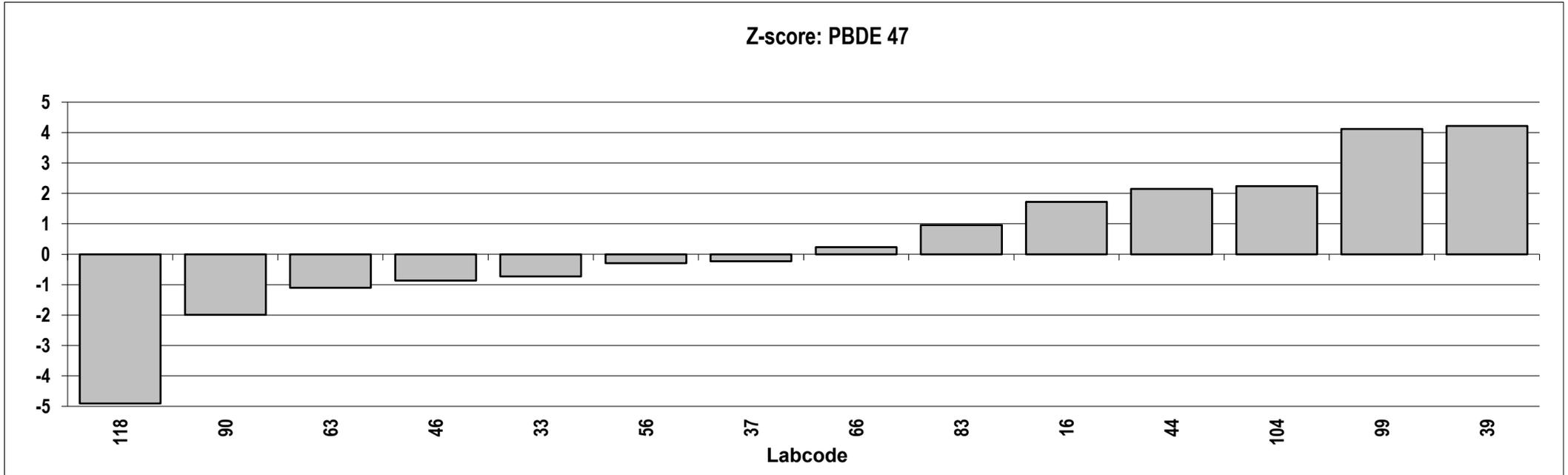
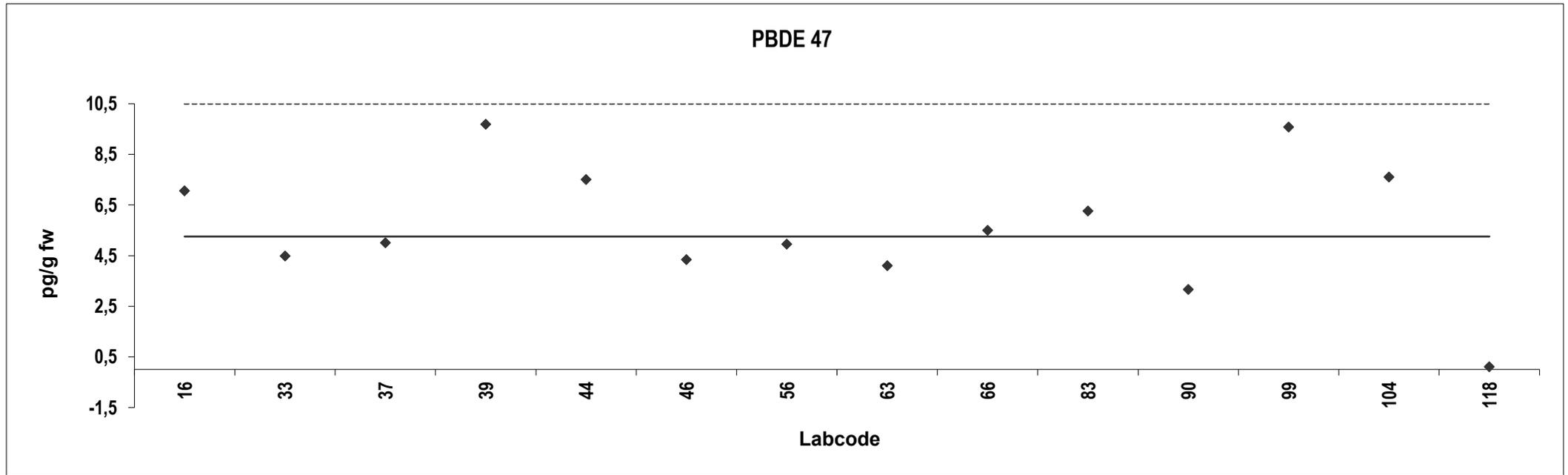


**Cream**  
Congener: PBDE 47

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	7,1	1,7				
33	4,5	-0,73				
37	5,0	-0,23				
39	9,7	4,2				
44	7,5	2,1				
46	4,3	-0,87				
56	4,9	-0,29				
63	4,1	-1,1				
66	5,5	0,23				
83	6,2	1,0				
90	3,2	-2,0				
99	9,6	4,1	ND			
104	7,6	2,2				
118	0,10	-4,9	ND			

**Consensus statistics**

Consensus median, pg/g	5,2
Median all values pg/g	5,2
Consensus mean, pg/g	5,7
Standard deviation, pg/g	2,5
Relative standard deviation, %	45
No. of values reported	14
No. of values removed	0
No. of reported non-detects	2

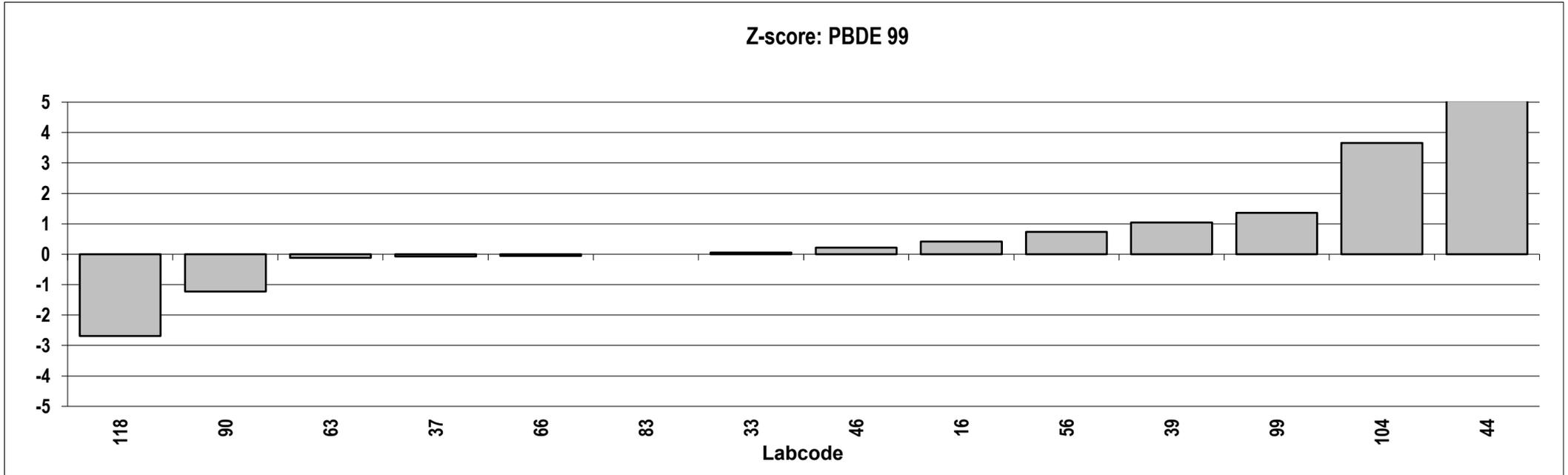
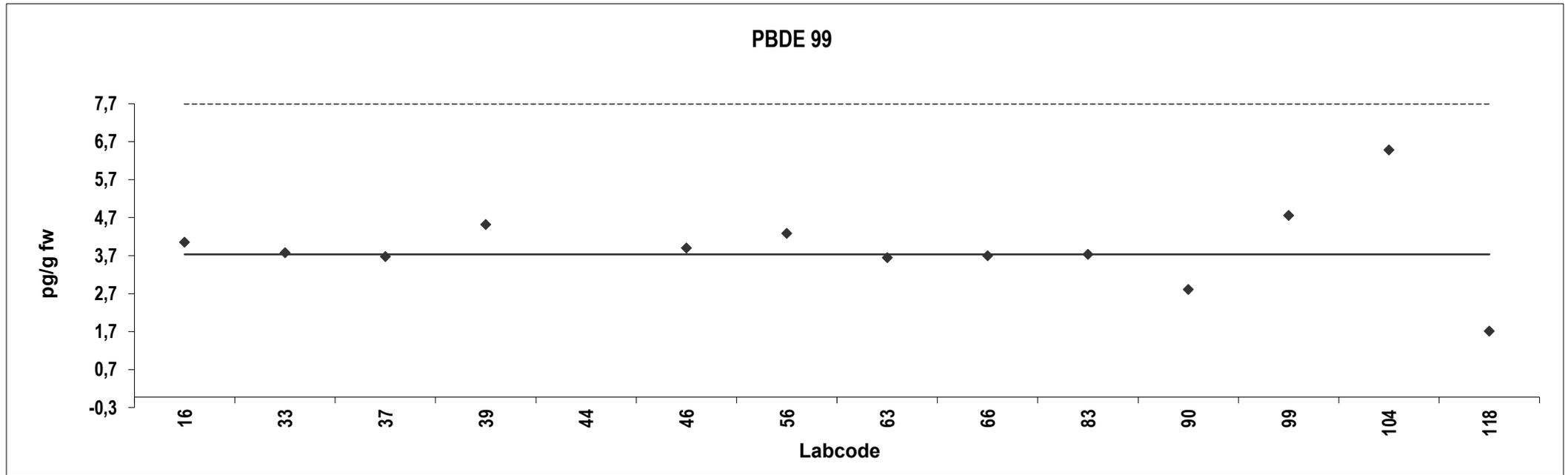


**Cream**  
**Congener: PBDE 99**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	4,1	0,42				
33	3,8	0,055	ND			
37	3,7	-0,078				
39	4,5	1,0				
44	13	12	Outlier			
46	3,9	0,22				
56	4,3	0,73				
63	3,7	-0,12				
66	3,7	-0,051				
83	3,8	0,00000				
90	2,8	-1,2				
99	4,8	1,4	ND			
104	6,5	3,7				
118	1,7	-2,7				

**Consensus statistics**

Consensus median, pg/g	3,8
Median all values pg/g	3,9
Consensus mean, pg/g	4,0
Standard deviation, pg/g	1,1
Relative standard deviation, %	27
No. of values reported	14
No. of values removed	1
No. of reported non-detects	2

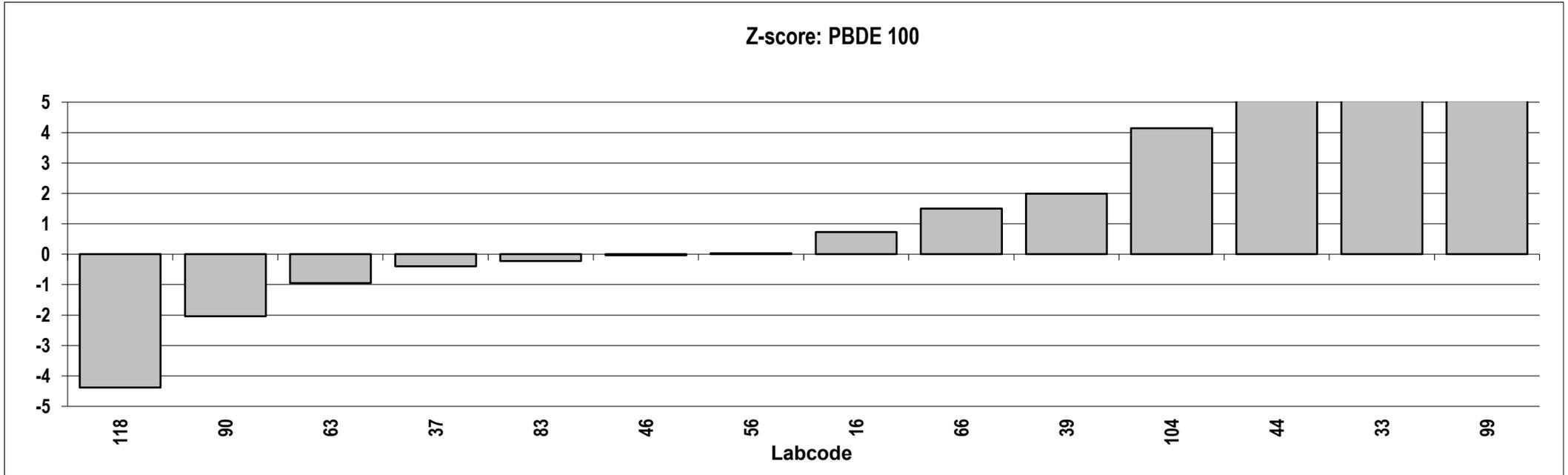
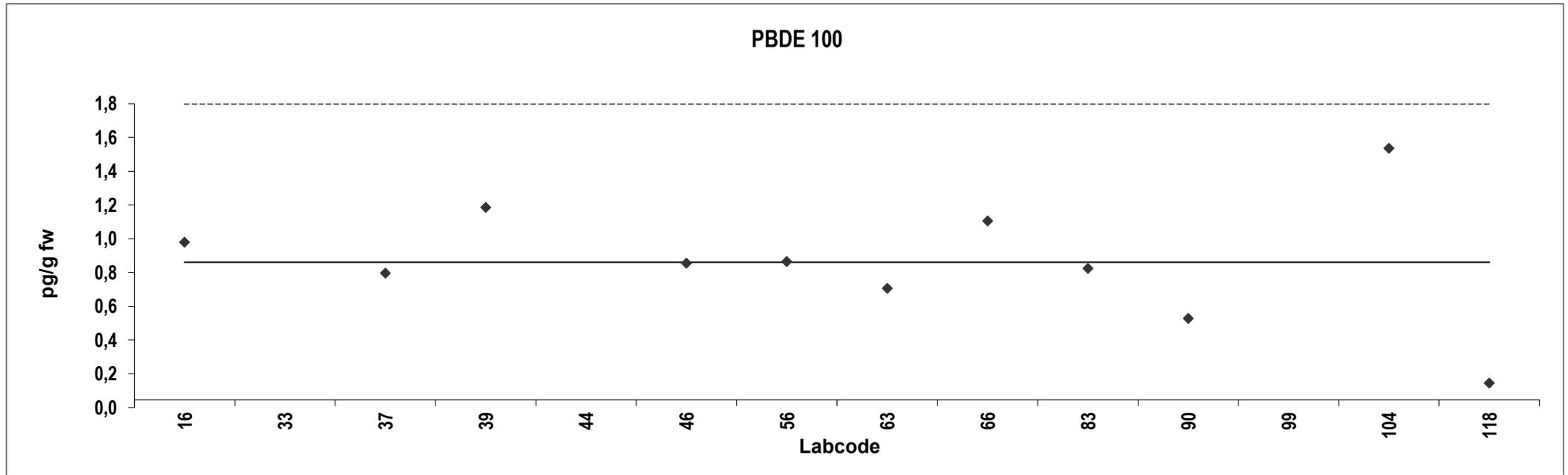


**Cream**  
Congener: PBDE 100

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,93	0,73				
33	3,8	18	Outlier,ND			
37	0,75	-0,40				
39	1,1	2,0				
44	2,2	8,5	Outlier			
46	0,81	-0,030				
56	0,82	0,030				
63	0,66	-0,95				
66	1,1	1,5				
83	0,78	-0,22				
90	0,48	-2,0				
99	4,8	24	Outlier,ND			
104	1,5	4,1				
118	0,10	-4,4	ND			

**Consensus statistics**

Consensus median, pg/g	0,82
Median all values pg/g	0,88
Consensus mean, pg/g	0,82
Standard deviation, pg/g	0,36
Relative standard deviation, %	44
No. of values reported	14
No. of values removed	3
No. of reported non-detects	3

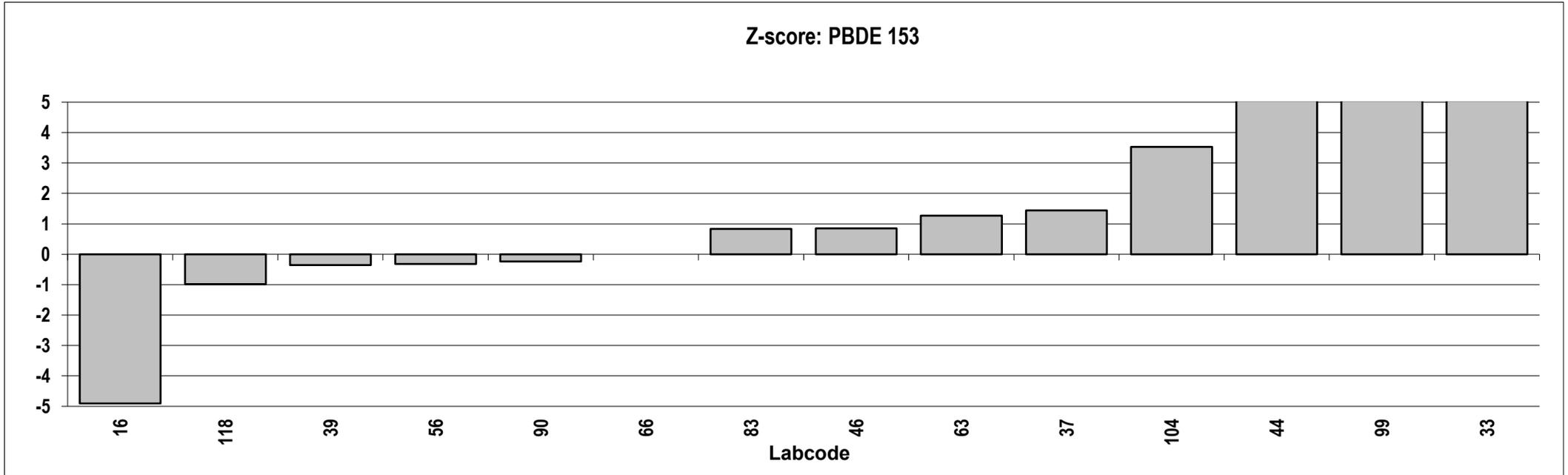
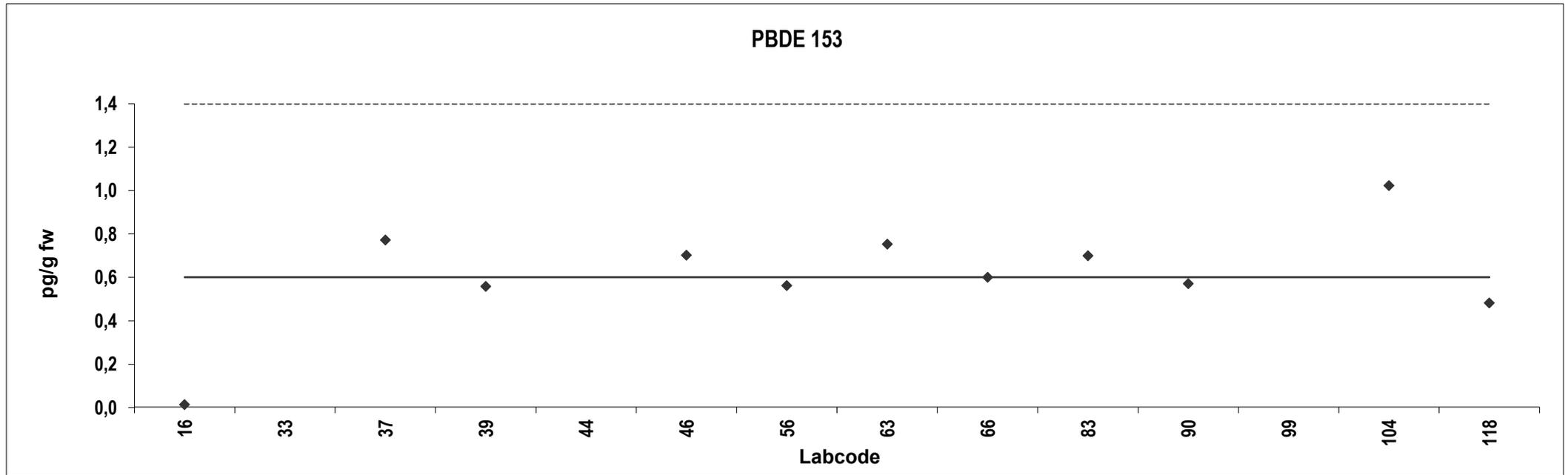


**Cream**  
Congener: PBDE 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,011	-4,9	ND			
33	5,8	43	Outlier,ND			
37	0,77	1,4				
39	0,56	-0,36				
44	1,6	8,4	Outlier			
46	0,70	0,85				
56	0,56	-0,32				
63	0,75	1,3				
66	0,60	0,00000				
83	0,70	0,83				
90	0,57	-0,24				
99	2,4	15	Outlier,ND			
104	1,0	3,5	ND			
118	0,48	-1,0				

**Consensus statistics**

Consensus median, pg/g	0,60
Median all values pg/g	0,70
Consensus mean, pg/g	0,61
Standard deviation, pg/g	0,25
Relative standard deviation, %	41
No. of values reported	14
No. of values removed	3
No. of reported non-detects	4

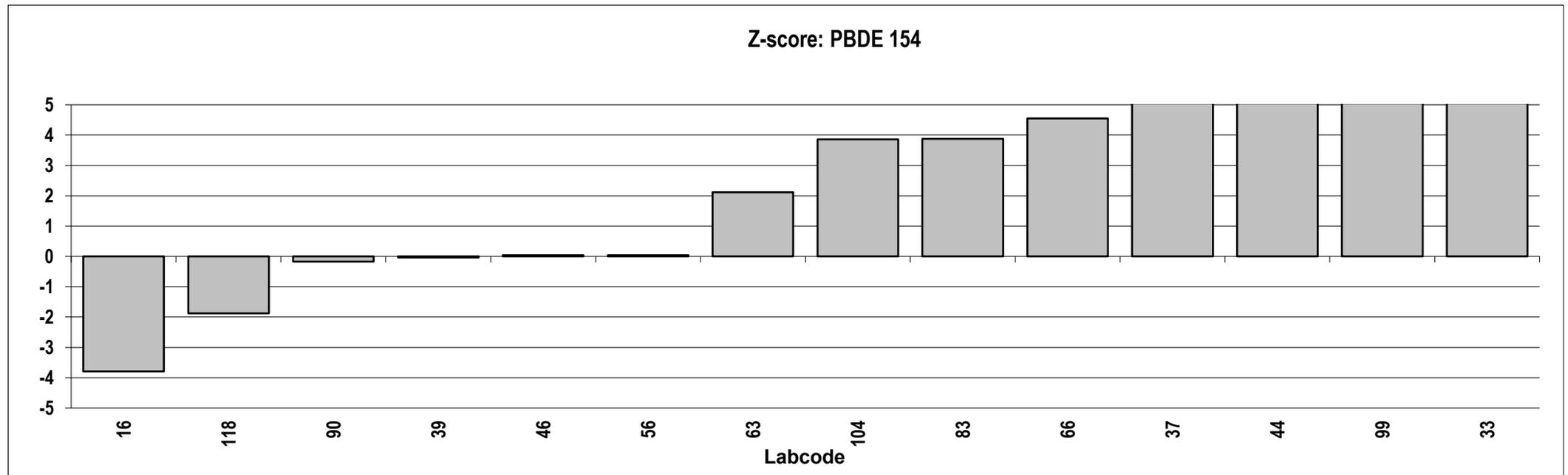
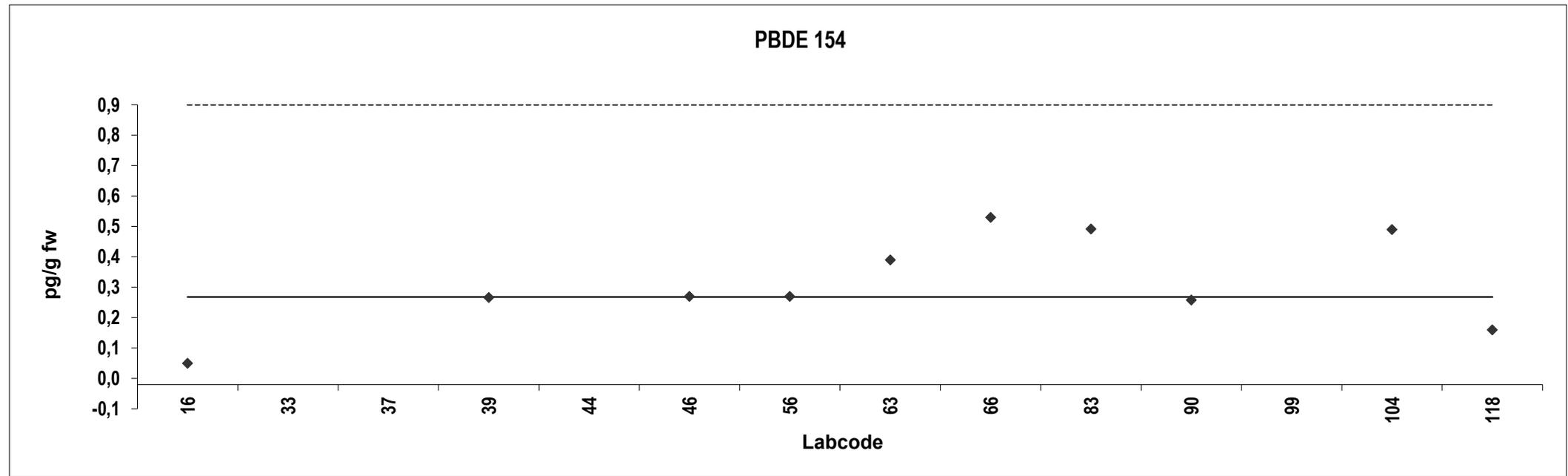


**Cream**  
Congener: PBDE 154

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,069	-3,8				
33	5,8	96	Outlier,ND			
37	1,2	16	Outlier			
39	0,29	-0,036				
44	1,3	18	Outlier			
46	0,29	0,036				
56	0,29	0,036				
63	0,41	2,1				
66	0,55	4,6	ND			
83	0,51	3,9				
90	0,28	-0,17				
99	2,4	37	Outlier,ND			
104	0,51	3,9	ND			
118	0,18	-1,9				

**Consensus statistics**

Consensus median, pg/g	0,29
Median all values pg/g	0,46
Consensus mean, pg/g	0,34
Standard deviation, pg/g	0,16
Relative standard deviation, %	46
No. of values reported	14
No. of values removed	4
No. of reported non-detects	4

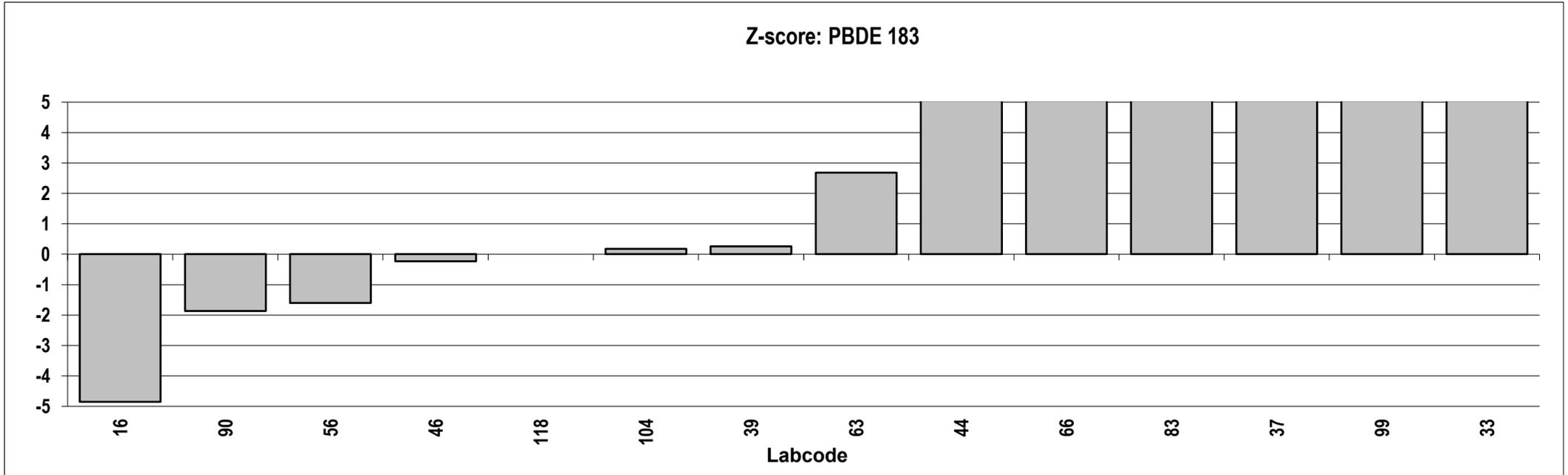
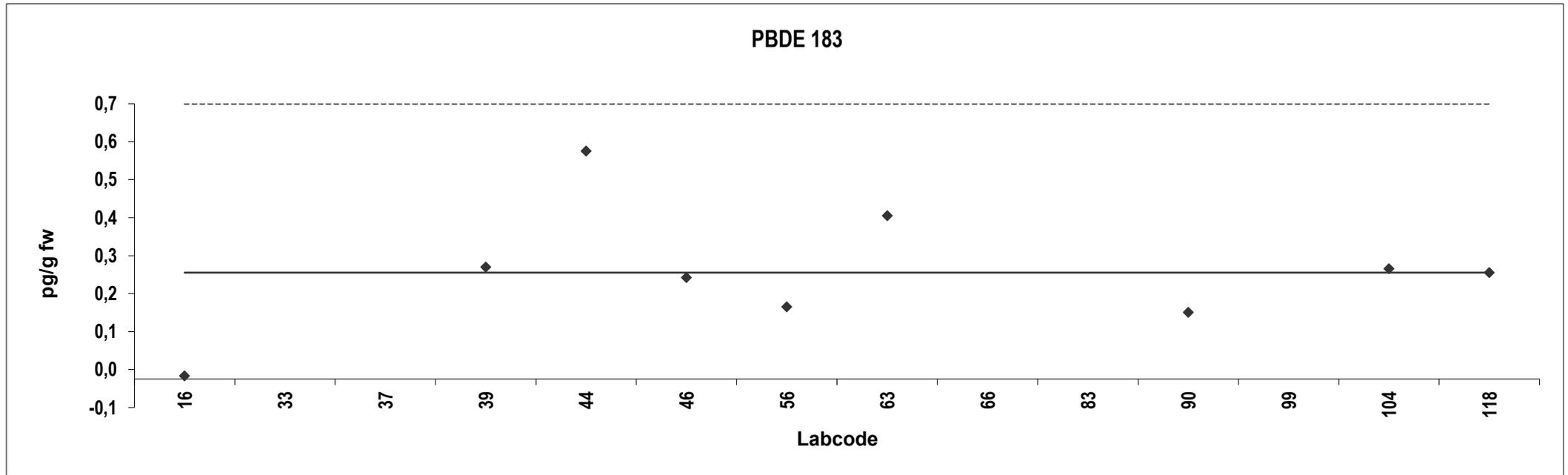


**Cream**  
Congener: PBDE 183

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0081	-4,9	ND			
33	9,5	165	Outlier,ND			
37	1,0	13	Outlier,ND			
39	0,29	0,26				
44	0,60	5,7				
46	0,27	-0,24				
56	0,19	-1,6				
63	0,43	2,7				
66	0,76	8,6	Outlier			
83	0,84	10	Outlier			
90	0,18	-1,9				
99	2,4	38	Outlier,ND			
104	0,29	0,2	ND			
118	0,28	0,00000				

**Consensus statistics**

Consensus median, pg/g	0,28
Median all values pg/g	0,36
Consensus mean, pg/g	0,28
Standard deviation, pg/g	0,17
Relative standard deviation, %	59
No. of values reported	14
No. of values removed	5
No. of reported non-detects	5

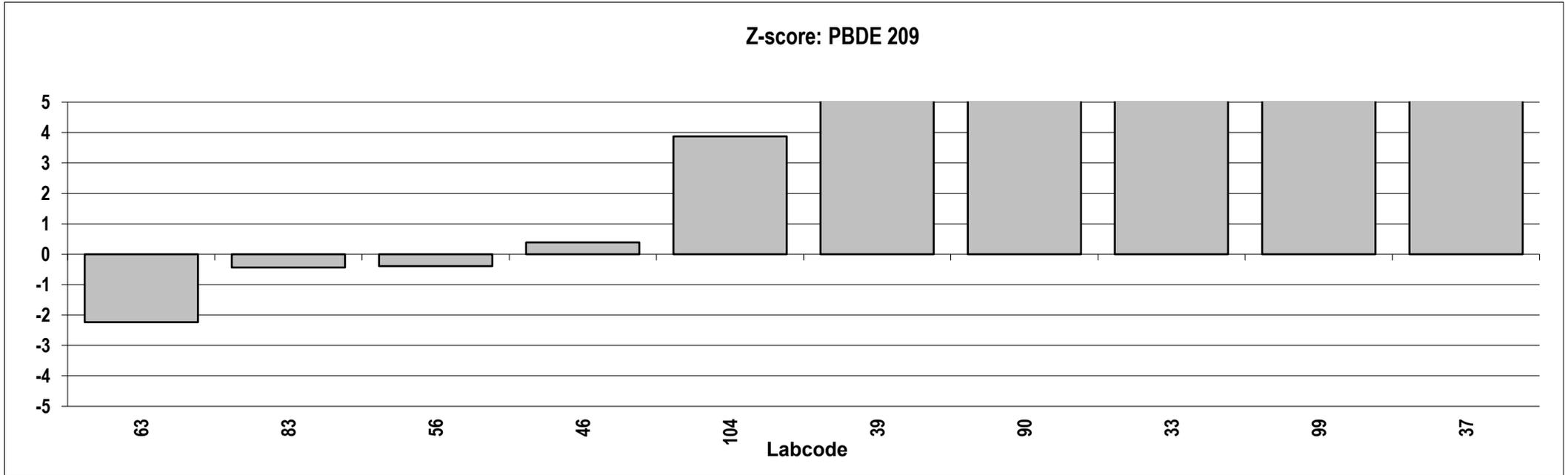
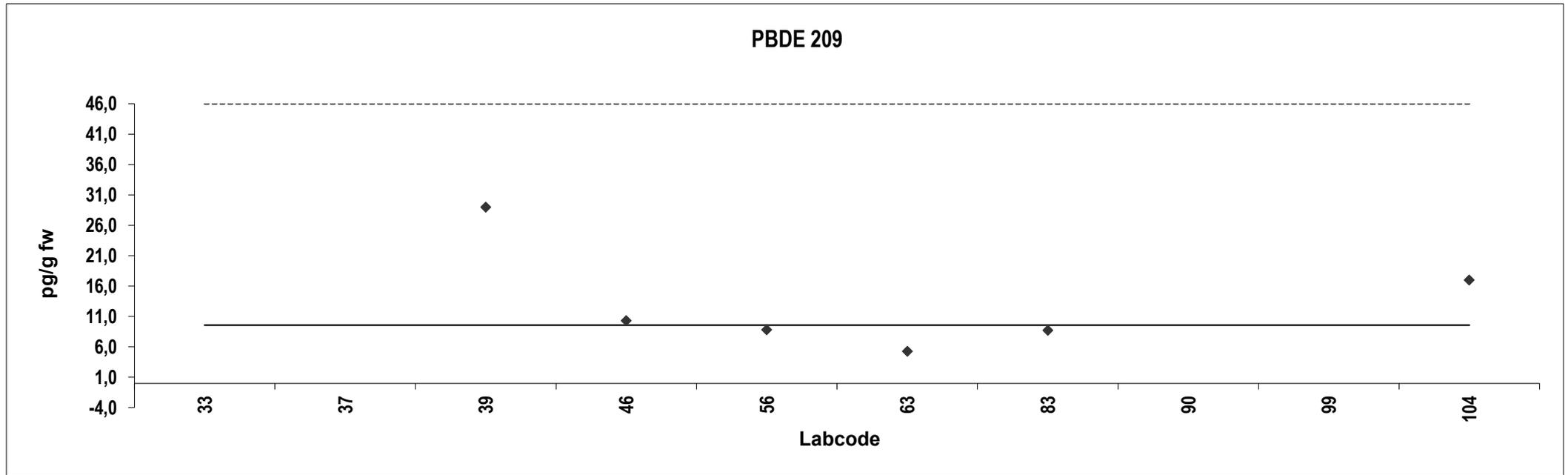


**Cream**  
**Congener: PBDE 209**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
33	190	94	Outlier,ND			
37	320	162	Outlier,ND			
39	29	10				
46	10	0,39				
56	8,8	-0,39				
63	5,3	-2,2				
83	8,7	-0,44				
90	53	23	Outlier			
99	191	95	Outlier,ND			
104	17	3,9				

**Consensus statistics**

Consensus median, pg/g	9,6
Median all values pg/g	23
Consensus mean, pg/g	13
Standard deviation, pg/g	8,7
Relative standard deviation, %	66
No. of values reported	10
No. of values removed	4
No. of reported non-detects	3

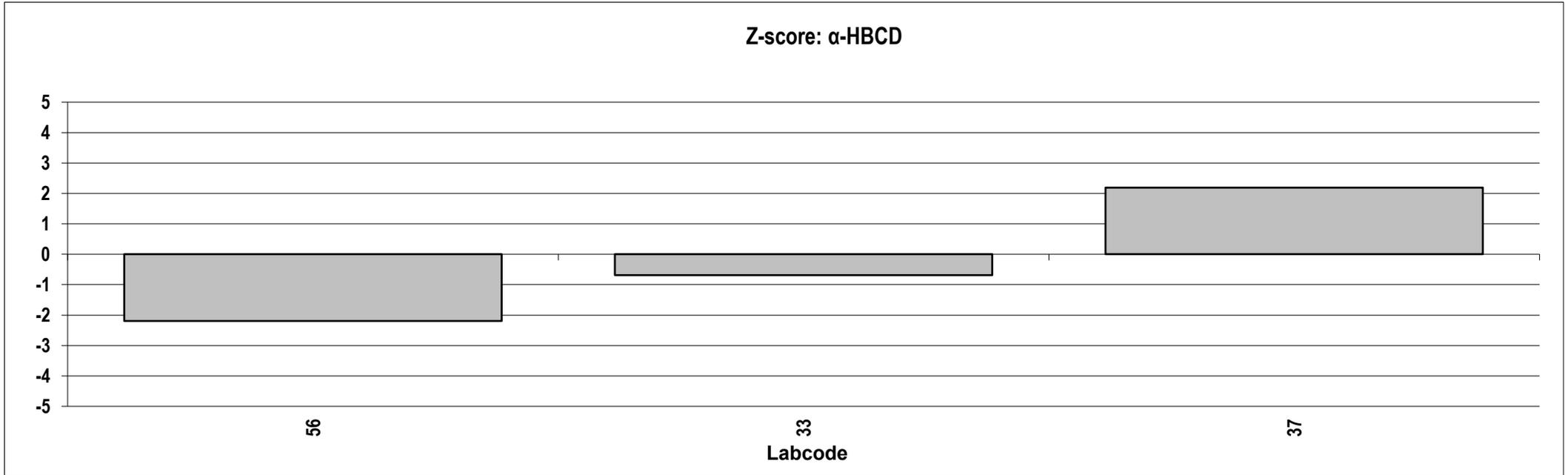
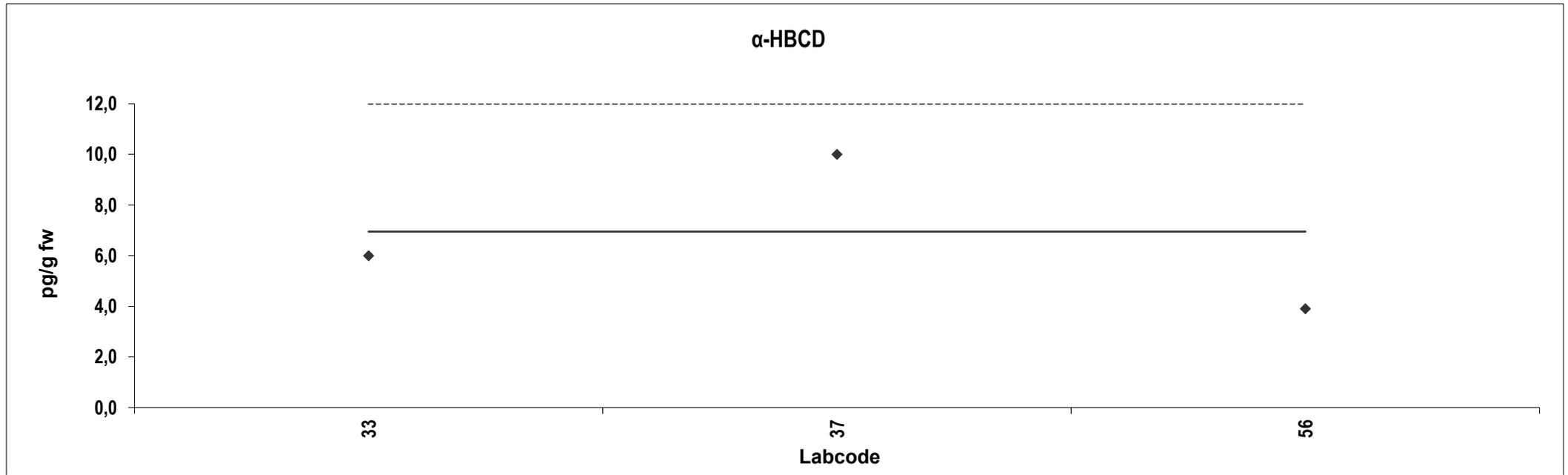


**Cream**  
Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
33	6,0	-0,68	ND			
37	10	2,2				
56	3,9	-2,2				

**Consensus statistics**

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

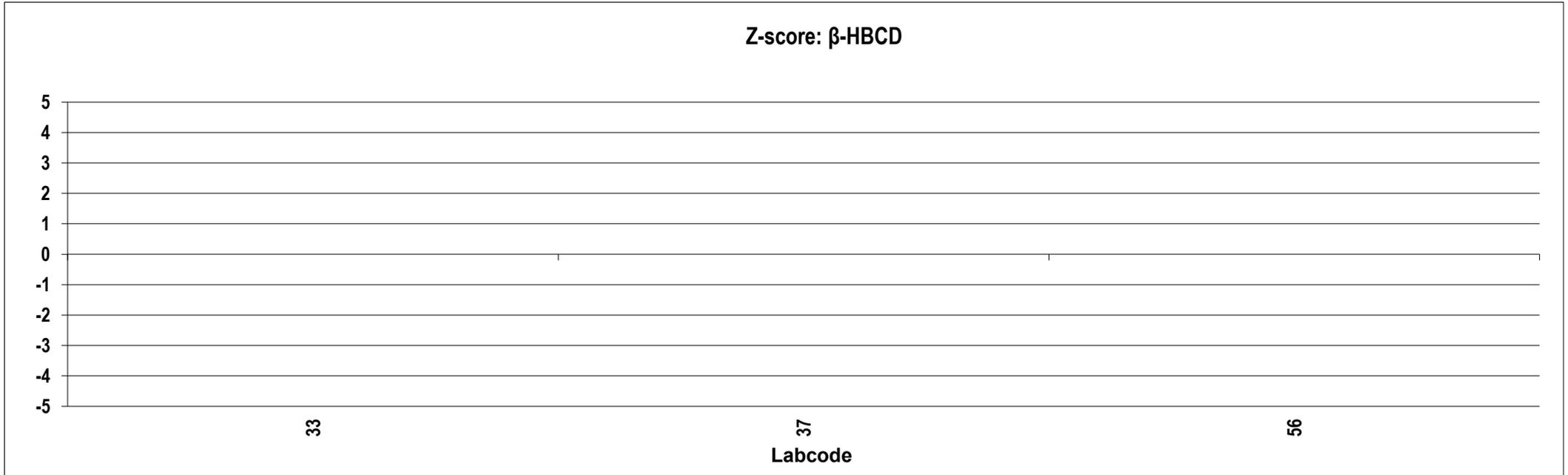
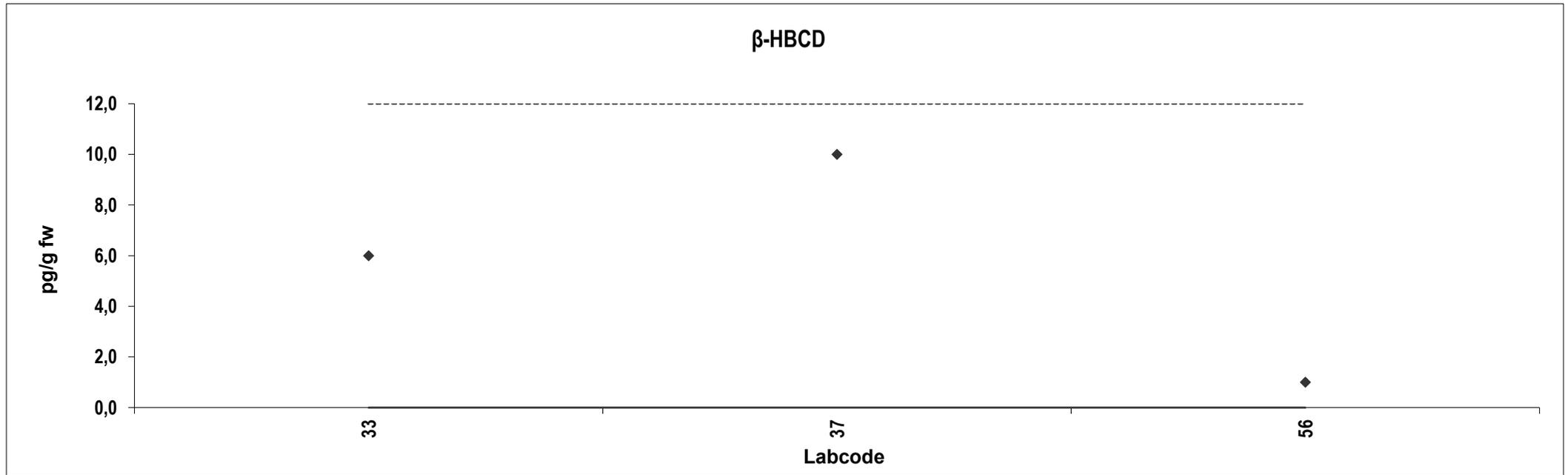


**Cream**  
Congener:  $\beta$ -HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
33	6,0	**	ND			
37	10	**	ND			
56	1,0	**	ND			

**Consensus statistics**

Consensus median, pg/g	**
Median all values pg/g	6,0
Consensus mean, pg/g	5,7
Standard deviation, pg/g	4,5
Relative standard deviation, %	80
No. of values reported	3
No. of values removed	0
No. of reported non-detects	3

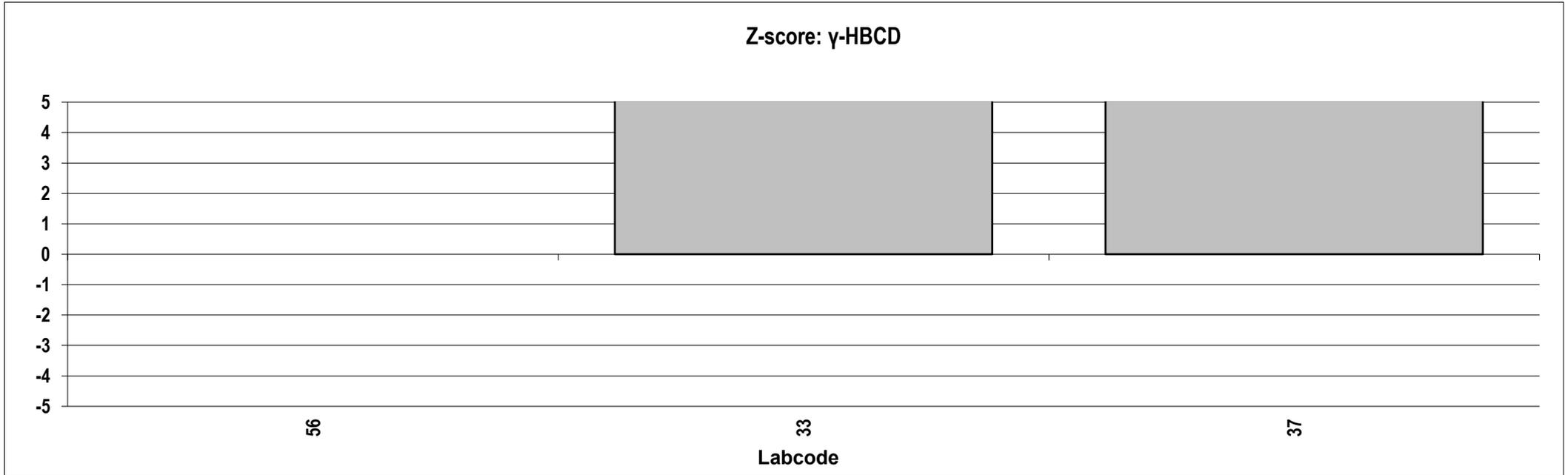
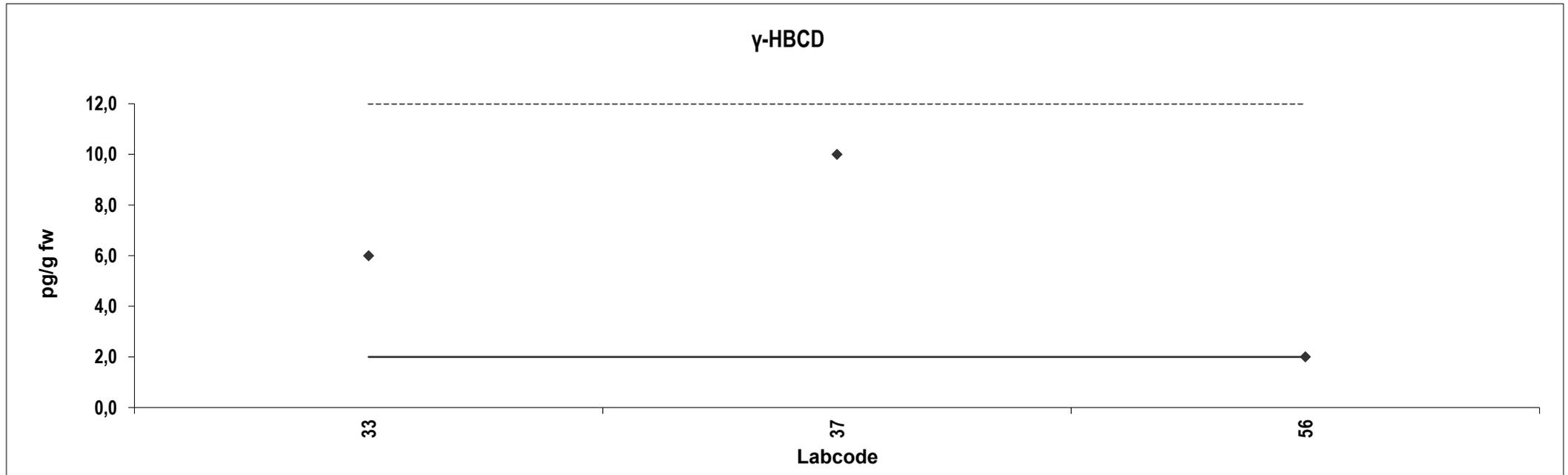


**Cream**  
Congener:  $\gamma$ -HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
33	6,0	10	ND			
37	10	20	ND			
56	2,0	0,00000				

**Consensus statistics**

Consensus median, pg/g	2,0
Median all values pg/g	6,0
Consensus mean, pg/g	6,0
Standard deviation, pg/g	4,0
Relative standard deviation, %	67
No. of values reported	3
No. of values removed	0
No. of reported non-detects	2

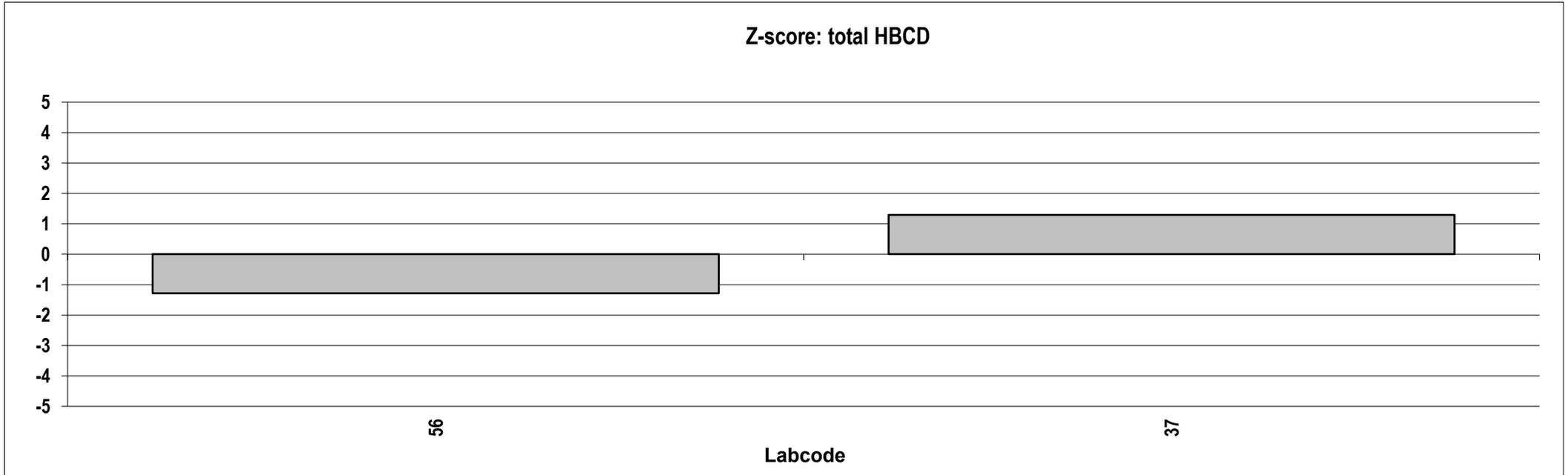
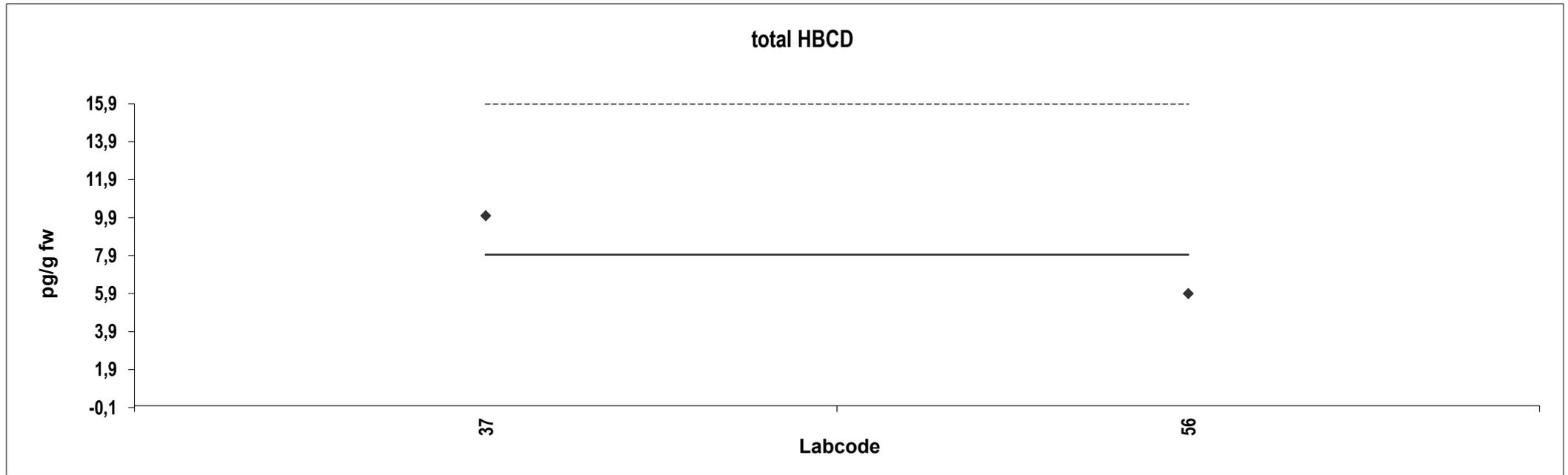


**Cream**  
Congener: total HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
37	10	1,3				
56	5,9	-1,3				

**Consensus statistics**

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





## **Appendix 4:**

---

Presentation of results for  
Egg yolk 2024



## Appendix 4: Presentation of results: Egg yolk 2024

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

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

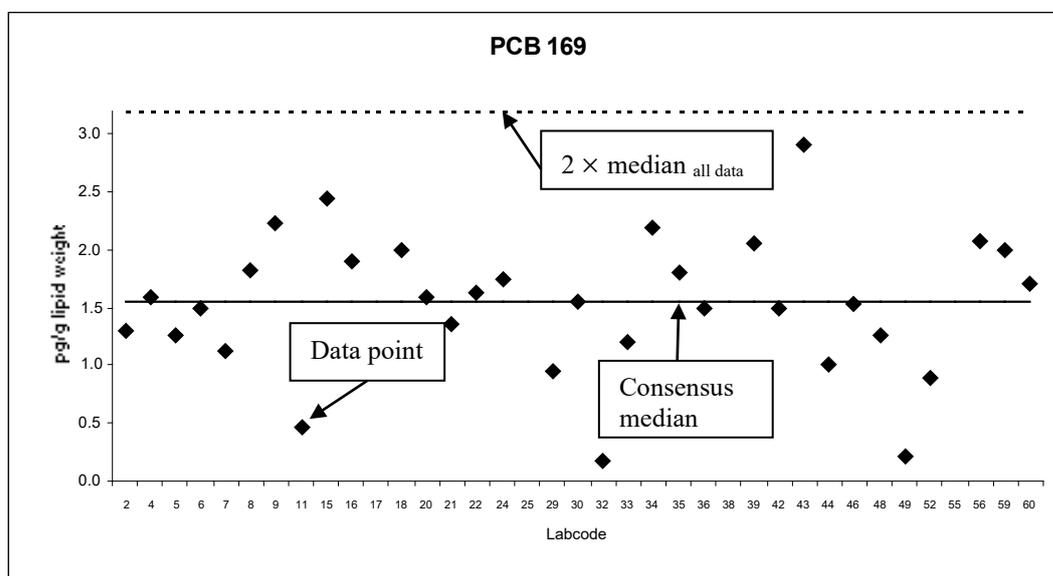
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding  $2 \times$  this median were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining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

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

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

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

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



### Z-Scores of individual congeners

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

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

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

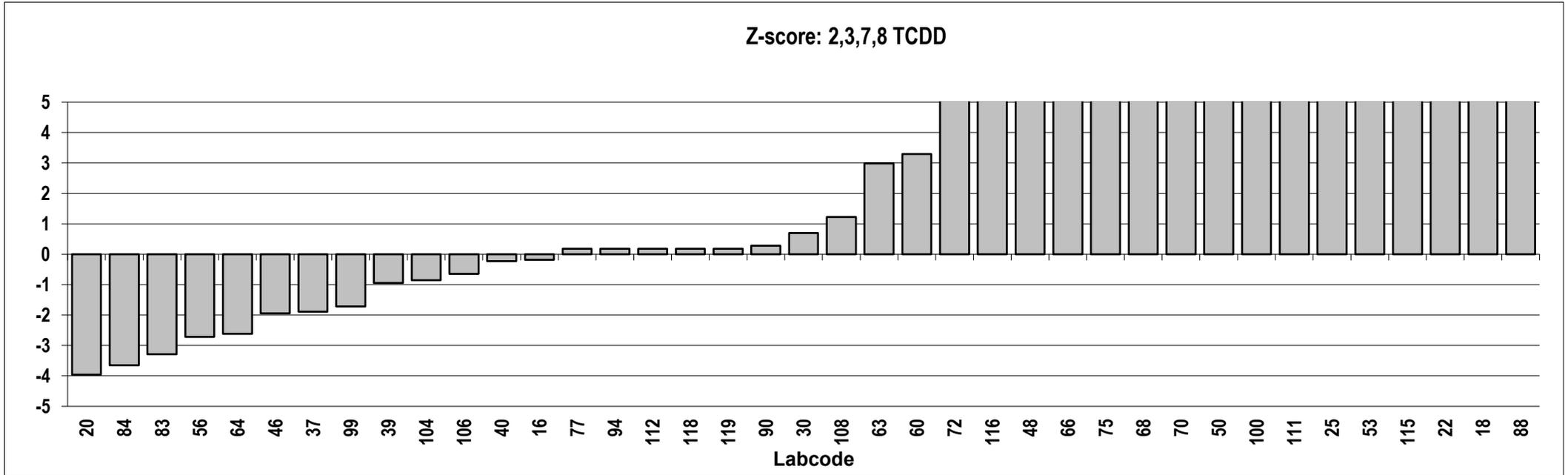
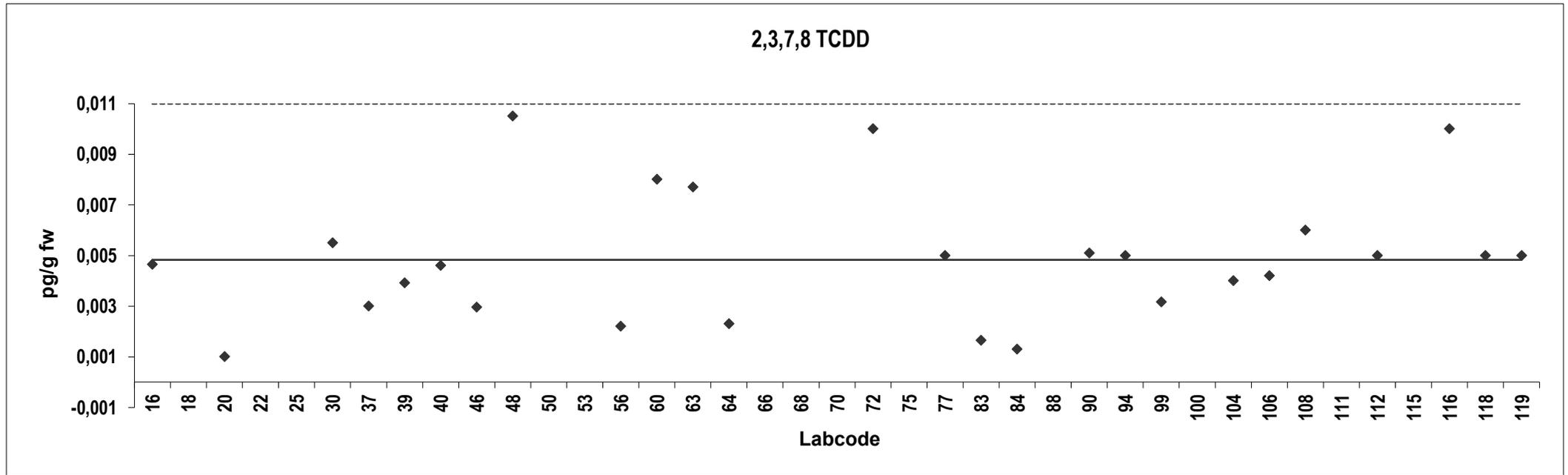


**Egg yolk**  
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0046	-0,18				
18	0,085	83	Outlier,ND			
20	0,0010	-4,0	ND			
22	0,078	75	Outlier			
25	0,050	47	Outlier,ND			
30	0,0055	0,70				
37	0,0030	-1,9				
39	0,0039	-0,94				
40	0,0046	-0,23	ND			
46	0,0030	-1,9				
48	0,011	5,9	ND			
50	0,028	24	Outlier,ND			
53	0,070	68	Outlier,ND			
56	0,0022	-2,7				
60	0,0080	3,3	ND			
63	0,0077	3,0	ND			
64	0,0023	-2,6				
66	0,012	7,4	Outlier			
68	0,019	15	Outlier,ND			
70	0,027	23	Outlier			
72	0,010	5,4	ND			
75	0,019	14	Outlier			
77	0,0050	0,18	ND			
83	0,0017	-3,3				
84	0,0013	-3,7				
88	0,15	146	Outlier,ND			
90	0,0051	0,28				
94	0,0050	0,18	ND			
99	0,0032	-1,7	ND			
100	0,039	35	Outlier			
104	0,0040	-0,85	ND			
106	0,0042	-0,65				
108	0,0060	1,2	ND			
111	0,040	36	Outlier,ND			
112	0,0050	0,18	ND			
115	0,073	71	Outlier,ND			
116	0,010	5,4				
118	0,0050	0,18	ND			
119	0,0050	0,18	ND			

**Consensus statistics**

Consensus median, pg/g	0,0048
Median all values pg/g	0,0055
Consensus mean, pg/g	0,0049
Standard deviation, pg/g	0,0026
Relative standard deviation, %	53
No. of values reported	39
No. of values removed	13
No. of reported non-detects	22

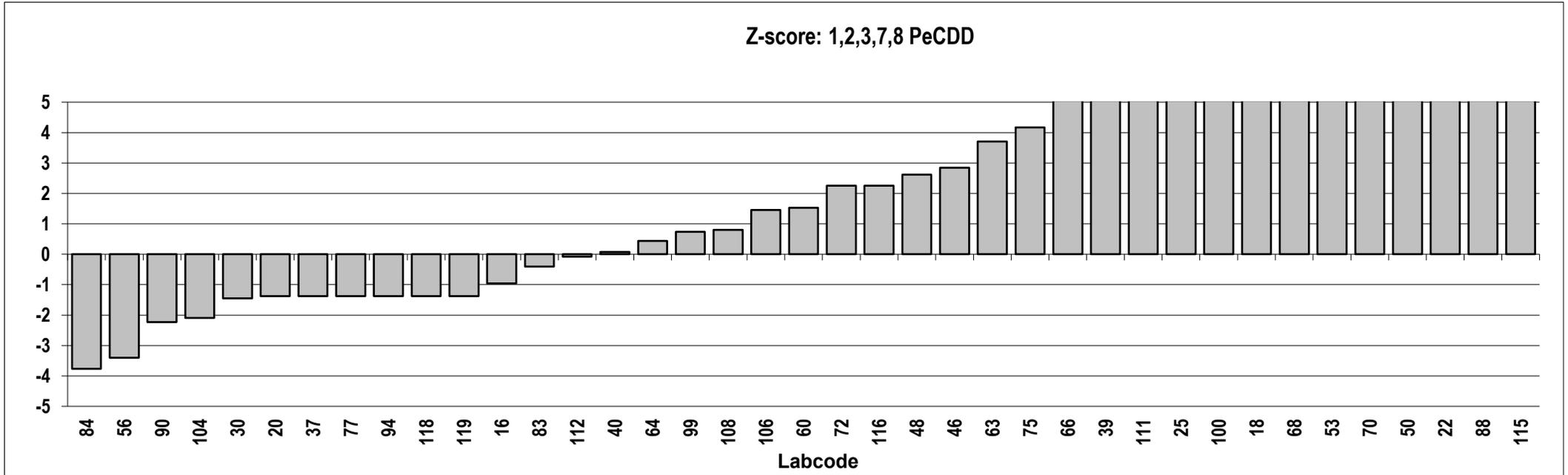
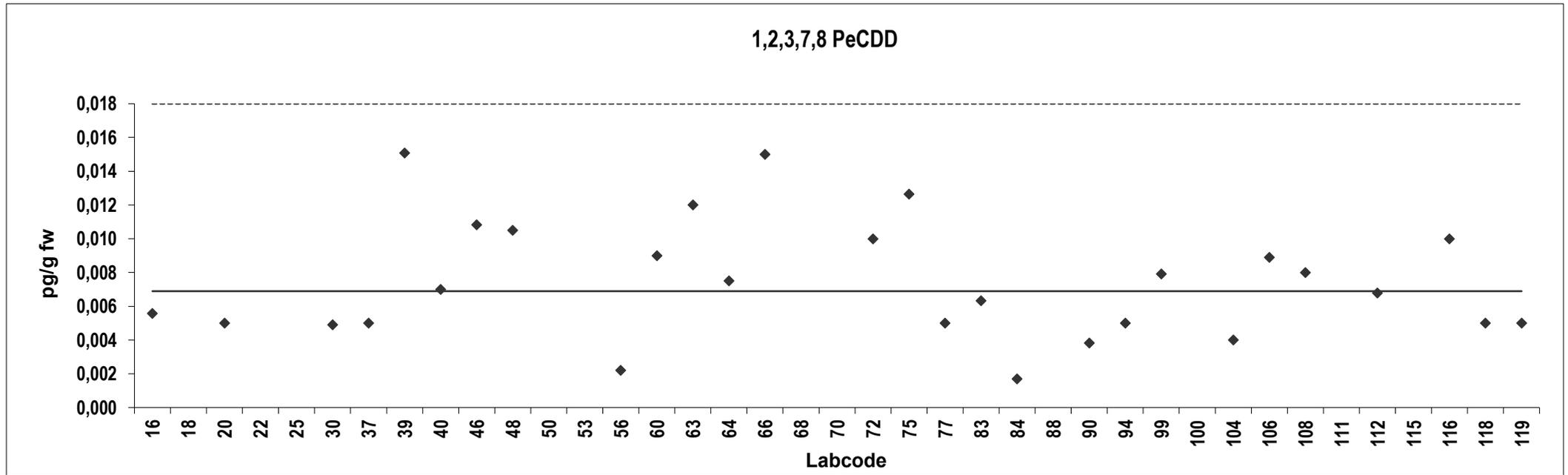


**Egg yolk**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0056	-0,96	ND			
18	0,060	39	Outlier,ND			
20	0,0050	-1,4	ND			
22	0,13	91	Outlier			
25	0,050	31	Outlier,ND			
30	0,0049	-1,4				
37	0,0050	-1,4				
39	0,015	5,9				
40	0,0070	0,076	ND			
46	0,011	2,8				
48	0,011	2,6	ND			
50	0,089	60	Outlier,ND			
53	0,070	46	Outlier,ND			
56	0,0022	-3,4				
60	0,0090	1,5	ND			
63	0,012	3,7				
64	0,0075	0,44				
66	0,015	5,9				
68	0,066	43	Outlier,ND			
70	0,082	54	Outlier			
72	0,010	2,3	ND			
75	0,013	4,2	ND			
77	0,0050	-1,4	ND			
83	0,0063	-0,41				
84	0,0017	-3,8	ND			
88	0,31	221	Outlier,ND			
90	0,0038	-2,2				
94	0,0050	-1,4	ND			
99	0,0079	0,74	ND			
100	0,051	32	Outlier			
104	0,0040	-2,1	ND			
106	0,0089	1,5				
108	0,0080	0,80	ND			
111	0,040	24	Outlier,ND			
112	0,0068	-0,076				
115	0,40	281	Outlier,ND			
116	0,010	2,3				
118	0,0050	-1,4	ND			
119	0,0050	-1,4	ND			

**Consensus statistics**

Consensus median, pg/g	0,0069
Median all values pg/g	0,0090
Consensus mean, pg/g	0,0075
Standard deviation, pg/g	0,0035
Relative standard deviation, %	47
No. of values reported	39
No. of values removed	11
No. of reported non-detects	23

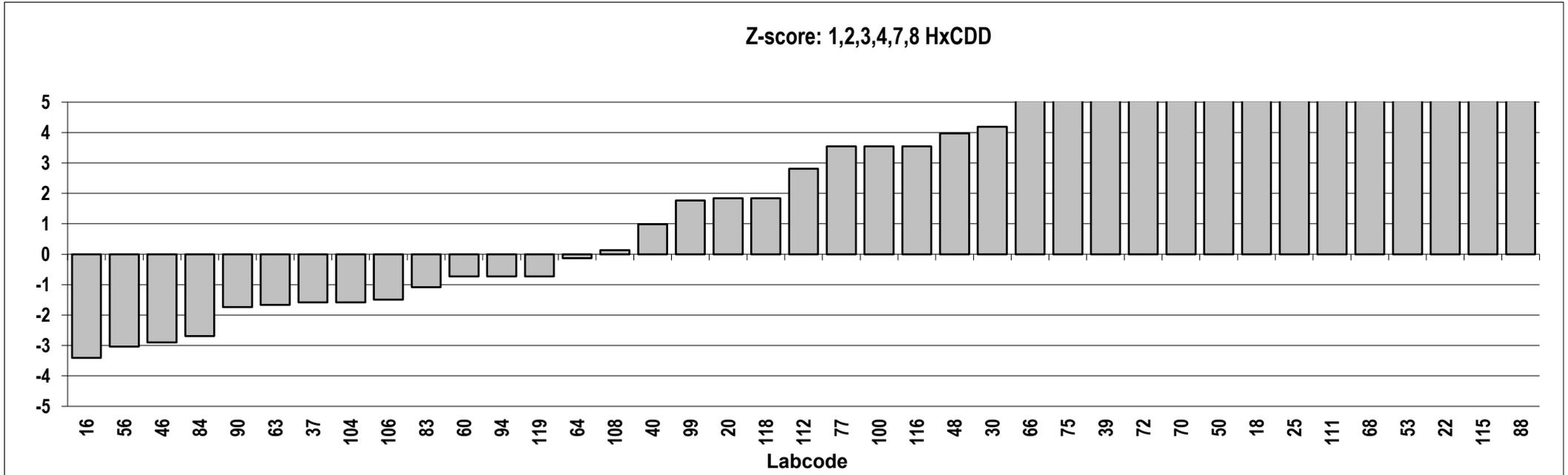
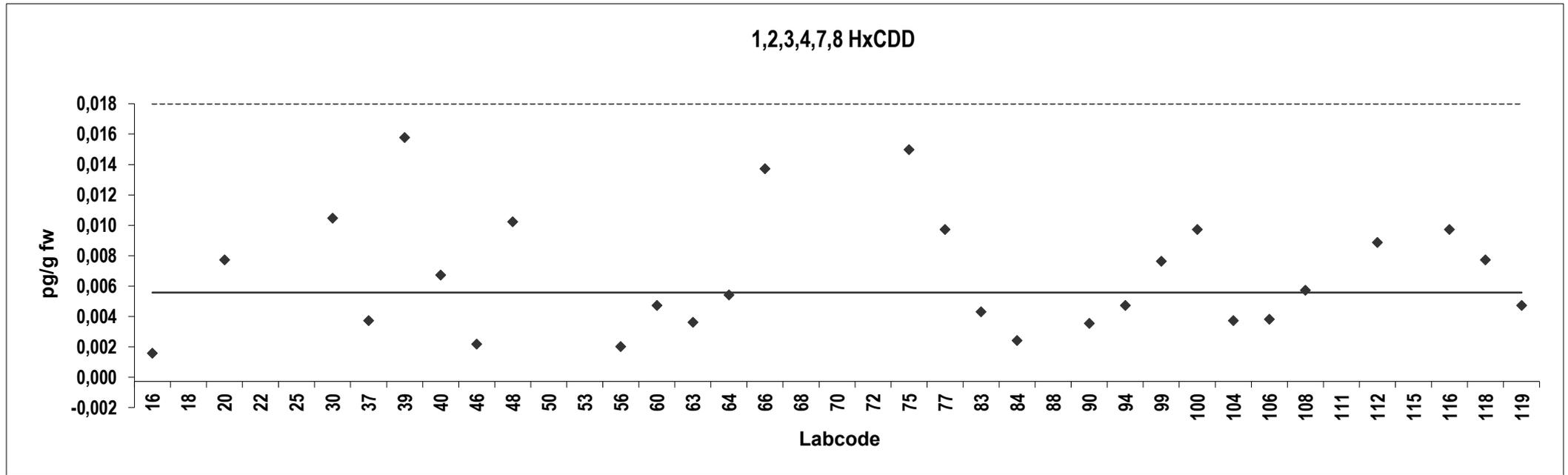


**Egg yolk**  
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0019	-3,4	ND			
18	0,046	34	Outlier,ND			
20	0,0080	1,8				
22	0,21	179	Outlier			
25	0,050	38	Outlier,ND			
30	0,011	4,2				
37	0,0040	-1,6				
39	0,016	8,7				
40	0,0070	1,0	ND			
46	0,0025	-2,9				
48	0,011	4,0	ND			
50	0,027	18	Outlier,ND			
53	0,070	55	Outlier,ND			
56	0,0023	-3,0				
60	0,0050	-0,73	ND			
63	0,0039	-1,7	ND			
64	0,0057	-0,13				
66	0,014	7,0				
68	0,069	54	Outlier,ND			
70	0,021	13	Outlier			
72	0,020	12	Outlier,ND			
75	0,015	8,0	ND			
77	0,010	3,5	ND			
83	0,0046	-1,1				
84	0,0027	-2,7				
88	0,53	447	Outlier,ND			
90	0,0038	-1,7				
94	0,0050	-0,73	ND			
99	0,0079	1,8	ND			
100	0,010	3,5				
104	0,0040	-1,6	ND			
106	0,0041	-1,5				
108	0,0060	0,13	ND			
111	0,050	38	Outlier,ND			
112	0,0091	2,8				
115	0,28	234	Outlier,ND			
116	0,010	3,5	ND			
118	0,0080	1,8				
119	0,0050	-0,73	ND			

**Consensus statistics**

Consensus median, pg/g	0,0059
Median all values pg/g	0,0091
Consensus mean, pg/g	0,0070
Standard deviation, pg/g	0,0039
Relative standard deviation, %	56
No. of values reported	39
No. of values removed	11
No. of reported non-detects	22

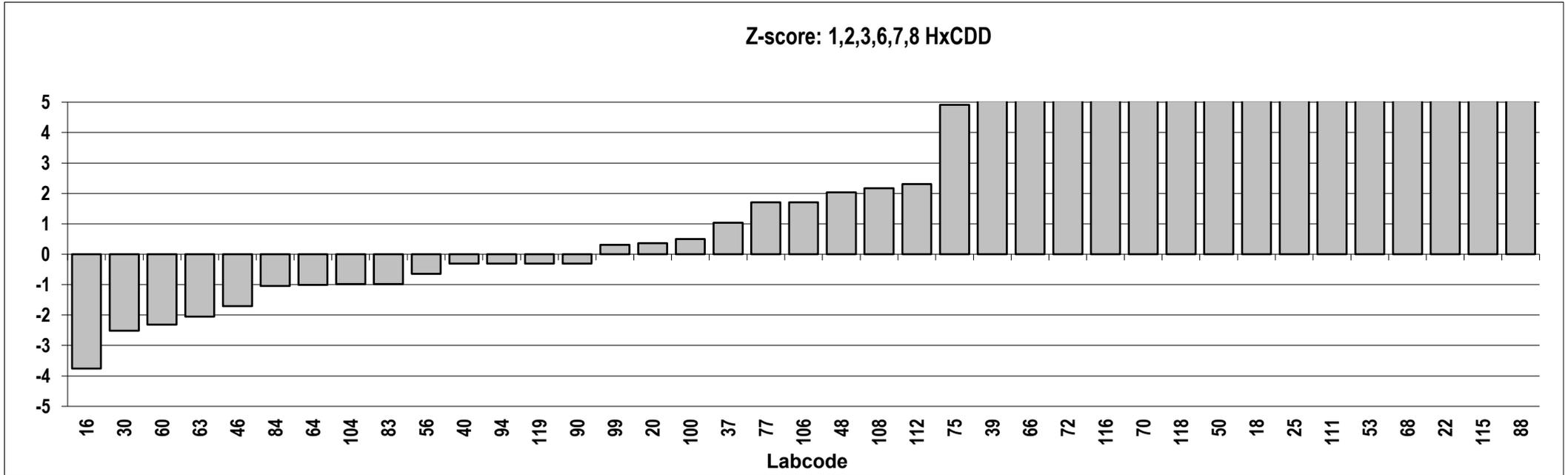
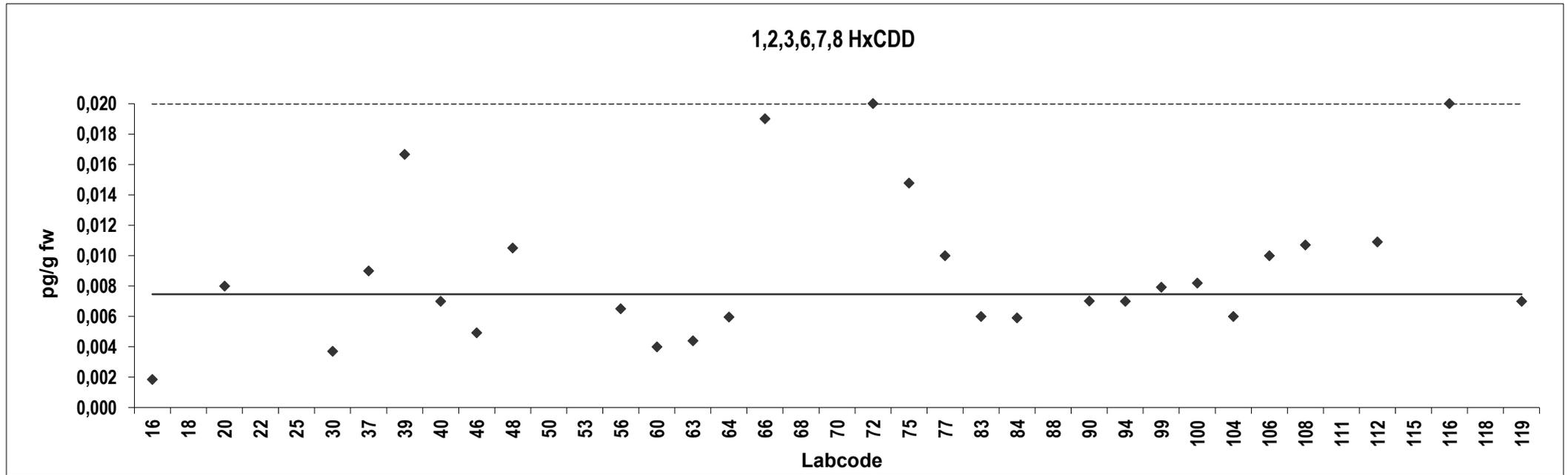


**Egg yolk**  
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0019	-3,8	ND			
18	0,042	23	Outlier,ND			
20	0,0080	0,36				
22	0,19	121	Outlier			
25	0,050	29	Outlier,ND			
30	0,0037	-2,5				
37	0,0090	1,0				
39	0,017	6,2				
40	0,0070	-0,31	ND			
46	0,0049	-1,7				
48	0,011	2,0	ND			
50	0,026	12	Outlier,ND			
53	0,070	42	Outlier,ND			
56	0,0065	-0,64				
60	0,0040	-2,3	ND			
63	0,0044	-2,1	ND			
64	0,0060	-1,0				
66	0,019	7,7	ND			
68	0,080	49	Outlier,ND			
70	0,022	9,6	Outlier			
72	0,020	8,4	ND			
75	0,015	4,9	ND			
77	0,010	1,7	ND			
83	0,0060	-1,0				
84	0,0059	-1,0				
88	0,54	357	Outlier,ND			
90	0,0070	-0,30				
94	0,0070	-0,31				
99	0,0079	0,30	ND			
100	0,0082	0,50	ND			
104	0,0060	-1,0	ND			
106	0,010	1,7				
108	0,011	2,2				
111	0,050	29	Outlier,ND			
112	0,011	2,3				
115	0,23	152	Outlier,ND			
116	0,020	8,4				
118	0,023	10	Outlier			
119	0,0070	-0,31				

**Consensus statistics**

Consensus median, pg/g	0,0075
Median all values pg/g	0,010
Consensus mean, pg/g	0,0090
Standard deviation, pg/g	0,0049
Relative standard deviation, %	54
No. of values reported	39
No. of values removed	11
No. of reported non-detects	20

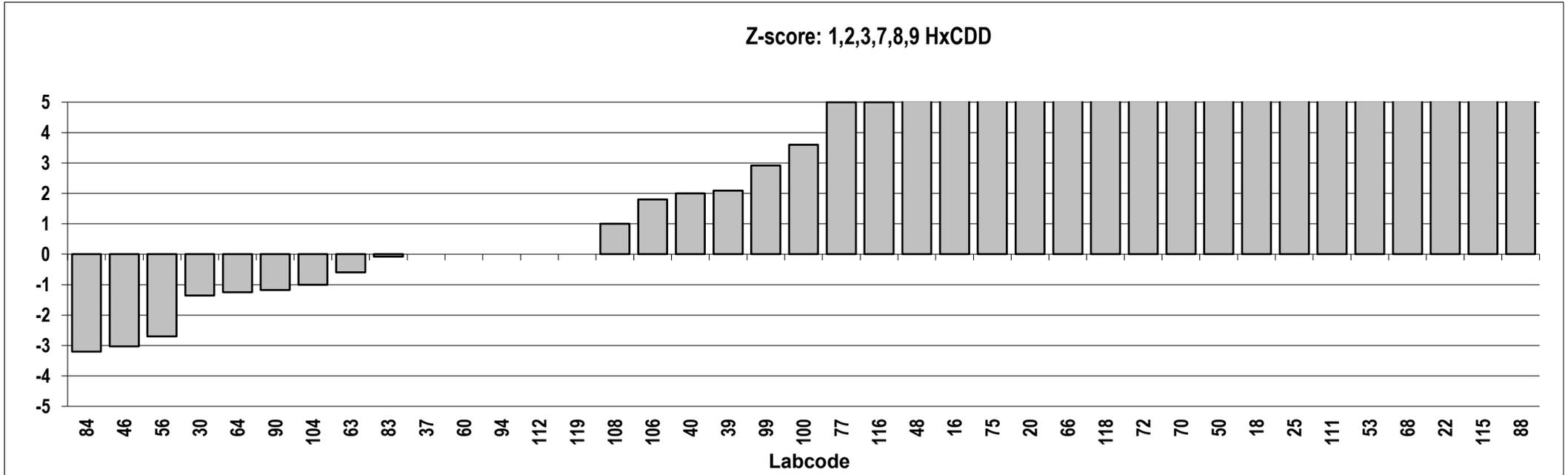
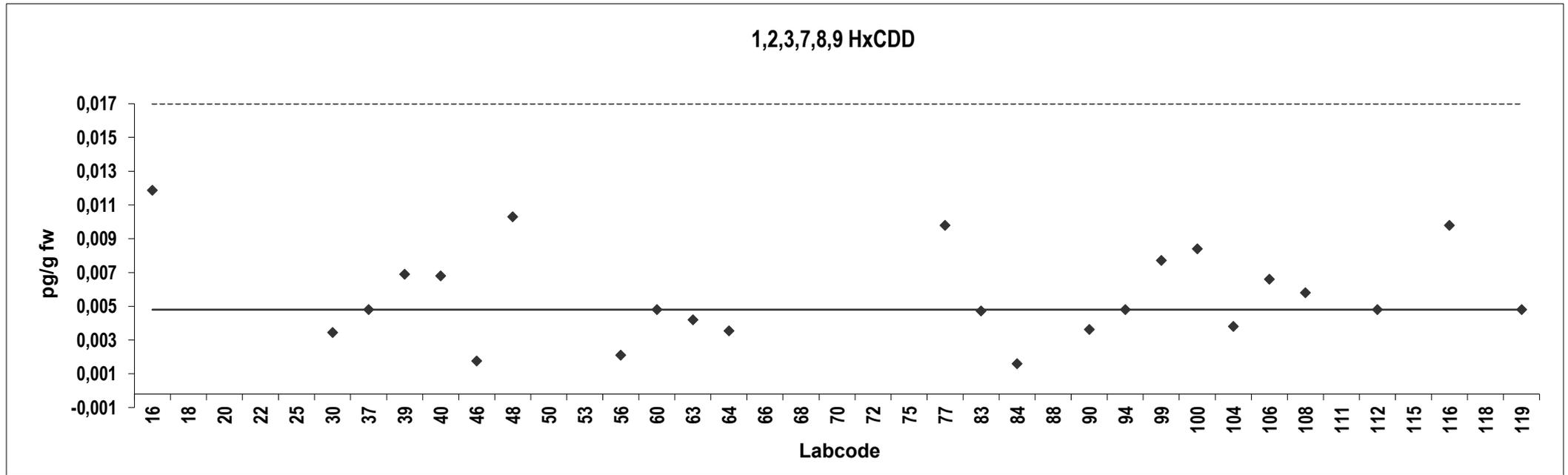


**Egg yolk**  
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,012	7,1				
18	0,045	40	Outlier,ND			
20	0,019	14	Outlier			
22	0,17	163	Outlier			
25	0,050	45	Outlier,ND			
30	0,0036	-1,4				
37	0,0050	0,00000				
39	0,0071	2,1				
40	0,0070	2,0	ND			
46	0,0020	-3,0				
48	0,011	5,5	ND			
50	0,023	18	Outlier,ND			
53	0,070	65	Outlier,ND			
56	0,0023	-2,7				
60	0,0050	0,00000	ND			
63	0,0044	-0,60	ND			
64	0,0038	-1,3				
66	0,019	14	Outlier,ND			
68	0,082	77	Outlier,ND			
70	0,022	17	Outlier			
72	0,020	15	Outlier,ND			
75	0,018	13	Outlier			
77	0,010	5,0	ND			
83	0,0049	-0,074				
84	0,0018	-3,2				
88	0,48	480	Outlier,ND			
90	0,0038	-1,2				
94	0,0050	0,00000	ND			
99	0,0079	2,9	ND			
100	0,0086	3,6	ND			
104	0,0040	-1,0	ND			
106	0,0068	1,8				
108	0,0060	1,0	ND			
111	0,050	45	Outlier,ND			
112	0,0050	0,00000	ND			
115	0,25	241	Outlier,ND			
116	0,010	5,0				
118	0,019	14	Outlier			
119	0,0050	0,00000	ND			

**Consensus statistics**

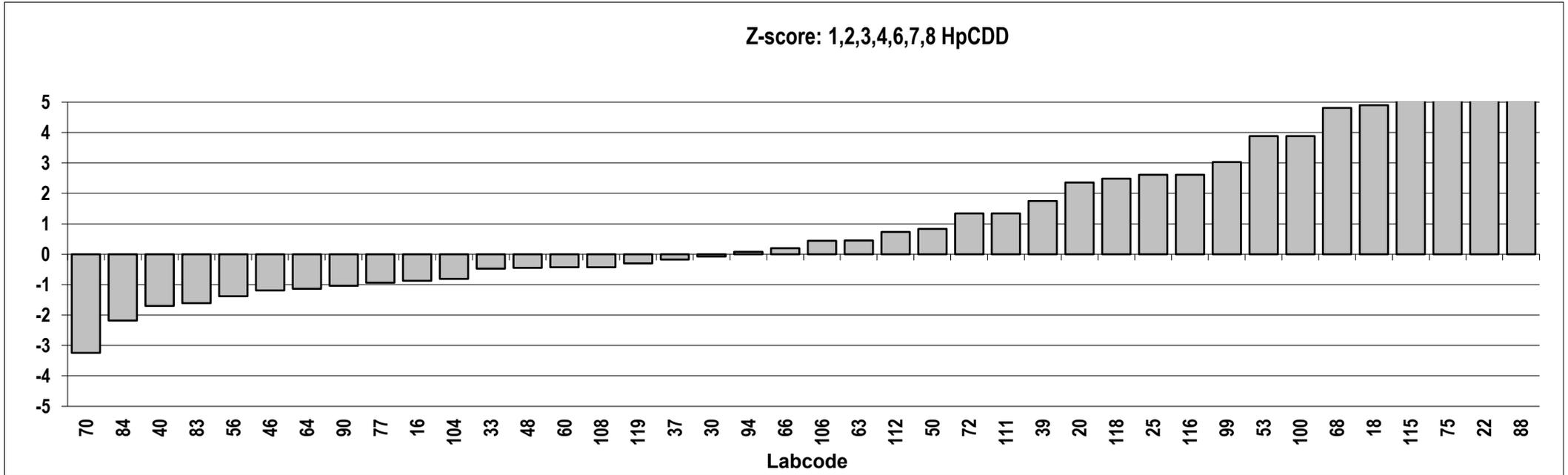
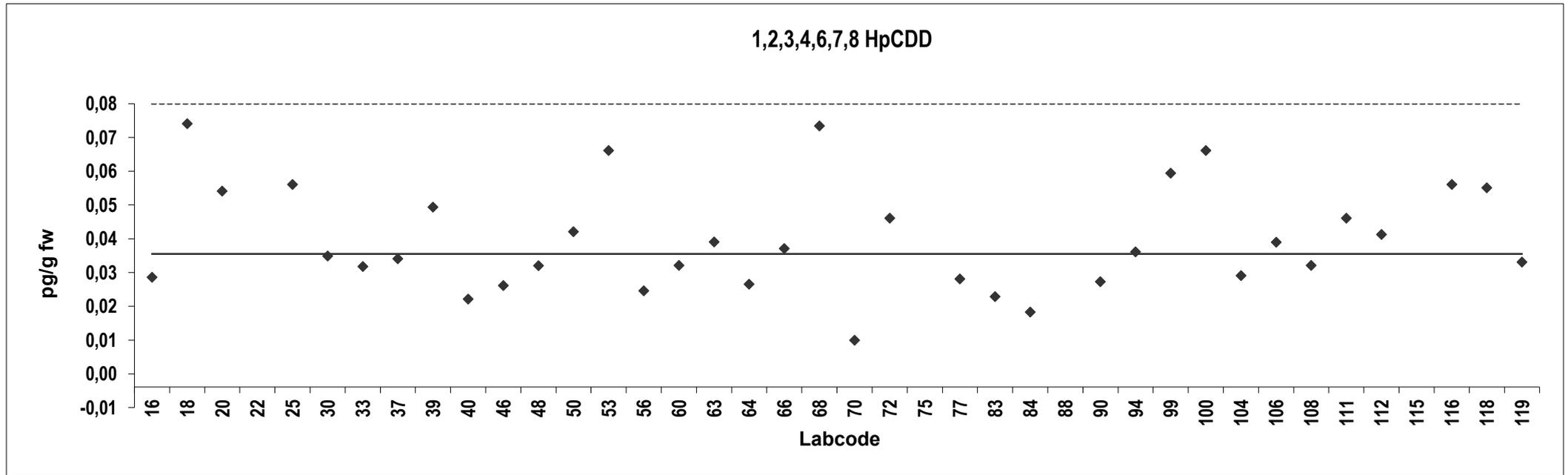
Consensus median, pg/g	0,0050
Median all values pg/g	0,0086
Consensus mean, pg/g	0,0059
Standard deviation, pg/g	0,0028
Relative standard deviation, %	47
No. of values reported	39
No. of values removed	15
No. of reported non-detects	22



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,033	-0,87				
18	0,078	4,9	ND			
20	0,058	2,4				
22	0,51	60	Outlier			
25	0,060	2,6				
30	0,039	-0,075				
33	0,036	-0,48				
37	0,038	-0,18				
39	0,053	1,8				
40	0,026	-1,7				
46	0,030	-1,2				
48	0,036	-0,45				
50	0,046	0,84				
53	0,070	3,9	ND			
56	0,029	-1,4				
60	0,036	-0,43				
63	0,043	0,46				
64	0,030	-1,1				
66	0,041	0,20				
68	0,077	4,8	ND			
70	0,014	-3,2				
72	0,050	1,3	ND			
75	0,30	33	Outlier			
77	0,032	-0,94				
83	0,027	-1,6				
84	0,022	-2,2				
88	0,56	67	Outlier,ND			
90	0,031	-1,0				
94	0,040	0,075				
99	0,063	3,0	ND			
100	0,070	3,9	ND			
104	0,033	-0,81				
106	0,043	0,44				
108	0,036	-0,43				
111	0,050	1,3	ND			
112	0,045	0,73				
115	0,21	21	Outlier,ND			
116	0,060	2,6				
118	0,059	2,5				
119	0,037	-0,31				

Consensus statistics	
Consensus median, pg/g	0,039
Median all values pg/g	0,042
Consensus mean, pg/g	0,044
Standard deviation, pg/g	0,016
Relative standard deviation, %	36
No. of values reported	40
No. of values removed	4
No. of reported non-detects	9

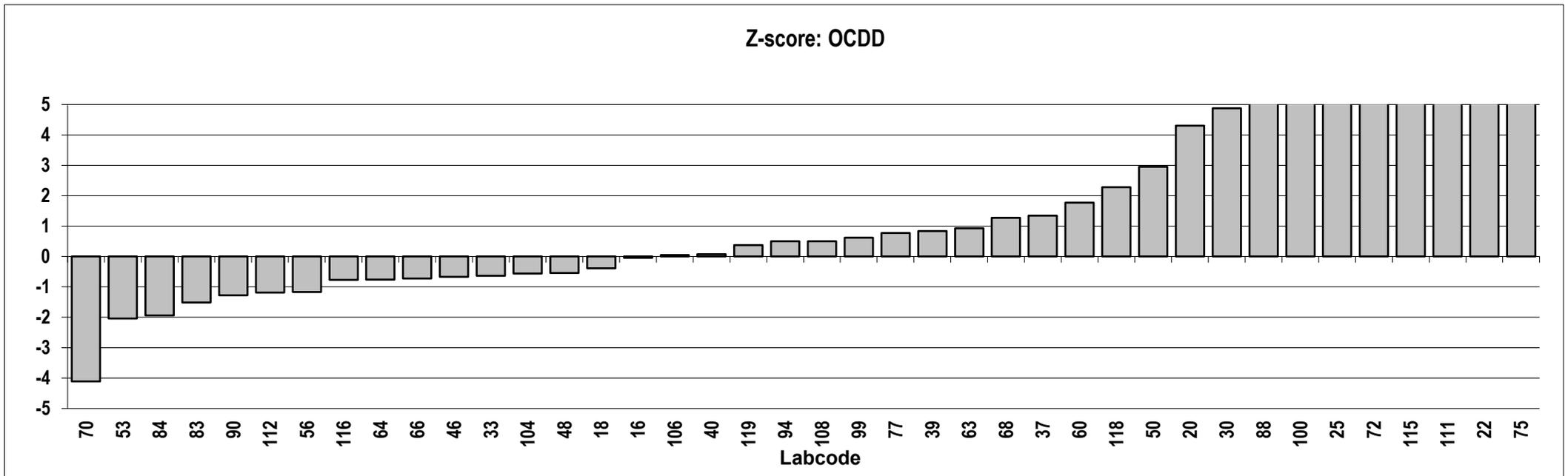
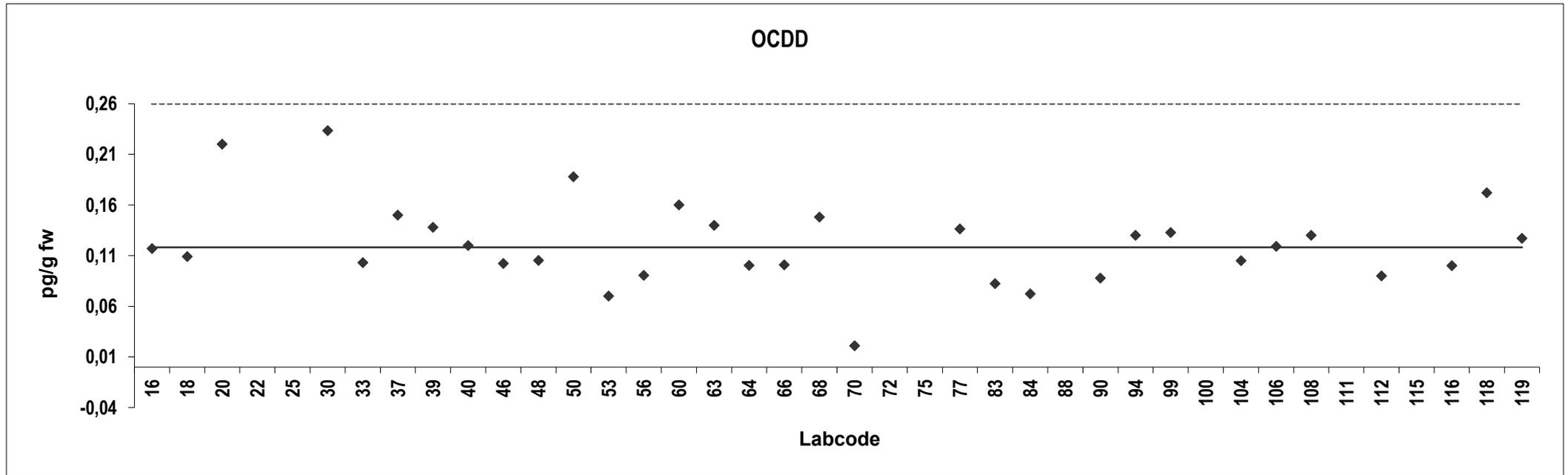


**Egg yolk**  
**Congener: OCDD**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,12	-0,047				
18	0,11	-0,39	ND			
20	0,22	4,3				
22	2,7	108	Outlier			
25	0,49	16	Outlier			
30	0,23	4,9				
33	0,10	-0,64				
37	0,15	1,3				
39	0,14	0,84				
40	0,12	0,077				
46	0,10	-0,67				
48	0,11	-0,55				
50	0,19	3,0				
53	0,070	-2,0	ND			
56	0,091	-1,2				
60	0,16	1,8				
63	0,14	0,92				
64	0,10	-0,76				
66	0,10	-0,73				
68	0,15	1,3	ND			
70	0,021	-4,1				
72	0,50	16	Outlier,ND			
75	3,1	124	Outlier			
77	0,14	0,77				
83	0,082	-1,5				
84	0,072	-1,9				
88	0,34	9,4	Outlier,ND			
90	0,088	-1,3				
94	0,13	0,50				
99	0,13	0,62				
100	0,46	14	Outlier,ND			
104	0,11	-0,56				
106	0,12	0,047				
108	0,13	0,50				
111	2,0	80	Outlier,ND			
112	0,090	-1,2				
115	0,74	26	Outlier,ND			
116	0,10	-0,77				
118	0,17	2,3				
119	0,13	0,37				

**Consensus statistics**

Consensus median, pg/g	0,12
Median all values pg/g	0,13
Consensus mean, pg/g	0,12
Standard deviation, pg/g	0,042
Relative standard deviation, %	35
No. of values reported	40
No. of values removed	8
No. of reported non-detects	8

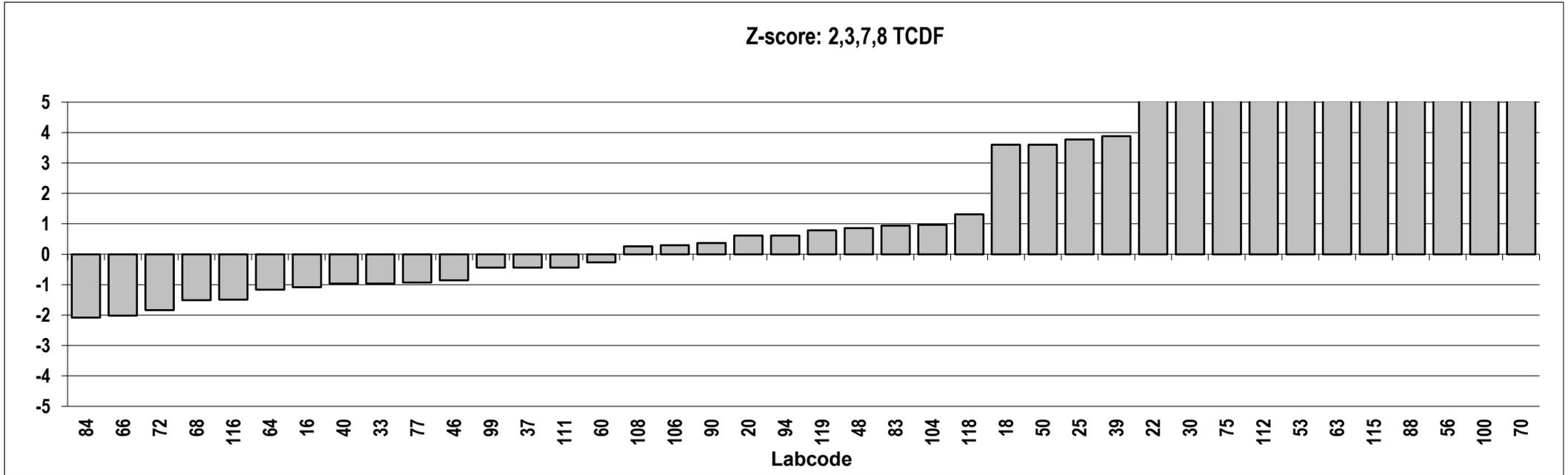
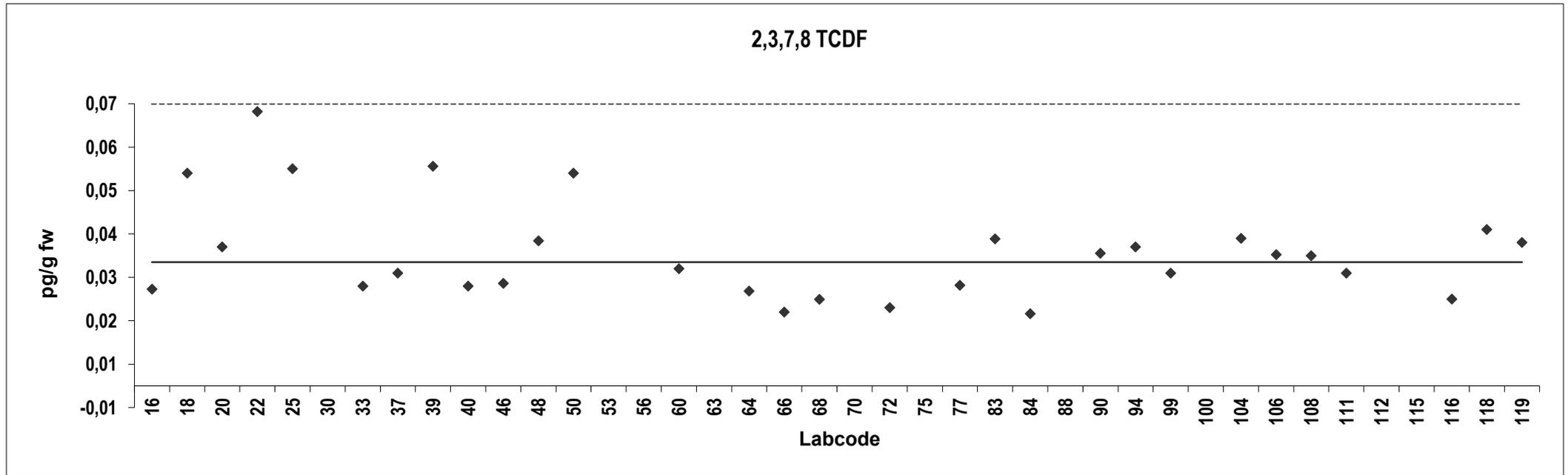


**Egg yolk**  
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,022	-1,1				
18	0,049	3,6				
20	0,032	0,61				
22	0,063	6,1				
25	0,050	3,8	ND			
30	0,065	6,4	Outlier			
33	0,023	-1,0				
37	0,026	-0,44				
39	0,051	3,9				
40	0,023	-1,0				
46	0,024	-0,86				
48	0,033	0,86				
50	0,049	3,6				
53	0,070	7,3	Outlier,ND			
56	0,23	35	Outlier			
60	0,027	-0,26				
63	0,070	7,3	Outlier			
64	0,022	-1,2				
66	0,017	-2,0				
68	0,020	-1,5	ND			
70	1,0	173	Outlier			
72	0,018	-1,8				
75	0,067	6,7	Outlier			
77	0,023	-0,93				
83	0,034	0,94				
84	0,017	-2,1				
88	0,13	18	Outlier,ND			
90	0,031	0,36				
94	0,032	0,61				
99	0,026	-0,44				
100	1,0	172	Outlier			
104	0,034	1,0				
106	0,030	0,30				
108	0,030	0,26				
111	0,026	-0,44				
112	0,068	6,9	Outlier			
115	0,079	8,8	Outlier,ND			
116	0,020	-1,5				
118	0,036	1,3				
119	0,033	0,8				

**Consensus statistics**

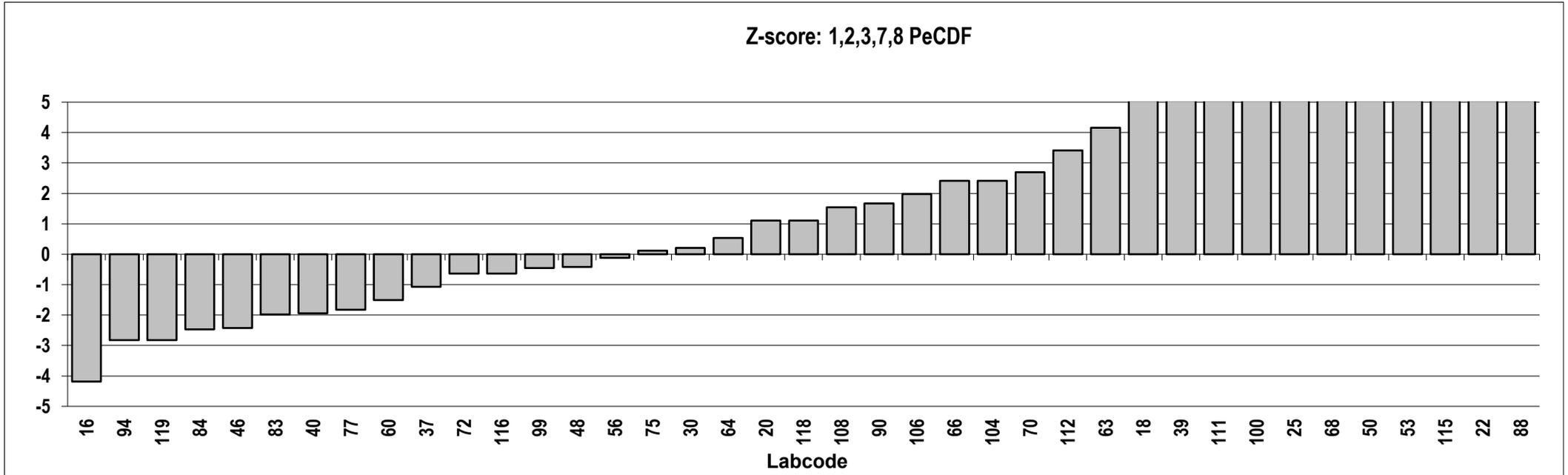
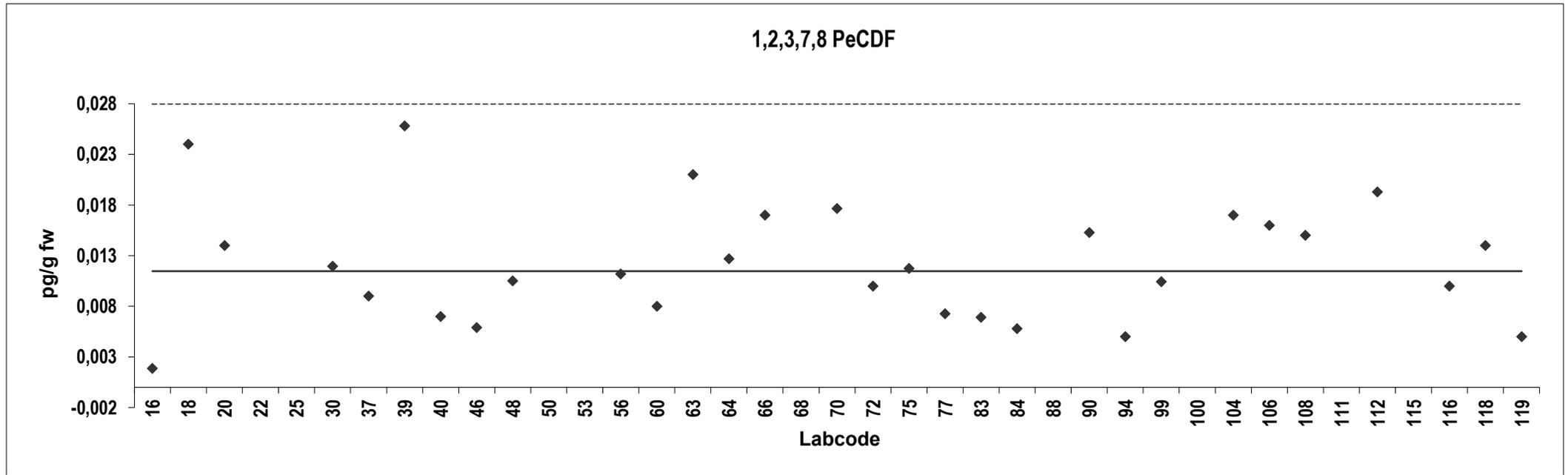
Consensus median, pg/g	0,029
Median all values pg/g	0,033
Consensus mean, pg/g	0,031
Standard deviation, pg/g	0,011
Relative standard deviation, %	37
No. of values reported	40
No. of values removed	10
No. of reported non-detects	5



**Egg yolk**  
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0019	-4,2	ND			
18	0,024	5,5	ND			
20	0,014	1,1				
22	0,100	39	Outlier			
25	0,050	17	Outlier,ND			
30	0,012	0,21				
37	0,0090	-1,1				
39	0,026	6,3				
40	0,0070	-1,9	ND			
46	0,0059	-2,4				
48	0,011	-0,42	ND			
50	0,058	20	Outlier			
53	0,070	26	Outlier,ND			
56	0,011	-0,12				
60	0,0080	-1,5	ND			
63	0,021	4,2				
64	0,013	0,54				
66	0,017	2,4				
68	0,051	17	Outlier,ND			
70	0,018	2,7				
72	0,010	-0,64	ND			
75	0,012	0,12				
77	0,0073	-1,8				
83	0,0069	-2,0				
84	0,0058	-2,5				
88	0,22	89	Outlier,ND			
90	0,015	1,7				
94	0,0050	-2,8	ND			
99	0,010	-0,46				
100	0,046	15	Outlier			
104	0,017	2,4				
106	0,016	2,0				
108	0,015	1,5	ND			
111	0,040	12	Outlier,ND			
112	0,019	3,4				
115	0,081	30	Outlier,ND			
116	0,010	-0,64				
118	0,014	1,1				
119	0,0050	-2,8	ND			

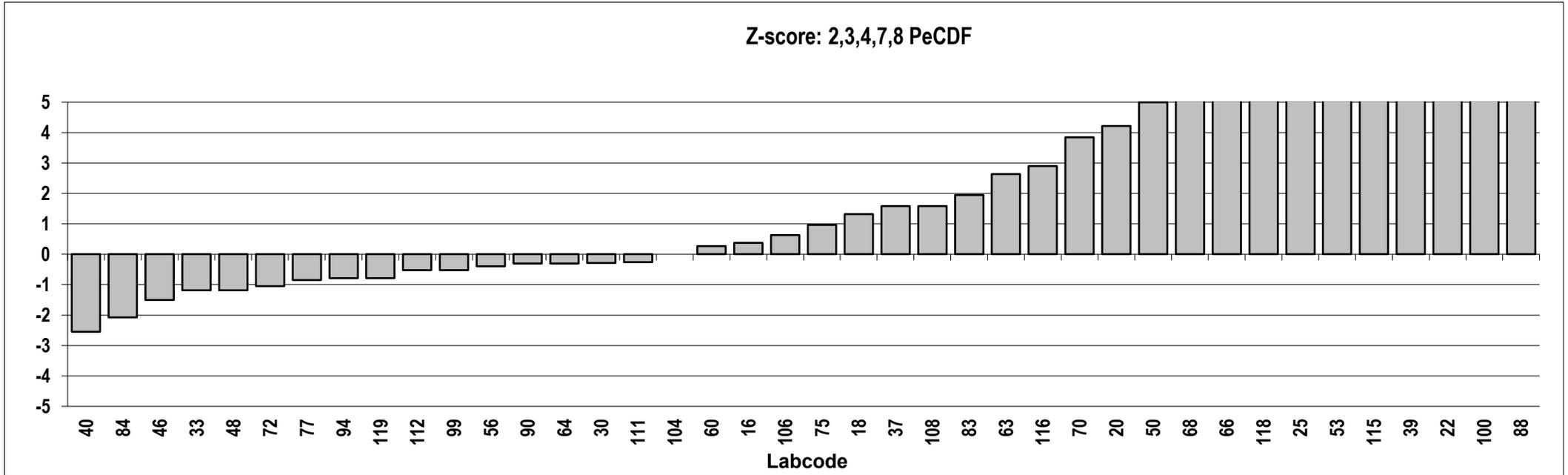
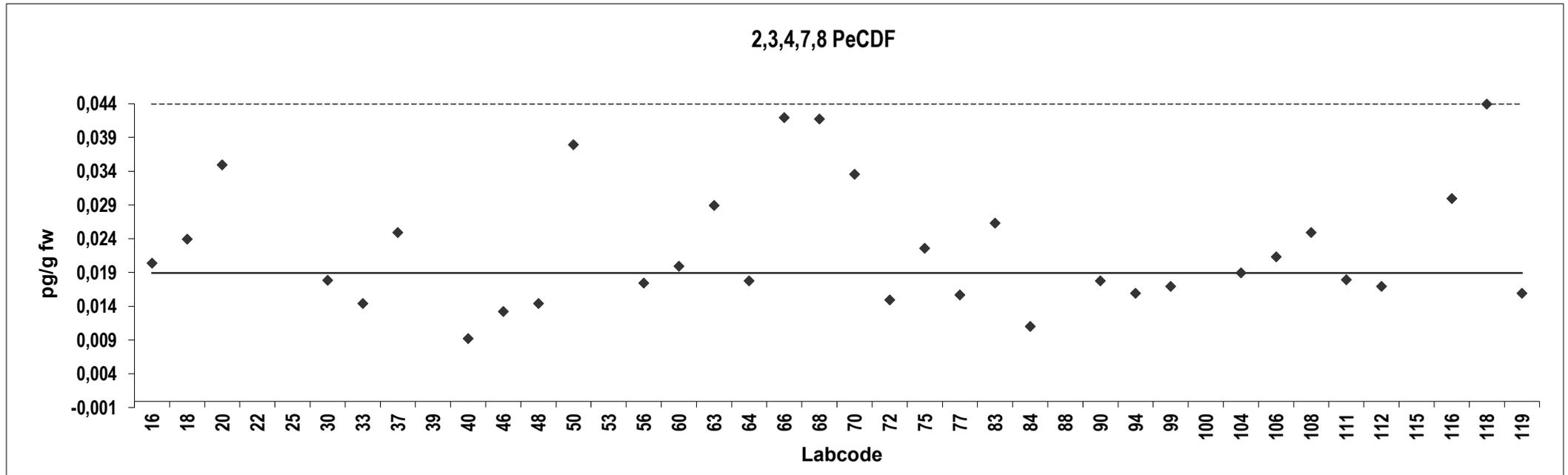
Consensus statistics	
Consensus median, pg/g	0,011
Median all values pg/g	0,014
Consensus mean, pg/g	0,012
Standard deviation, pg/g	0,0058
Relative standard deviation, %	48
No. of values reported	39
No. of values removed	9
No. of reported non-detects	15



**Egg yolk**  
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,020	0,38				
18	0,024	1,3	ND			
20	0,035	4,2				
22	0,100	21	Outlier			
25	0,050	8,2	Outlier,ND			
30	0,018	-0,29				
33	0,015	-1,2				
37	0,025	1,6				
39	0,084	17	Outlier			
40	0,0093	-2,6				
46	0,013	-1,5				
48	0,015	-1,2				
50	0,038	5,0	ND			
53	0,070	13	Outlier,ND			
56	0,018	-0,39				
60	0,020	0,26				
63	0,029	2,6				
64	0,018	-0,30				
66	0,042	6,1				
68	0,042	6,0	ND			
70	0,034	3,8				
72	0,015	-1,1				
75	0,023	0,97				
77	0,016	-0,85				
83	0,026	1,9				
84	0,011	-2,1				
88	0,21	51	Outlier,ND			
90	0,018	-0,31				
94	0,016	-0,79				
99	0,017	-0,52				
100	0,17	40	Outlier			
104	0,019	0,00000				
106	0,021	0,63				
108	0,025	1,6				
111	0,018	-0,26				
112	0,017	-0,53				
115	0,083	17	Outlier,ND			
116	0,030	2,9				
118	0,044	6,6				
119	0,016	-0,79				

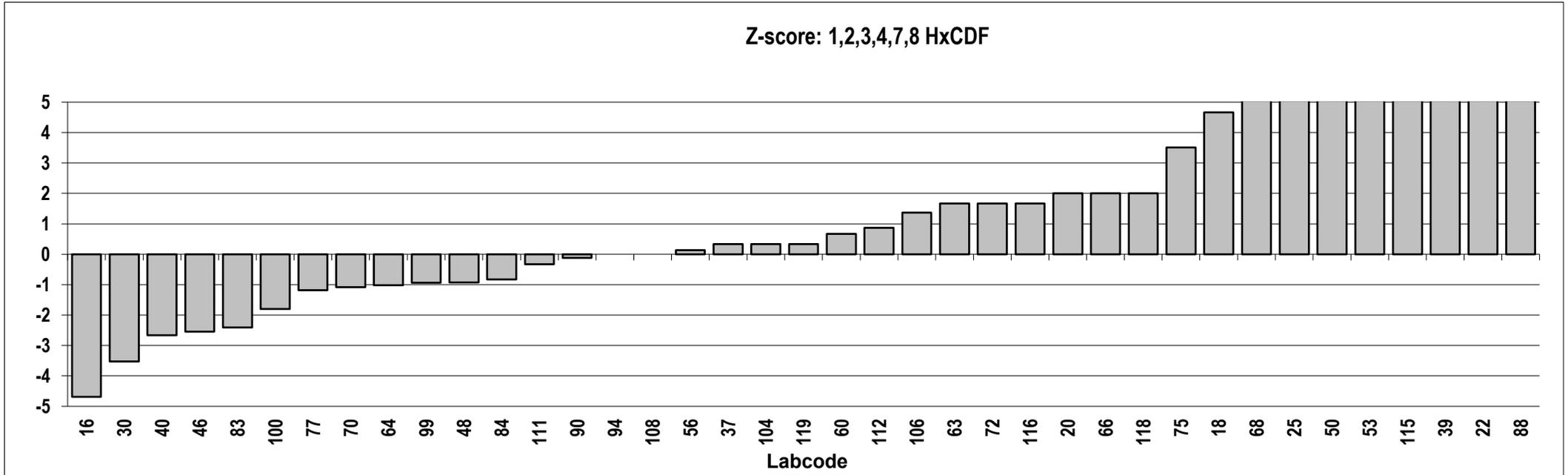
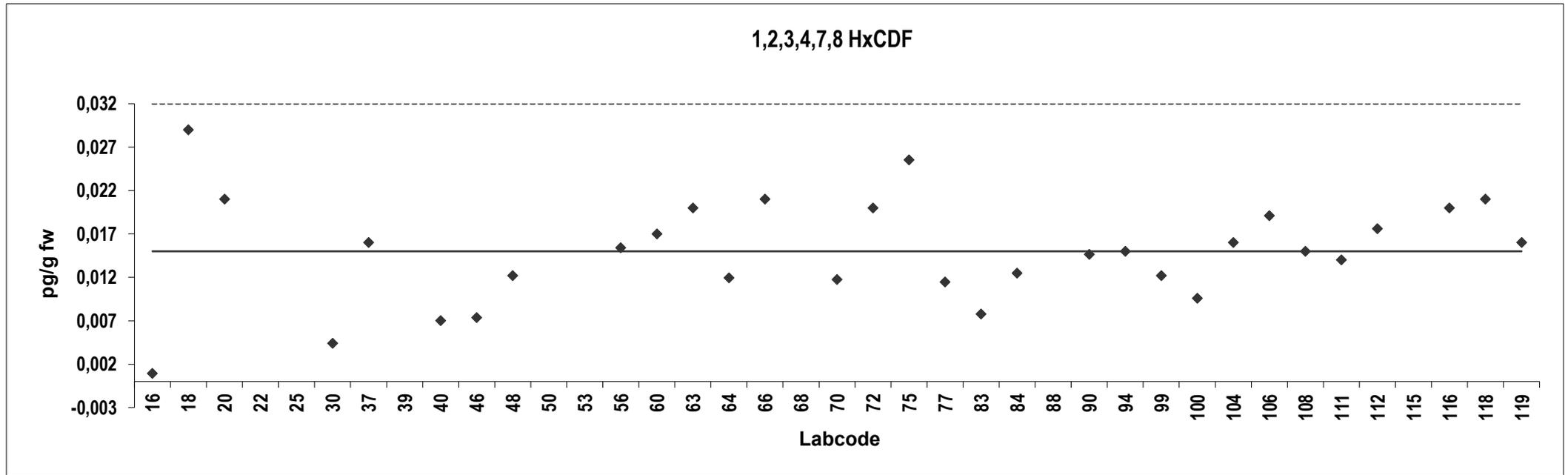
Consensus statistics	
Consensus median, pg/g	0,019
Median all values pg/g	0,022
Consensus mean, pg/g	0,023
Standard deviation, pg/g	0,0093
Relative standard deviation, %	41
No. of values reported	40
No. of values removed	7
No. of reported non-detects	7



**Egg yolk**  
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00093	-4,7	ND			
18	0,029	4,7	ND			
20	0,021	2,0				
22	0,17	53	Outlier			
25	0,050	12	Outlier			
30	0,0044	-3,5				
37	0,016	0,33				
39	0,15	44	Outlier			
40	0,0070	-2,7	ND			
46	0,0074	-2,5				
48	0,012	-0,93				
50	0,051	12	Outlier,ND			
53	0,070	18	Outlier,ND			
56	0,015	0,13				
60	0,017	0,67				
63	0,020	1,7				
64	0,012	-1,0				
66	0,021	2,0				
68	0,050	12	Outlier,ND			
70	0,012	-1,1				
72	0,020	1,7	ND			
75	0,026	3,5				
77	0,011	-1,2				
83	0,0078	-2,4				
84	0,013	-0,83				
88	0,29	91	Outlier,ND			
90	0,015	-0,12				
94	0,015	0,00000				
99	0,012	-0,94				
100	0,0096	-1,8	ND			
104	0,016	0,33				
106	0,019	1,4				
108	0,015	0,00000				
111	0,014	-0,33				
112	0,018	0,87				
115	0,073	19	Outlier,ND			
116	0,020	1,7				
118	0,021	2,0				
119	0,016	0,33				

Consensus statistics	
Consensus median, pg/g	0,015
Median all values pg/g	0,016
Consensus mean, pg/g	0,015
Standard deviation, pg/g	0,0060
Relative standard deviation, %	40
No. of values reported	39
No. of values removed	8
No. of reported non-detects	10

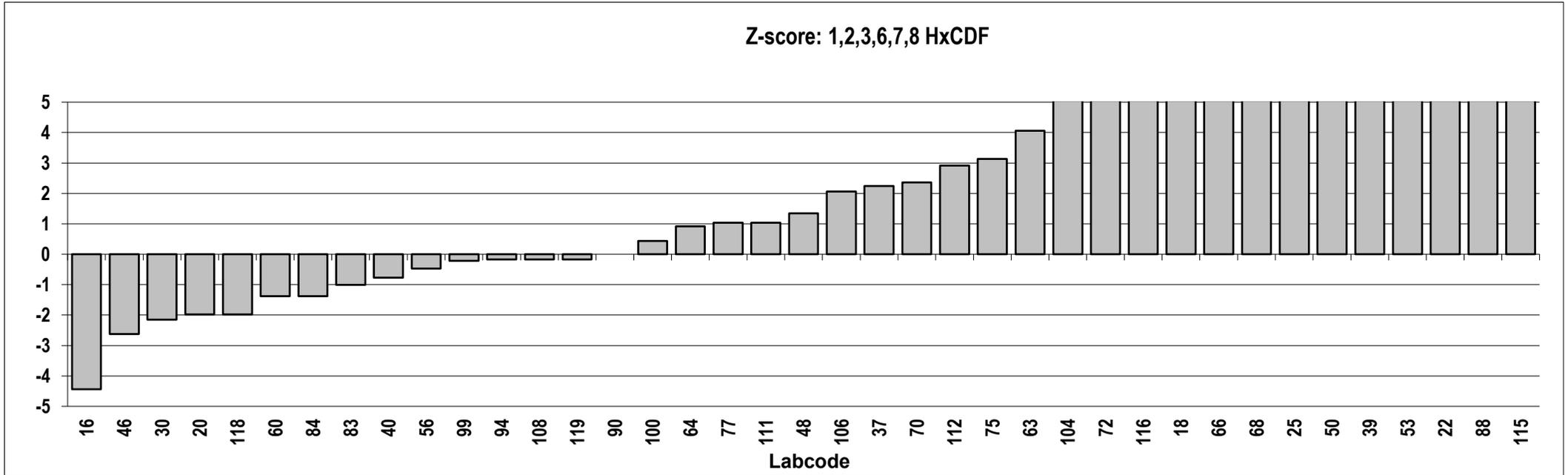
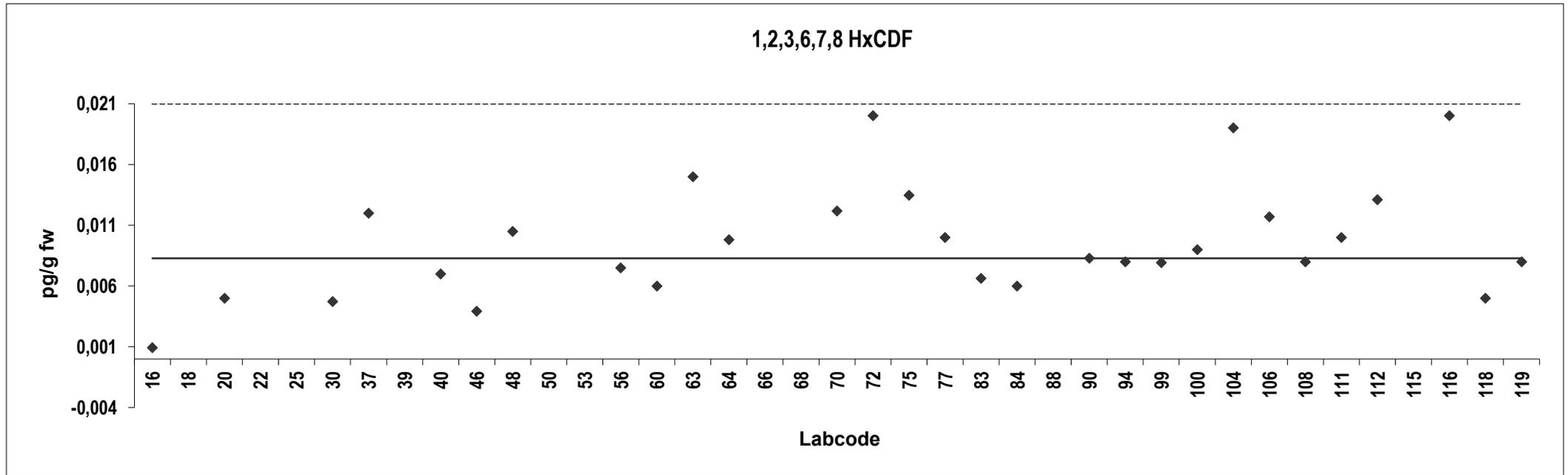


**Egg yolk**  
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00093	-4,4				
18	0,025	10	Outlier,ND			
20	0,0050	-2,0	ND			
22	0,16	92	Outlier			
25	0,050	25	Outlier,ND			
30	0,0047	-2,2				
37	0,012	2,2				
39	0,063	33	Outlier			
40	0,0070	-0,77	ND			
46	0,0039	-2,6				
48	0,011	1,3	ND			
50	0,050	25	Outlier,ND			
53	0,070	37	Outlier,ND			
56	0,0075	-0,47				
60	0,0060	-1,4				
63	0,015	4,1				
64	0,0098	0,92				
66	0,029	13	Outlier			
68	0,044	21	Outlier,ND			
70	0,012	2,4				
72	0,020	7,1	ND			
75	0,013	3,1				
77	0,010	1,0	ND			
83	0,0066	-1,0				
84	0,0060	-1,4				
88	0,27	156	Outlier,ND			
90	0,0083	0,00000				
94	0,0080	-0,17				
99	0,0079	-0,22	ND			
100	0,0090	0,43				
104	0,019	6,5				
106	0,012	2,1				
108	0,0080	-0,17				
111	0,010	1,0				
112	0,013	2,9				
115	0,70	415	Outlier,ND			
116	0,020	7,1				
118	0,0050	-2,0	ND			
119	0,0080	-0,17				

**Consensus statistics**

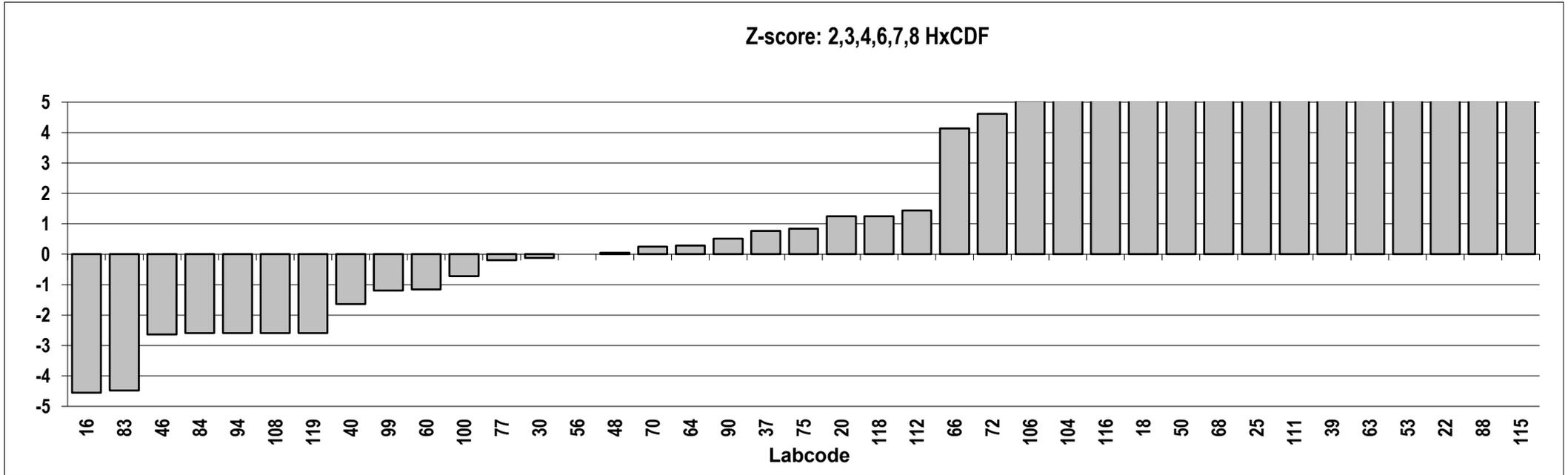
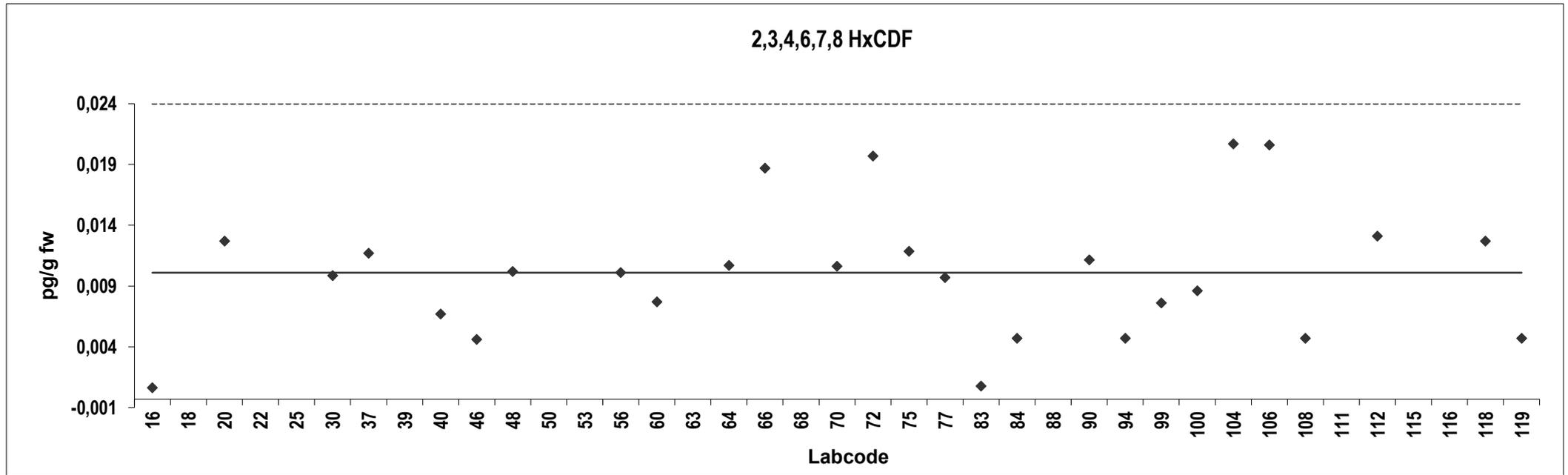
Consensus median, pg/g	0,0083
Median all values pg/g	0,011
Consensus mean, pg/g	0,010
Standard deviation, pg/g	0,0047
Relative standard deviation, %	49
No. of values reported	39
No. of values removed	10
No. of reported non-detects	14



**Egg yolk**  
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00093	-4,6	ND			
18	0,031	9,9	Outlier,ND			
20	0,013	1,3				
22	0,12	51	Outlier			
25	0,050	19	Outlier,ND			
30	0,010	-0,12				
37	0,012	0,77				
39	0,056	22	Outlier			
40	0,0070	-1,6	ND			
46	0,0049	-2,6				
48	0,011	0,048	ND			
50	0,035	12	Outlier,ND			
53	0,070	29	Outlier,ND			
56	0,010	0,00000				
60	0,0080	-1,2				
63	0,057	22	Outlier,ND			
64	0,011	0,29				
66	0,019	4,1				
68	0,042	15	Outlier,ND			
70	0,011	0,25				
72	0,020	4,6	ND			
75	0,012	0,84				
77	0,010	-0,19	ND			
83	0,0011	-4,5				
84	0,0050	-2,6				
88	0,29	135	Outlier,ND			
90	0,011	0,51				
94	0,0050	-2,6	ND			
99	0,0079	-1,2	ND			
100	0,0089	-0,72	ND			
104	0,021	5,1				
106	0,021	5,0				
108	0,0050	-2,6	ND			
111	0,050	19	Outlier,ND			
112	0,013	1,4				
115	0,68	321	Outlier,ND			
116	0,030	9,4	Outlier			
118	0,013	1,3				
119	0,0050	-2,6	ND			

Consensus statistics	
Consensus median, pg/g	0,010
Median all values pg/g	0,012
Consensus mean, pg/g	0,010
Standard deviation, pg/g	0,0054
Relative standard deviation, %	53
No. of values reported	39
No. of values removed	12
No. of reported non-detects	19

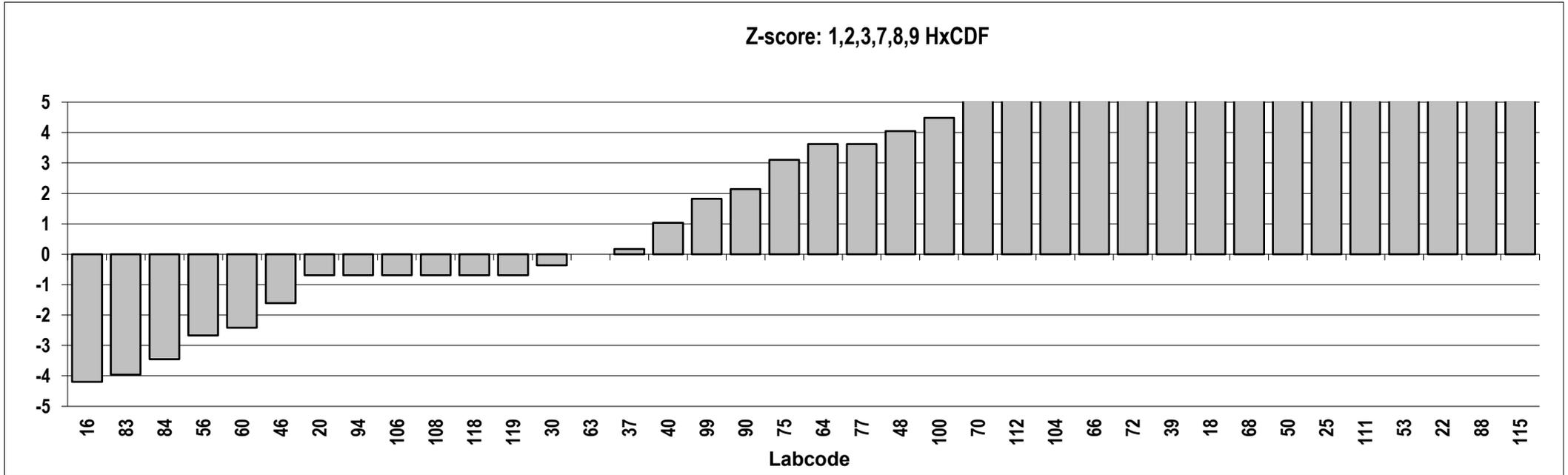
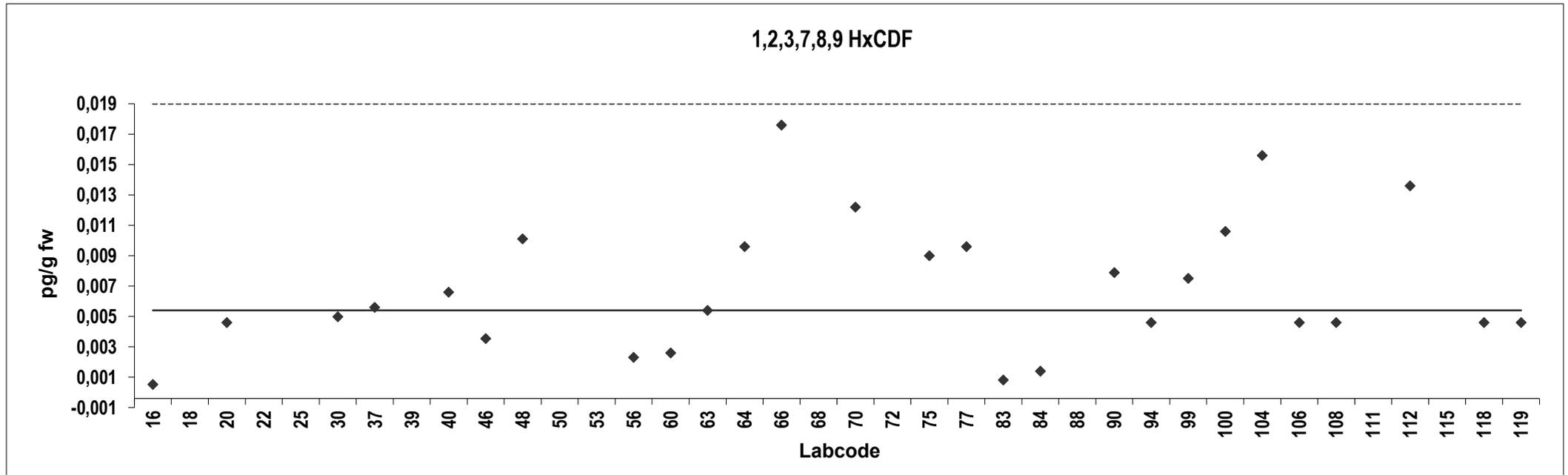


**Egg yolk**  
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,00093	-4,2	ND			
18	0,039	29	Outlier,ND			
20	0,0050	-0,69	ND			
22	0,088	71	Outlier			
25	0,050	38	Outlier,ND			
30	0,0054	-0,37				
37	0,0060	0,17				
39	0,022	14	Outlier			
40	0,0070	1,0	ND			
46	0,0039	-1,6				
48	0,011	4,1	ND			
50	0,043	32	Outlier,ND			
53	0,070	55	Outlier,ND			
56	0,0027	-2,7				
60	0,0030	-2,4	ND			
63	0,0058	0,00000	ND			
64	0,010	3,6				
66	0,018	11				
68	0,042	31	Outlier,ND			
70	0,013	5,9				
72	0,020	12	Outlier,ND			
75	0,0094	3,1				
77	0,010	3,6	ND			
83	0,0012	-4,0				
84	0,0018	-3,4	ND			
88	0,30	251	Outlier,ND			
90	0,0083	2,1				
94	0,0050	-0,69	ND			
99	0,0079	1,8	ND			
100	0,011	4,5	ND			
104	0,016	8,8	ND			
106	0,0050	-0,69				
108	0,0050	-0,69	ND			
111	0,050	38	Outlier,ND			
112	0,014	7,1				
115	1,1	965	Outlier,ND			
118	0,0050	-0,69	ND			
119	0,0050	-0,69	ND			

**Consensus statistics**

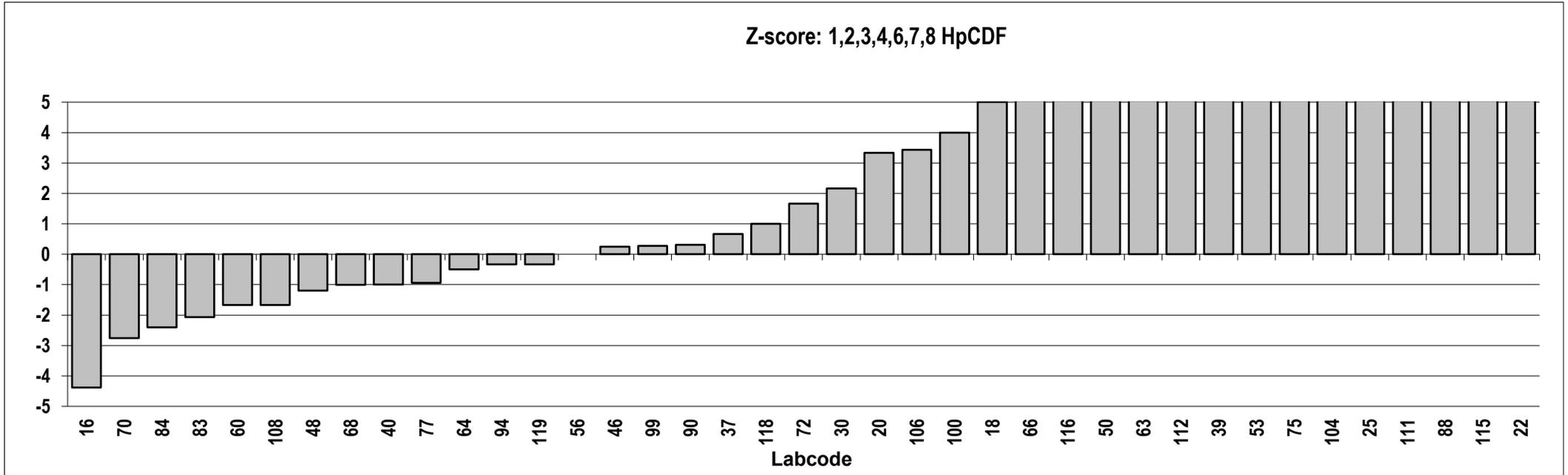
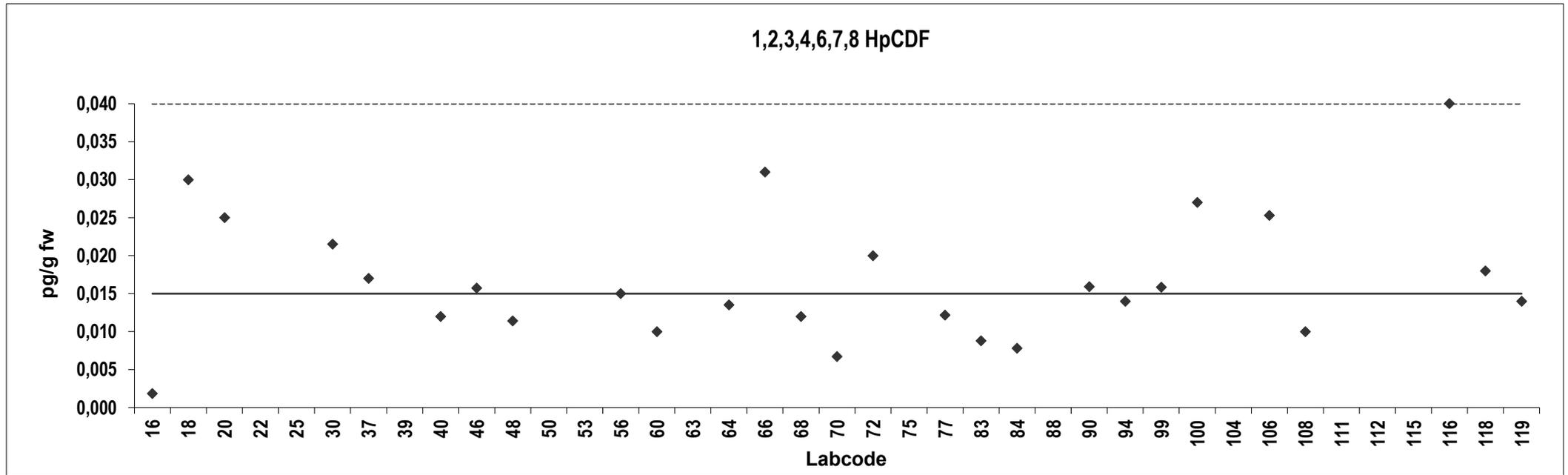
Consensus median, pg/g	0,0058
Median all values pg/g	0,010
Consensus mean, pg/g	0,0072
Standard deviation, pg/g	0,0044
Relative standard deviation, %	61
No. of values reported	38
No. of values removed	11
No. of reported non-detects	24



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0019	-4,4	ND			
18	0,030	5,0	ND			
20	0,025	3,3				
22	0,28	87	Outlier			
25	0,13	38	Outlier			
30	0,021	2,2				
37	0,017	0,67				
39	0,067	17	Outlier			
40	0,012	-1,0				
46	0,016	0,25				
48	0,011	-1,2				
50	0,042	9,0	Outlier			
53	0,070	18	Outlier,ND			
56	0,015	0,00000				
60	0,010	-1,7				
63	0,045	10	Outlier			
64	0,014	-0,50				
66	0,031	5,3				
68	0,012	-1,0	ND			
70	0,0067	-2,8				
72	0,020	1,7	ND			
75	0,073	19	Outlier			
77	0,012	-0,94				
83	0,0088	-2,1				
84	0,0078	-2,4				
88	0,17	52	Outlier,ND			
90	0,016	0,31				
94	0,014	-0,33				
99	0,016	0,28	ND			
100	0,027	4,0	ND			
104	0,093	26	Outlier			
106	0,025	3,4				
108	0,010	-1,7	ND			
111	0,15	45	Outlier,ND			
112	0,049	11	Outlier			
115	0,17	53	Outlier,ND			
116	0,040	8,3				
118	0,018	1,0				
119	0,014	-0,33				

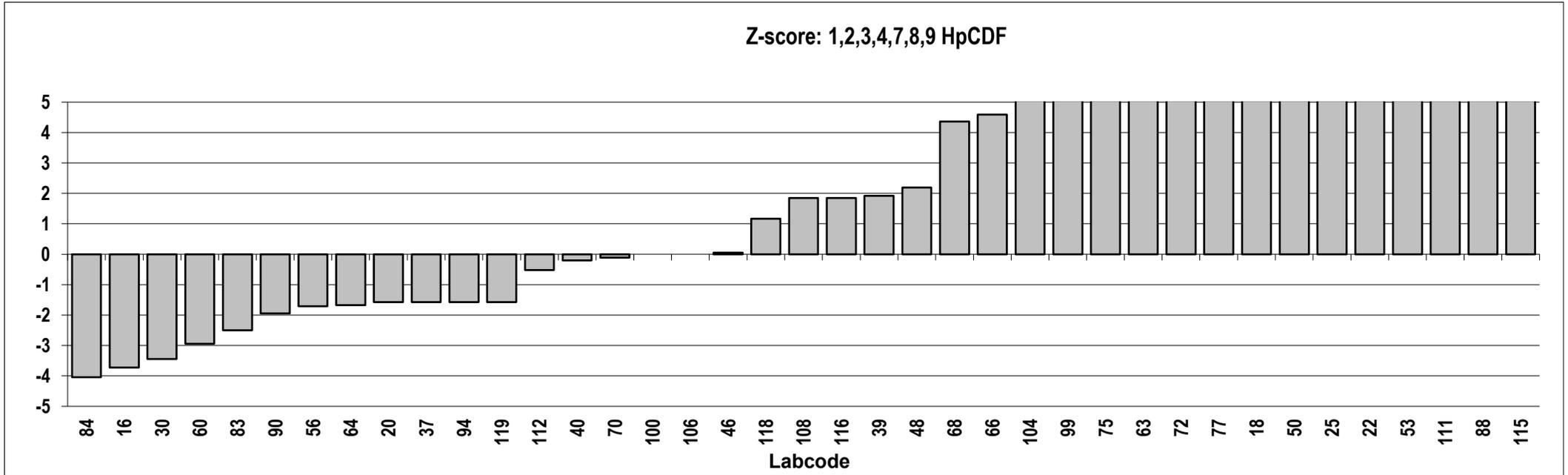
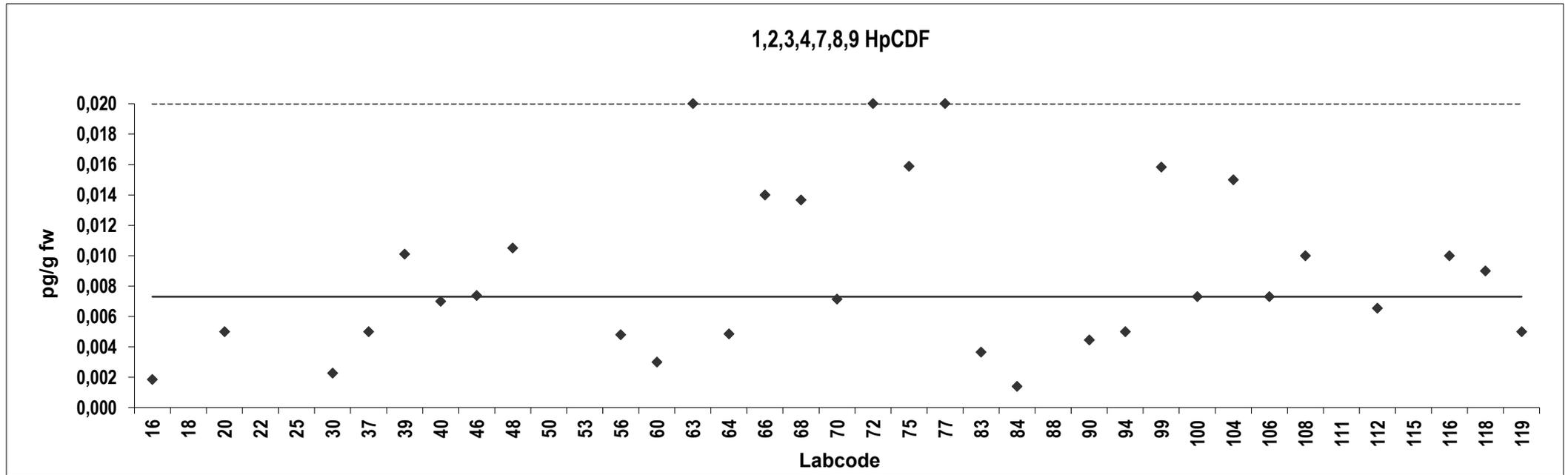
Consensus statistics	
Consensus median, pg/g	0,015
Median all values pg/g	0,020
Consensus mean, pg/g	0,017
Standard deviation, pg/g	0,0085
Relative standard deviation, %	51
No. of values reported	39
No. of values removed	12
No. of reported non-detects	11



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

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0019	-3,7	ND			
18	0,042	24	Outlier,ND			
20	0,0050	-1,6	ND			
22	0,069	42	Outlier			
25	0,050	29	Outlier,ND			
30	0,0023	-3,4				
37	0,0050	-1,6				
39	0,010	1,9				
40	0,0070	-0,21	ND			
46	0,0074	0,054				
48	0,011	2,2	ND			
50	0,044	25	Outlier,ND			
53	0,070	43	Outlier,ND			
56	0,0048	-1,7				
60	0,0030	-2,9	ND			
63	0,020	8,7				
64	0,0049	-1,7				
66	0,014	4,6				
68	0,014	4,4	ND			
70	0,0071	-0,11				
72	0,020	8,7	ND			
75	0,016	5,9				
77	0,020	8,7	ND			
83	0,0036	-2,5				
84	0,0014	-4,0	ND			
88	0,19	128	Outlier,ND			
90	0,0045	-1,9				
94	0,0050	-1,6	ND			
99	0,016	5,8	ND			
100	0,0073	0,00000	ND			
104	0,015	5,3				
106	0,0073	0,00000				
108	0,010	1,8	ND			
111	0,15	98	Outlier,ND			
112	0,0065	-0,52				
115	0,31	207	Outlier,ND			
116	0,010	1,8				
118	0,0090	1,2	ND			
119	0,0050	-1,6	ND			

Consensus statistics	
Consensus median, pg/g	0,0073
Median all values pg/g	0,010
Consensus mean, pg/g	0,0088
Standard deviation, pg/g	0,0055
Relative standard deviation, %	62
No. of values reported	39
No. of values removed	8
No. of reported non-detects	22

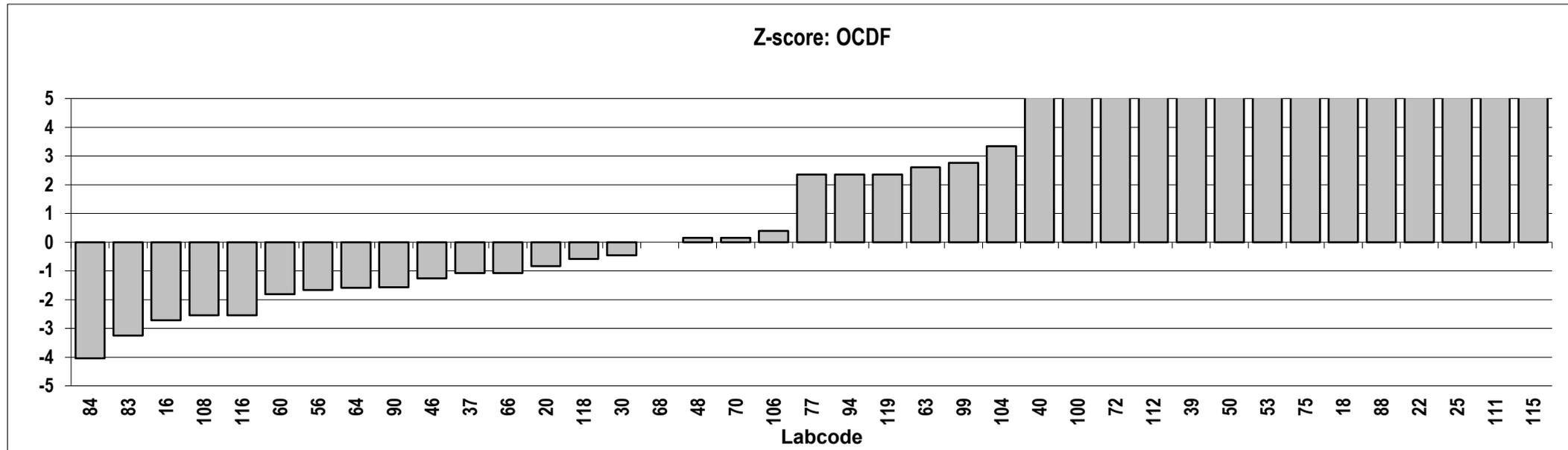
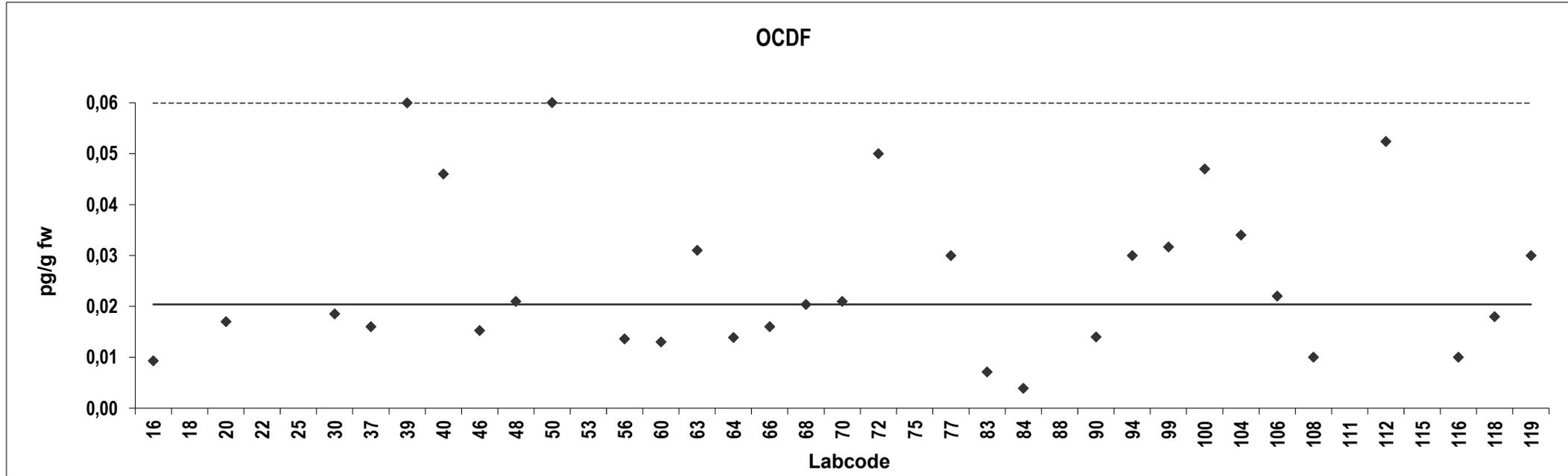


**Egg yolk**  
Congener: OCDF

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,0093	-2,7	ND			
18	0,13	27	Outlier,ND			
20	0,017	-0,83				
22	0,35	82	Outlier			
25	0,45	105	Outlier			
30	0,019	-0,46				
37	0,016	-1,1				
39	0,060	9,7				
40	0,046	6,3	ND			
46	0,015	-1,3				
48	0,021	0,15	ND			
50	0,060	9,7				
53	0,070	12	Outlier,ND			
56	0,014	-1,7				
60	0,013	-1,8				
63	0,031	2,6				
64	0,014	-1,6				
66	0,016	-1,1				
68	0,020	0,00000	ND			
70	0,021	0,15				
72	0,050	7,3	ND			
75	0,10	20	Outlier			
77	0,030	2,4	ND			
83	0,0071	-3,2				
84	0,0039	-4,0	ND			
88	0,16	33	Outlier,ND			
90	0,014	-1,6				
94	0,030	2,4	ND			
99	0,032	2,8	ND			
100	0,047	6,5	ND			
104	0,034	3,3				
106	0,022	0,39				
108	0,010	-2,5	ND			
111	2,0	485	Outlier,ND			
112	0,052	8				
115	2,4	572	Outlier,ND			
116	0,010	-2,5				
118	0,018	-0,59	ND			
119	0,030	2,4	ND			

**Consensus statistics**

Consensus median, pg/g	0,020
Median all values pg/g	0,030
Consensus mean, pg/g	0,025
Standard deviation, pg/g	0,016
Relative standard deviation, %	62
No. of values reported	39
No. of values removed	8
No. of reported non-detects	18

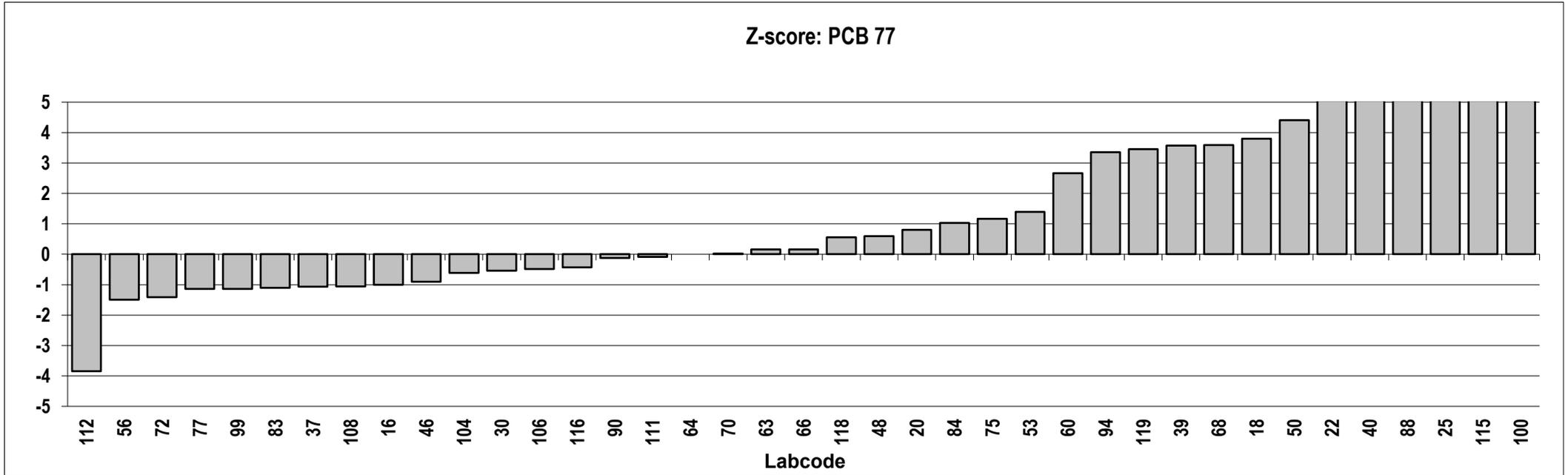
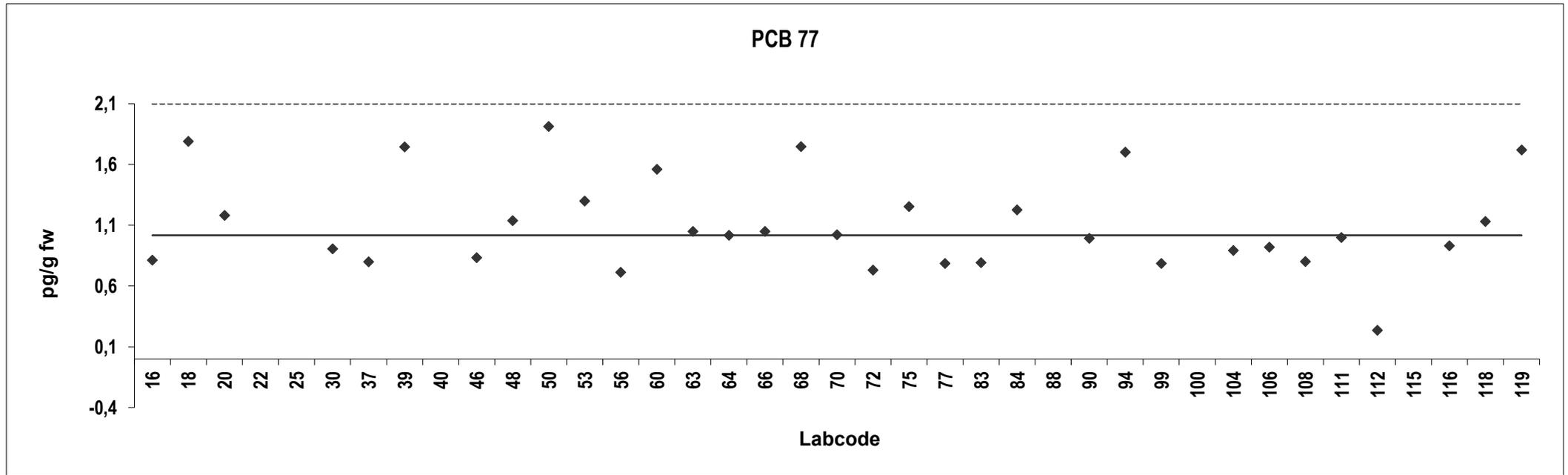


**Egg yolk**  
**Congener: PCB 77**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,81	-1,0				
18	1,8	3,8				
20	1,2	0,80				
22	2,2	6,0	Outlier			
25	3,8	13	Outlier			
30	0,91	-0,54				
37	0,80	-1,1				
39	1,7	3,6				
40	2,3	6,3	Outlier			
46	0,83	-0,91				
48	1,1	0,60				
50	1,9	4,4				
53	1,3	1,4				
56	0,71	-1,5				
60	1,6	2,7				
63	1,1	0,16				
64	1,0	0,00000				
66	1,1	0,16				
68	1,7	3,6				
70	1,0	0,017				
72	0,73	-1,4				
75	1,3	1,2				
77	0,79	-1,1				
83	0,79	-1,1				
84	1,2	1,0				
88	3,2	11	Outlier,ND			
90	0,99	-0,13				
94	1,7	3,4				
99	0,79	-1,1				
100	21	100	Outlier			
104	0,89	-0,62				
106	0,92	-0,48				
108	0,80	-1,1				
111	1,0	-0,085	ND			
112	0,24	-3,8				
115	3,9	14	Outlier			
116	0,93	-0,43				
118	1,1	0,55				
119	1,7	3,5				

**Consensus statistics**

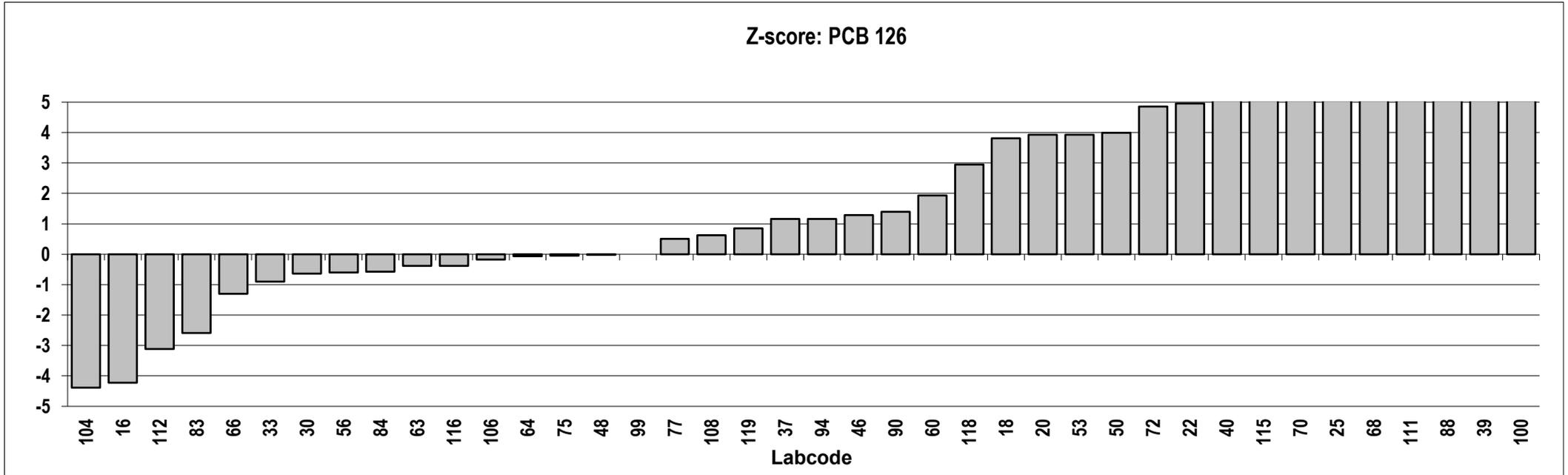
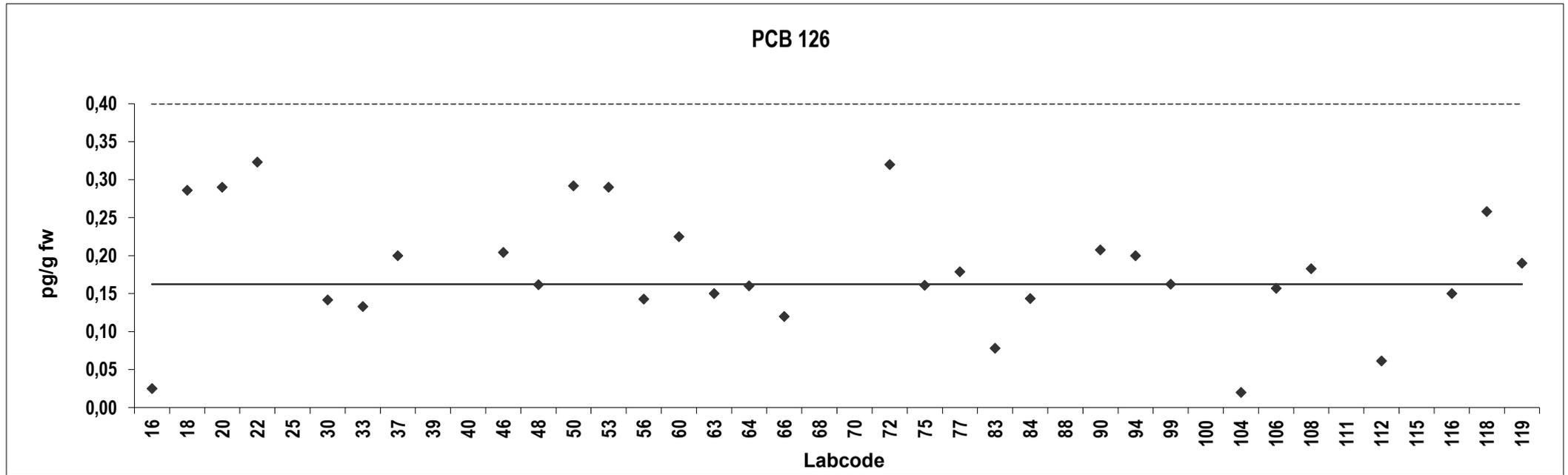
Consensus median, pg/g	1,0
Median all values pg/g	1,1
Consensus mean, pg/g	1,1
Standard deviation, pg/g	0,39
Relative standard deviation, %	35
No. of values reported	39
No. of values removed	6
No. of reported non-detects	2



**Egg yolk**  
**Congener: PCB 126**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,025	-4,2	ND			
18	0,29	3,8				
20	0,29	3,9				
22	0,32	5,0				
25	0,58	13	Outlier			
30	0,14	-0,64				
33	0,13	-0,90				
37	0,20	1,2				
39	3,2	92	Outlier			
40	0,44	8,6	Outlier			
46	0,20	1,3				
48	0,16	-0,017				
50	0,29	4,0				
53	0,29	3,9				
56	0,14	-0,61				
60	0,23	1,9				
63	0,15	-0,38				
64	0,16	-0,068				
66	0,12	-1,3				
68	0,71	17	Outlier,ND			
70	0,57	13	Outlier			
72	0,32	4,9	ND			
75	0,16	-0,044				
77	0,18	0,50				
83	0,078	-2,6				
84	0,14	-0,58				
88	2,8	80	Outlier,ND			
90	0,21	1,4				
94	0,20	1,2				
99	0,16	0,00000				
100	4,5	134	Outlier			
104	0,020	-4,4	ND			
106	0,16	-0,17				
108	0,18	0,63				
111	1,0	26	Outlier,ND			
112	0,061	-3,1				
115	0,53	11	Outlier			
116	0,15	-0,38				
118	0,26	2,9				
119	0,19	0,85				

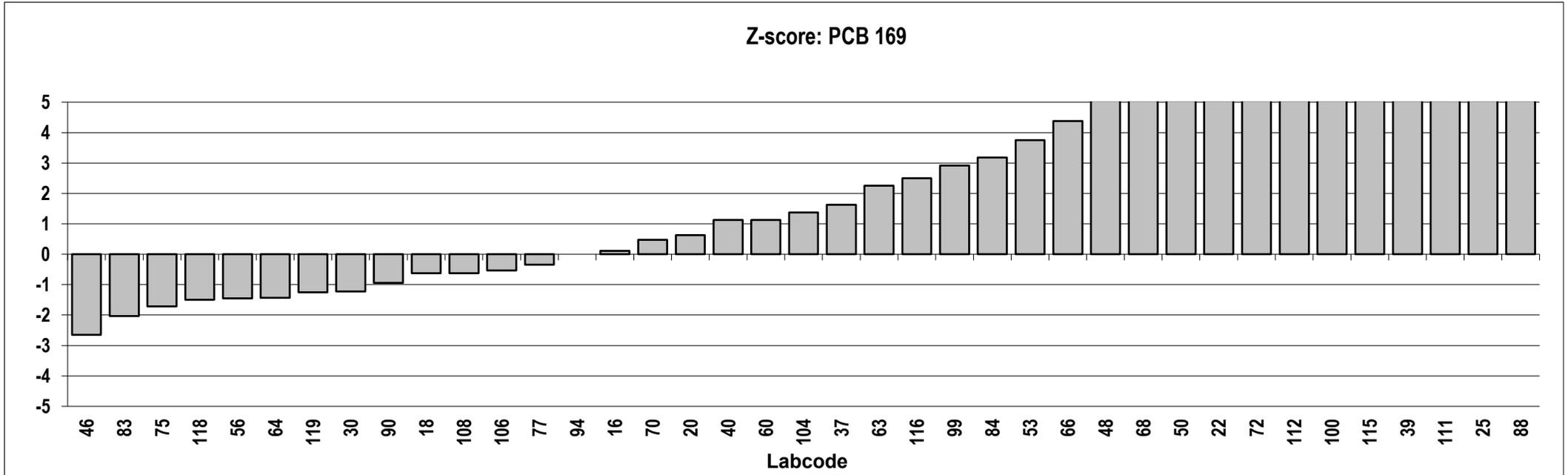
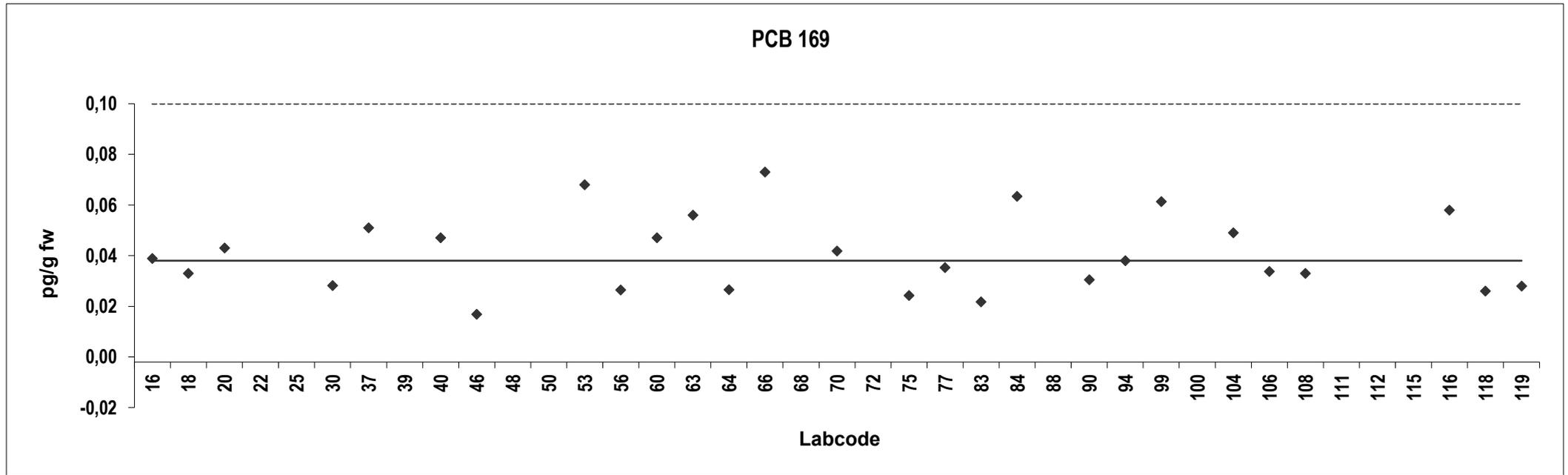
Consensus statistics	
Consensus median, pg/g	0,16
Median all values pg/g	0,20
Consensus mean, pg/g	0,18
Standard deviation, pg/g	0,079
Relative standard deviation, %	44
No. of values reported	40
No. of values removed	9
No. of reported non-detects	6



**Egg yolk**  
**Congener: PCB 169**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,041	0,11	ND			
18	0,035	-0,63	ND			
20	0,045	0,63				
22	0,27	29	Outlier			
25	2,0	245	Outlier,ND			
30	0,030	-1,2				
37	0,053	1,6				
39	0,85	101	Outlier			
40	0,049	1,1				
46	0,019	-2,6				
48	0,13	11	Outlier,ND			
50	0,24	25	Outlier,ND			
53	0,070	3,8	ND			
56	0,028	-1,5				
60	0,049	1,1				
63	0,058	2,3				
64	0,029	-1,4				
66	0,075	4,4				
68	0,18	17	Outlier,ND			
70	0,044	0,47	ND			
72	0,32	35	Outlier,ND			
75	0,026	-1,7				
77	0,037	-0,34				
83	0,024	-2,0				
84	0,065	3,2	ND			
88	2,7	336	Outlier,ND			
90	0,032	-0,94				
94	0,040	0,00000				
99	0,063	2,9	ND			
100	0,65	76	Outlier			
104	0,051	1,4				
106	0,036	-0,54				
108	0,035	-0,63				
111	1,0	120	Outlier,ND			
112	0,63	74	Outlier			
115	0,77	91	Outlier,ND			
116	0,060	2,5				
118	0,028	-1,5				
119	0,030	-1,3				

Consensus statistics	
Consensus median, pg/g	0,040
Median all values pg/g	0,051
Consensus mean, pg/g	0,043
Standard deviation, pg/g	0,015
Relative standard deviation, %	36
No. of values reported	39
No. of values removed	12
No. of reported non-detects	14

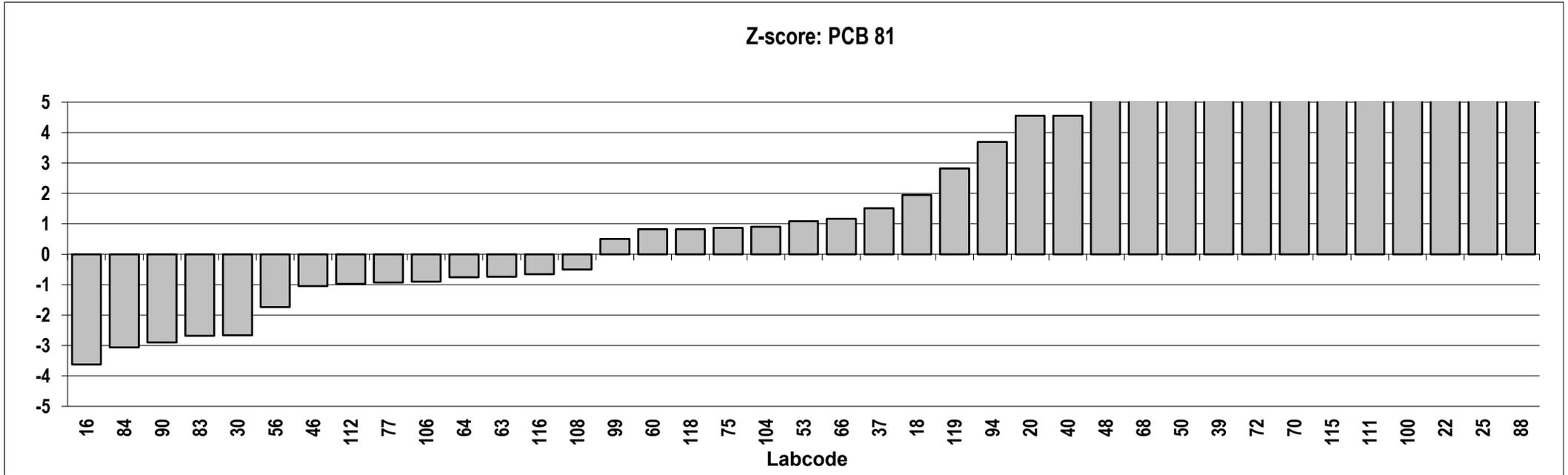
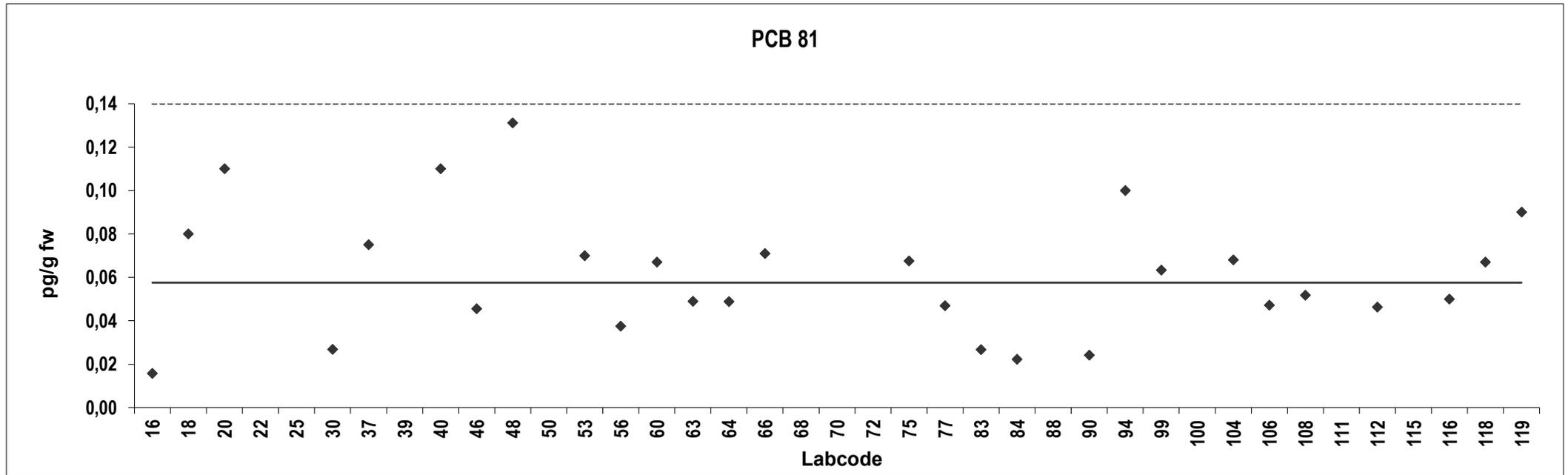


**Egg yolk**  
Congener: PCB 81

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,016	-3,6				
18	0,080	1,9				
20	0,11	4,6				
22	1,9	158	Outlier			
25	2,0	169	Outlier,ND			
30	0,027	-2,7				
37	0,075	1,5				
39	0,26	17	Outlier			
40	0,11	4,6				
46	0,045	-1,0				
48	0,13	6,4	ND			
50	0,17	9,4	Outlier,ND			
53	0,070	1,1	ND			
56	0,038	-1,7				
60	0,067	0,82				
63	0,049	-0,74				
64	0,049	-0,76				
66	0,071	1,2				
68	0,16	9,2	Outlier,ND			
70	0,40	30	Outlier			
72	0,32	23	Outlier,ND			
75	0,067	0,86				
77	0,047	-0,93				
83	0,027	-2,7				
84	0,022	-3,1	ND			
88	2,8	239	Outlier,ND			
90	0,024	-2,9				
94	0,10	3,7				
99	0,063	0,50	ND			
100	1,3	107	Outlier			
104	0,068	0,91				
106	0,047	-0,90				
108	0,052	-0,50				
111	1,0	82	Outlier,ND			
112	0,046	-1,0				
115	0,46	35	Outlier			
116	0,050	-0,66				
118	0,067	0,82				
119	0,090	2,8				

**Consensus statistics**

Consensus median, pg/g	0,058
Median all values pg/g	0,070
Consensus mean, pg/g	0,061
Standard deviation, pg/g	0,029
Relative standard deviation, %	47
No. of values reported	39
No. of values removed	11
No. of reported non-detects	10

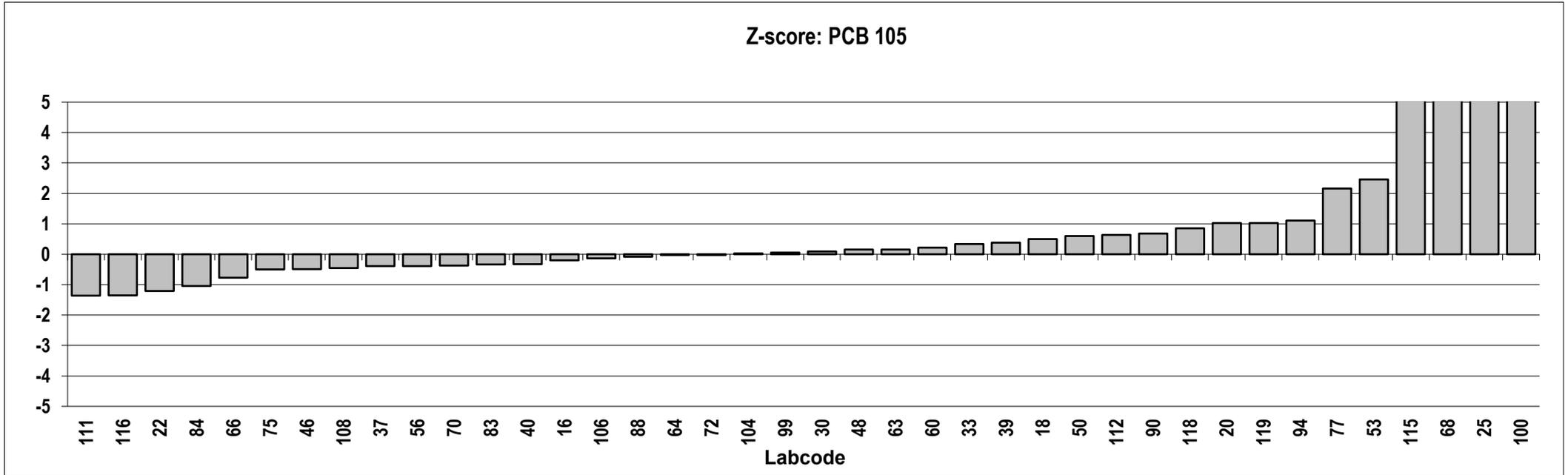
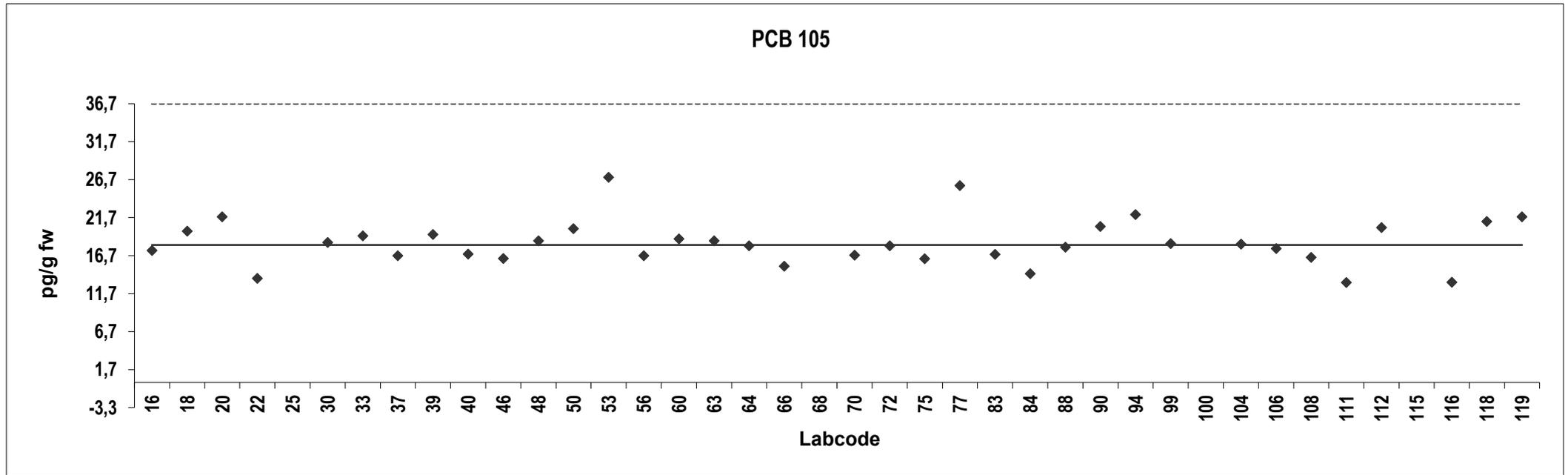


**Egg yolk**  
**Congener: PCB 105**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	17	-0,20				
18	20	0,50				
20	22	1,0				
22	14	-1,2				
25	76	16	Outlier			
30	18	0,086				
33	19	0,33				
37	17	-0,39				
39	19	0,38				
40	17	-0,33				
46	16	-0,49				
48	19	0,15				
50	20	0,60				
53	27	2,5				
56	17	-0,39				
60	19	0,22				
63	19	0,15				
64	18	-0,030				
66	15	-0,77				
68	75	16	Outlier			
70	17	-0,37				
72	18	-0,028				
75	16	-0,50				
77	26	2,2				
83	17	-0,34				
84	14	-1,0				
88	18	-0,083				
90	21	0,68				
94	22	1,1				
99	18	0,051				
100	184	46	Outlier			
104	18	0,028				
106	18	-0,13				
108	16	-0,45				
111	13	-1,4				
112	20	0,64				
115	74	16	Outlier			
116	13	-1,4				
118	21	0,86				
119	22	1,0				

**Consensus statistics**

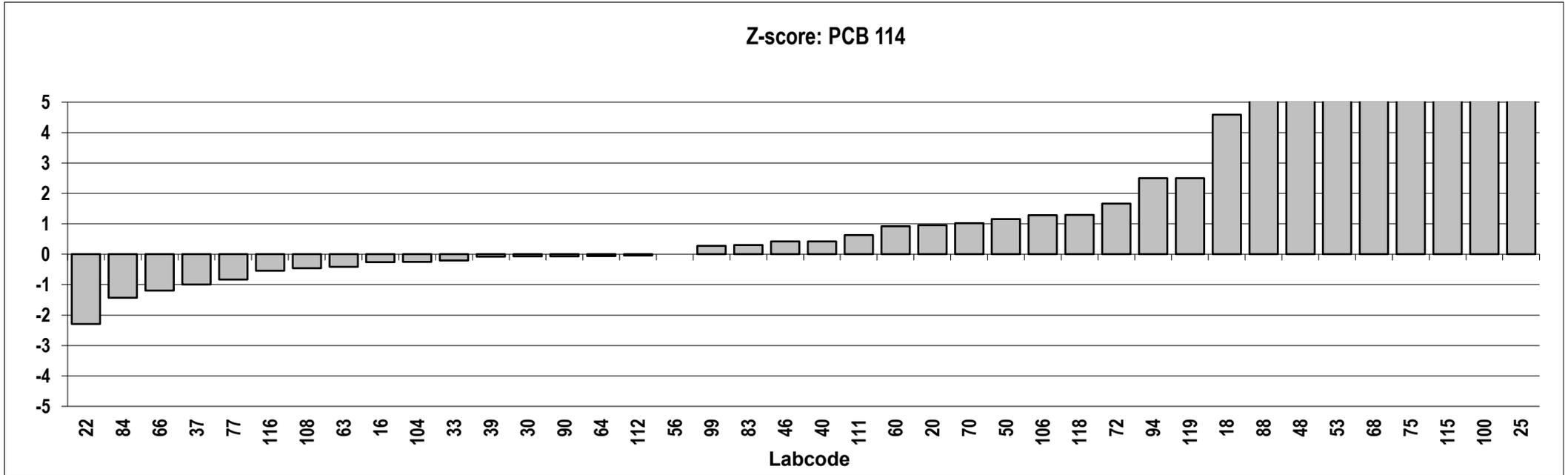
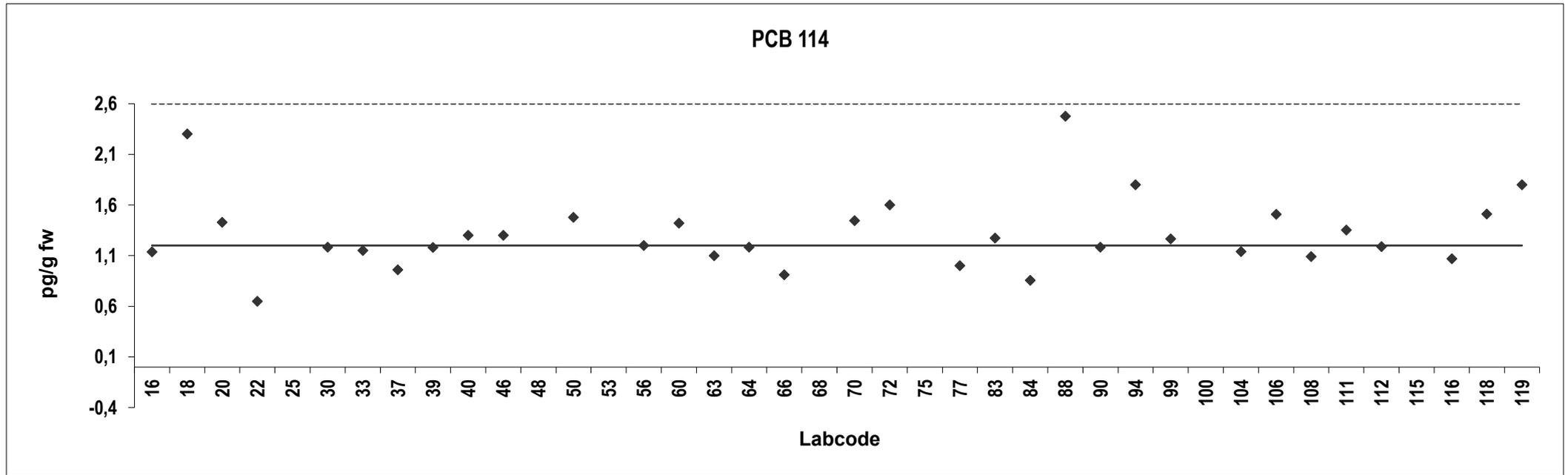
Consensus median, pg/g	18
Median all values pg/g	18
Consensus mean, pg/g	18
Standard deviation, pg/g	3,0
Relative standard deviation, %	17
No. of values reported	40
No. of values removed	4
No. of reported non-detects	0



**Egg yolk**  
**Congener: PCB 114**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	1,1	-0,26				
18	2,3	4,6				
20	1,4	0,96				
22	0,65	-2,3				
25	10	37	Outlier,ND			
30	1,2	-0,073				
33	1,2	-0,21				
37	0,96	-1,0				
39	1,2	-0,075				
40	1,3	0,42				
46	1,3	0,42				
48	2,6	5,9	Outlier,ND			
50	1,5	1,2				
53	2,7	6,3	Outlier,ND			
56	1,2	0,00000				
60	1,4	0,92				
63	1,1	-0,42				
64	1,2	-0,064				
66	0,91	-1,2				
68	4,0	12	Outlier			
70	1,4	1,0				
72	1,6	1,7				
75	4,9	16	Outlier,ND			
77	1,0	-0,83	ND			
83	1,3	0,30				
84	0,86	-1,4				
88	2,5	5,3	ND			
90	1,2	-0,069				
94	1,8	2,5				
99	1,3	0,28	ND			
100	9,0	32	Outlier			
104	1,1	-0,25				
106	1,5	1,3				
108	1,1	-0,46				
111	1,4	0,63				
112	1,2	-0,042				
115	5,8	19	Outlier			
116	1,1	-0,54				
118	1,5	1,3				
119	1,8	2,5				

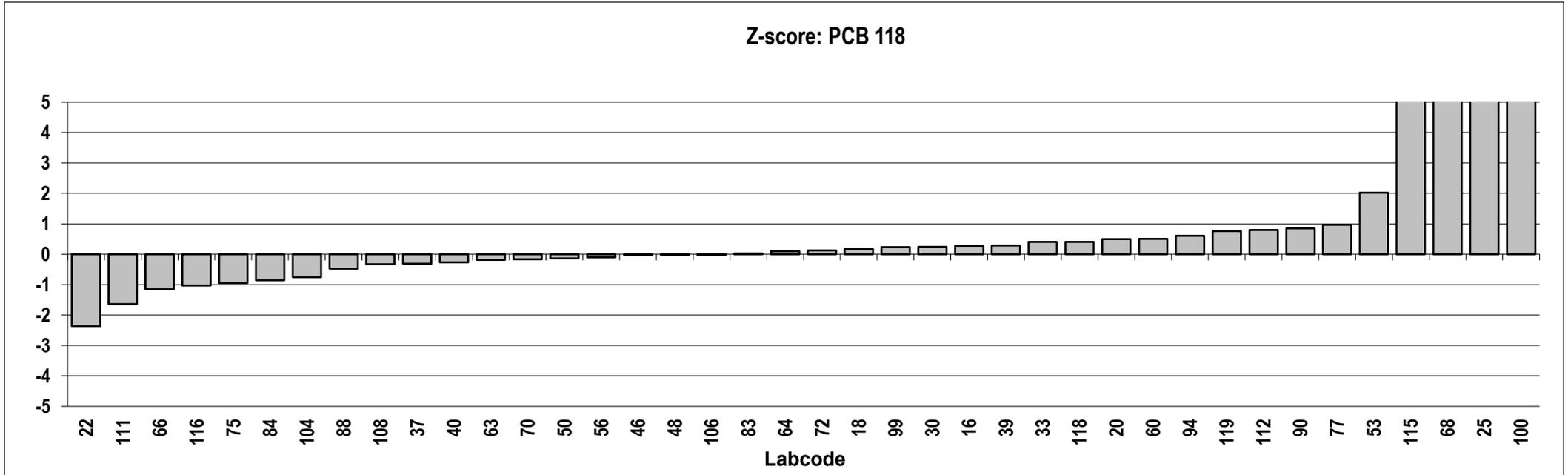
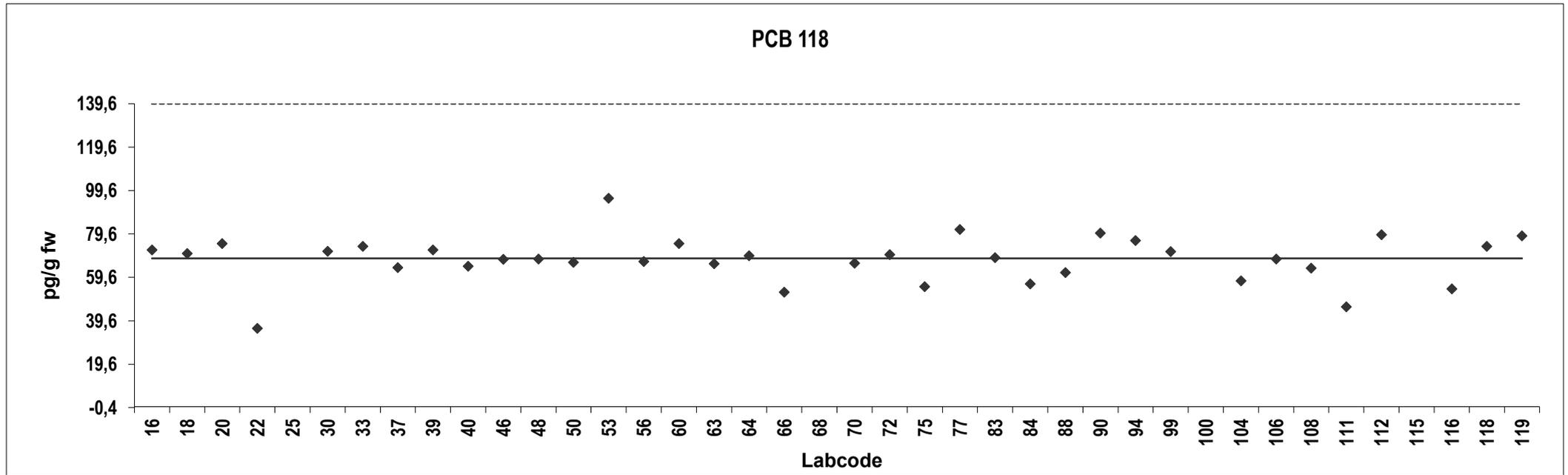
Consensus statistics	
Consensus median, pg/g	1,2
Median all values pg/g	1,3
Consensus mean, pg/g	1,3
Standard deviation, pg/g	0,37
Relative standard deviation, %	28
No. of values reported	40
No. of values removed	7
No. of reported non-detects	7



**Egg yolk**  
**Congener: PCB 118**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	72	0,28				
18	71	0,17				
20	75	0,50				
22	36	-2,4				
25	363	22	Outlier			
30	72	0,24				
33	74	0,41				
37	64	-0,31				
39	72	0,28				
40	65	-0,27				
46	68	-0,031				
48	68	-0,025				
50	66	-0,14				
53	96	2,0				
56	67	-0,10				
60	75	0,50				
63	66	-0,18				
64	70	0,093				
66	53	-1,1				
68	283	16	Outlier			
70	66	-0,17				
72	70	0,12				
75	55	-0,95				
77	82	0,97				
83	69	0,024				
84	57	-0,86				
88	62	-0,48				
90	80	0,85				
94	77	0,61				
99	72	0,23				
100	625	41	Outlier			
104	58	-0,76				
106	68	-0,024				
108	64	-0,33				
111	46	-1,6				
112	79	0,80				
115	265	14	Outlier			
116	54	-1,0				
118	74	0,41				
119	79	0,76				

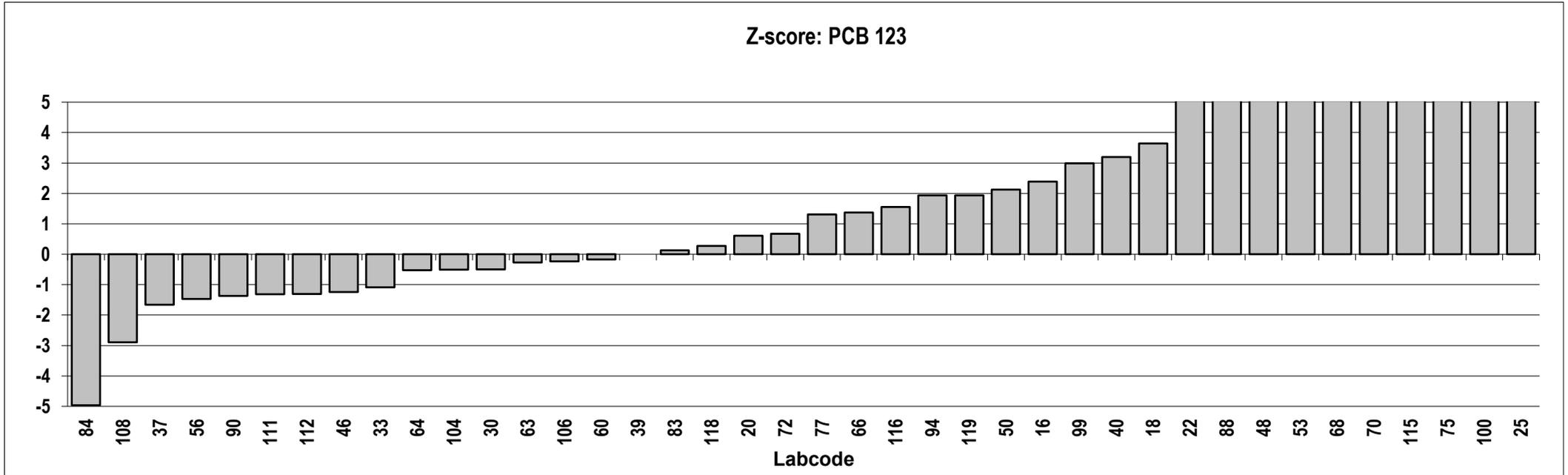
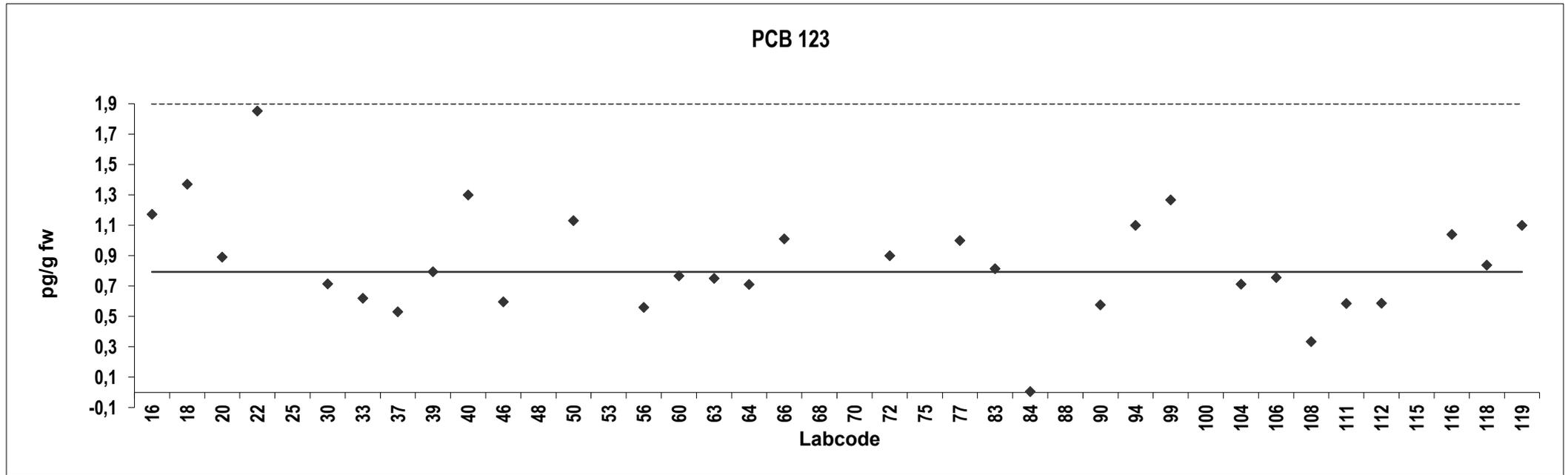
<b>Consensus statistics</b>	
Consensus median, pg/g	68
Median all values pg/g	70
Consensus mean, pg/g	68
Standard deviation, pg/g	11
Relative standard deviation, %	16
No. of values reported	40
No. of values removed	4
No. of reported non-detects	0



**Egg yolk**  
Congener: PCB 123

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	1,2	2,4				
18	1,4	3,6				
20	0,89	0,61				
22	1,9	6,7				
25	10	58	Outlier,ND			
30	0,71	-0,50				
33	0,62	-1,1				
37	0,53	-1,7				
39	0,79	0,0000				
40	1,3	3,2				
46	0,60	-1,2				
48	2,6	12	Outlier,ND			
50	1,1	2,1				
53	2,7	12	Outlier,ND			
56	0,56	-1,5				
60	0,77	-0,17				
63	0,75	-0,27				
64	0,71	-0,52				
66	1,0	1,4				
68	3,4	17	Outlier			
70	4,2	21	Outlier			
72	0,90	0,67				
75	5,9	32	Outlier,ND			
77	1,0	1,3	ND			
83	0,81	0,13				
84	0,0060	-5,0	ND			
88	2,6	12	Outlier,ND			
90	0,58	-1,4				
94	1,1	1,9				
99	1,3	3,0	ND			
100	9,2	53	Outlier			
104	0,71	-0,50				
106	0,76	-0,24				
108	0,33	-2,9				
111	0,59	-1,3				
112	0,59	-1,3				
115	5,1	27	Outlier			
116	1,0	1,6				
118	0,84	0,28				
119	1,1	1,9				

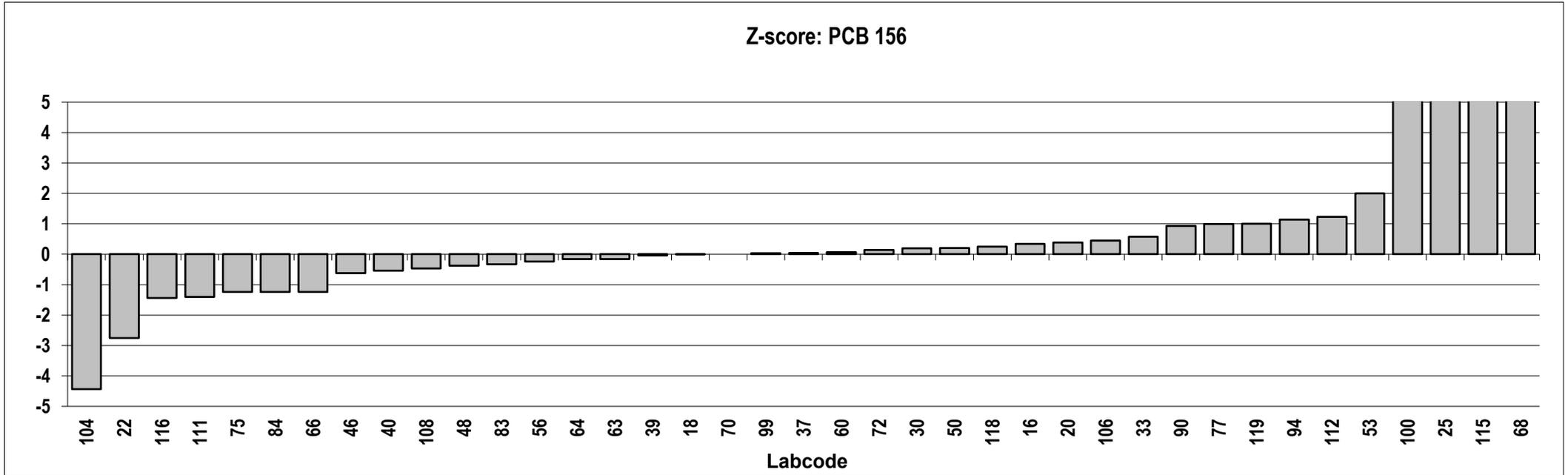
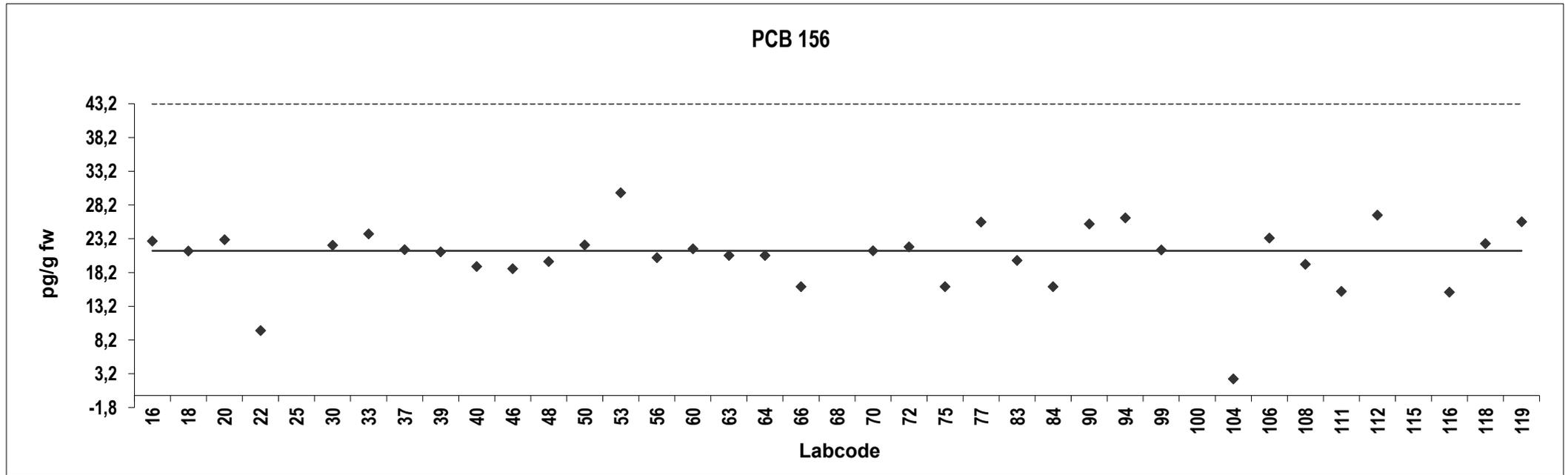
Consensus statistics	
Consensus median, pg/g	0,79
Median all values pg/g	0,95
Consensus mean, pg/g	0,85
Standard deviation, pg/g	0,35
Relative standard deviation, %	41
No. of values reported	40
No. of values removed	9
No. of reported non-detects	8



**Egg yolk**  
Congener: PCB 156

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	23	0,34				
18	21	-0,0038				
20	23	0,38				
22	9,6	-2,8				
25	95	17	Outlier			
30	22	0,20				
33	24	0,58				
37	22	0,043				
39	21	-0,039				
40	19	-0,54				
46	19	-0,62				
48	20	-0,37				
50	22	0,20				
53	30	2,00				
56	20	-0,24				
60	22	0,066				
63	21	-0,16				
64	21	-0,16				
66	16	-1,2				
68	100	18	Outlier			
70	21	0,00000				
72	22	0,14				
75	16	-1,2				
77	26	0,99				
83	20	-0,33				
84	16	-1,2				
90	25	0,93				
94	26	1,1				
99	22	0,032				
100	56	8,0	Outlier			
104	2,4	-4,4				
106	23	0,44				
108	19	-0,47				
111	15	-1,4				
112	27	1,2				
115	97	18	Outlier			
116	15	-1,4				
118	23	0,25				
119	26	1,0				

Consensus statistics	
Consensus median, pg/g	21
Median all values pg/g	22
Consensus mean, pg/g	21
Standard deviation, pg/g	5,0
Relative standard deviation, %	24
No. of values reported	39
No. of values removed	4
No. of reported non-detects	0

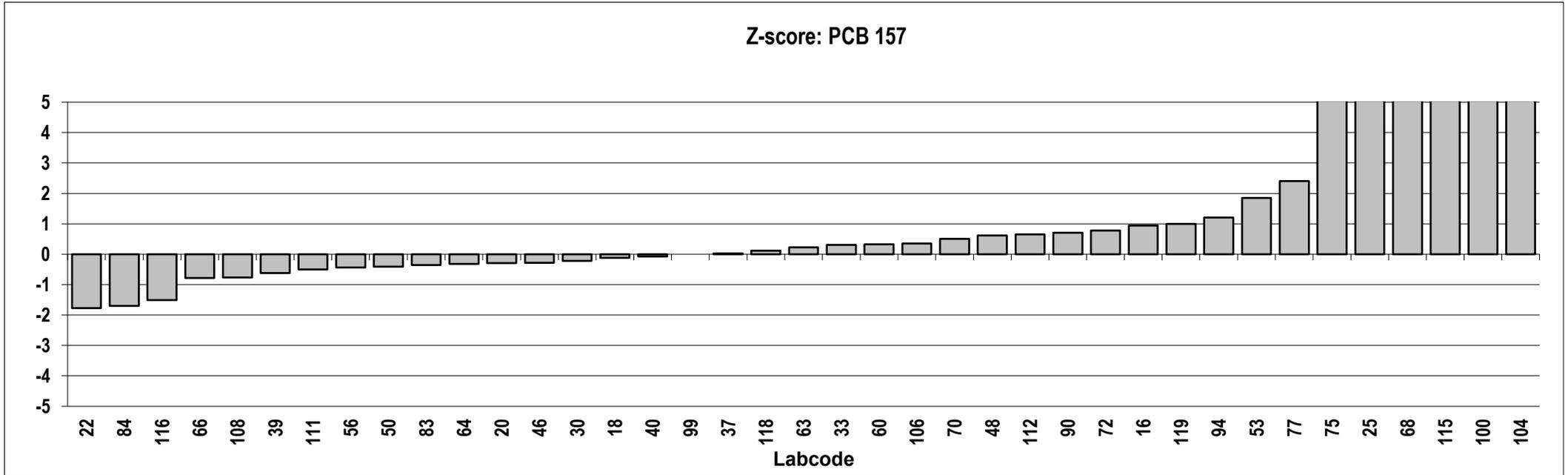
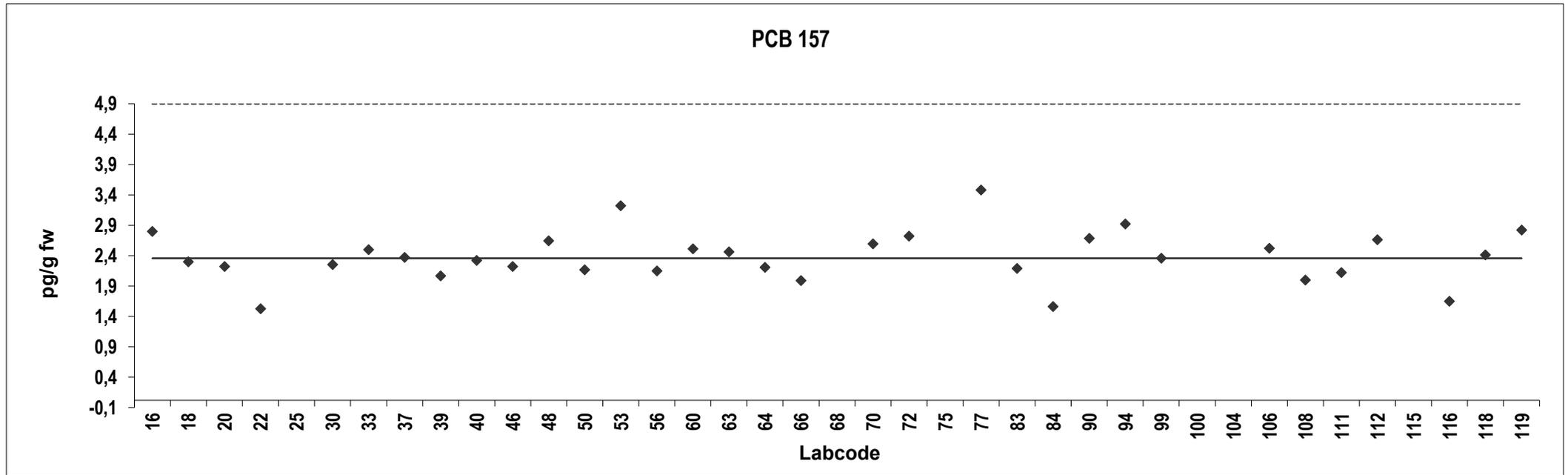


**Egg yolk**  
Congener: PCB 157

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	2,8	0,95				
18	2,3	-0,12				
20	2,2	-0,29				
22	1,5	-1,8				
25	10	16	Outlier,ND			
30	2,2	-0,22				
33	2,5	0,31				
37	2,4	0,030				
39	2,0	-0,62				
40	2,3	-0,077				
46	2,2	-0,29				
48	2,6	0,61	ND			
50	2,1	-0,41				
53	3,2	1,8				
56	2,1	-0,44				
60	2,5	0,33				
63	2,4	0,22				
64	2,2	-0,32				
66	2,0	-0,78				
68	12	20	Outlier			
70	2,6	0,51				
72	2,7	0,78				
75	5,3	6,3	Outlier,ND			
77	3,5	2,4				
83	2,2	-0,36				
84	1,5	-1,7				
90	2,7	0,70				
94	2,9	1,2				
99	2,3	0,00000				
100	19	35	Outlier			
104	24	46	Outlier			
106	2,5	0,35				
108	2,0	-0,76				
111	2,1	-0,50				
112	2,6	0,65				
115	16	30	Outlier			
116	1,6	-1,5				
118	2,4	0,12				
119	2,8	0,99				

**Consensus statistics**

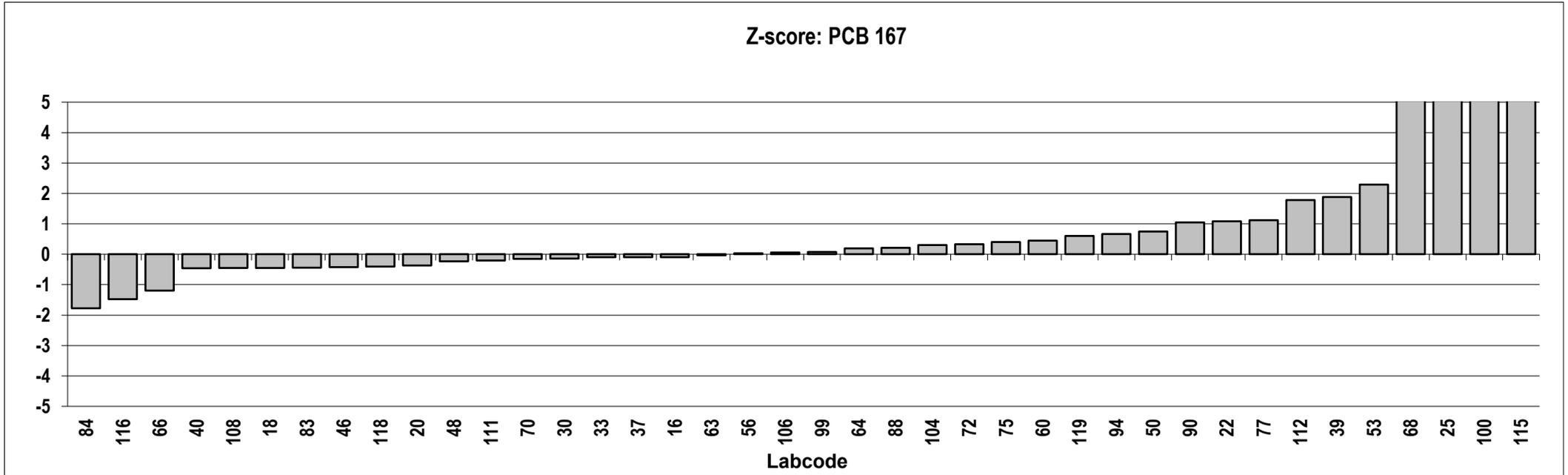
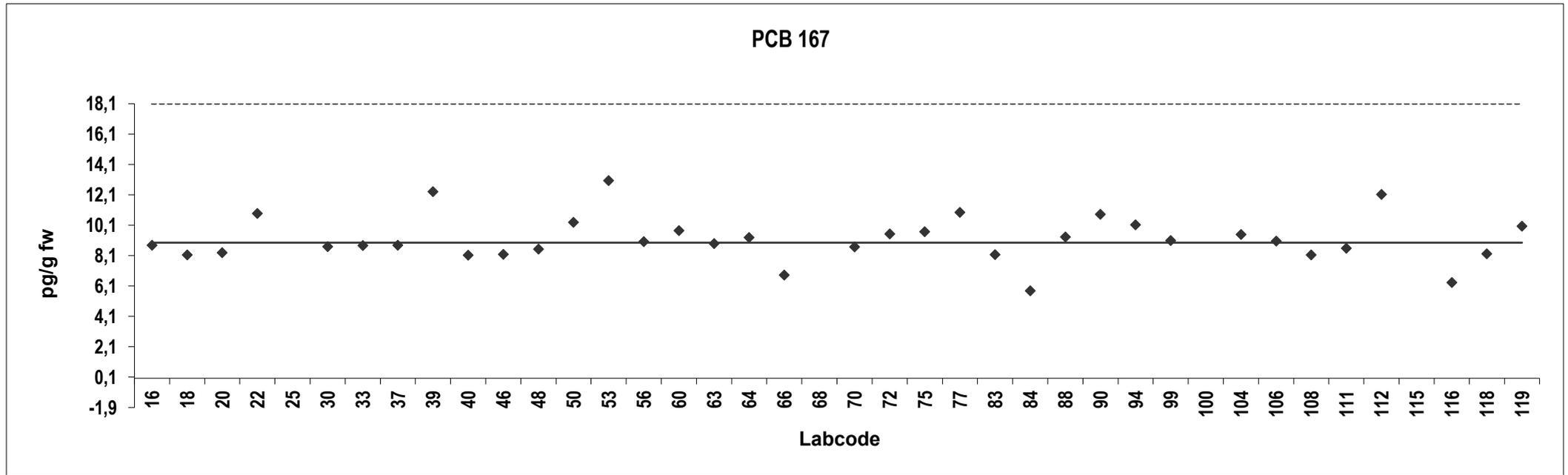
Consensus median, pg/g	2,3
Median all values pg/g	2,4
Consensus mean, pg/g	2,4
Standard deviation, pg/g	0,42
Relative standard deviation, %	18
No. of values reported	39
No. of values removed	6
No. of reported non-detects	3



**Egg yolk**  
Congener: PCB 167

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	8,8	-0,10				
18	8,1	-0,45				
20	8,3	-0,37				
22	11	1,1				
25	44	19	Outlier			
30	8,7	-0,15				
33	8,7	-0,10				
37	8,8	-0,10				
39	12	1,9				
40	8,1	-0,46				
46	8,2	-0,43				
48	8,5	-0,23				
50	10	0,75				
53	13	2,3				
56	9,0	0,034				
60	9,7	0,44				
63	8,9	-0,034				
64	9,3	0,19				
66	6,8	-1,2				
68	40	17	Outlier			
70	8,6	-0,16				
72	9,5	0,33				
75	9,6	0,40				
77	11	1,1				
83	8,1	-0,44				
84	5,7	-1,8				
88	9,3	0,21				
90	11	1,0				
94	10	0,66				
99	9,1	0,073				
100	53	24	Outlier			
104	9,5	0,30				
106	9,0	0,054				
108	8,1	-0,45				
111	8,6	-0,20				
112	12	1,8				
115	67	33	Outlier			
116	6,3	-1,5				
118	8,2	-0,41				
119	10	0,61				

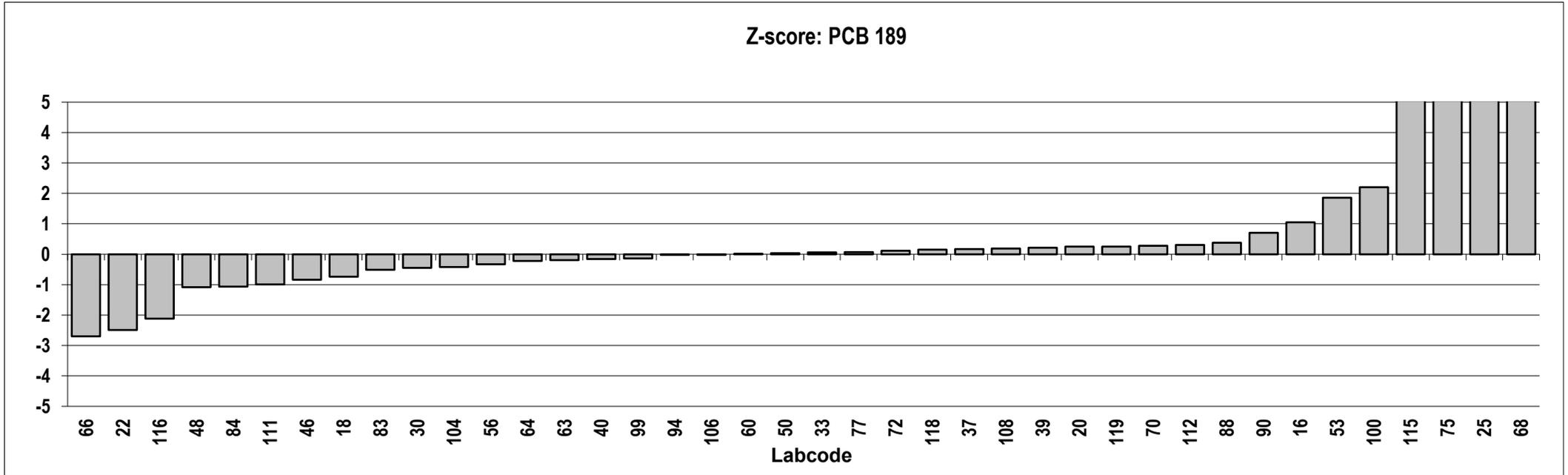
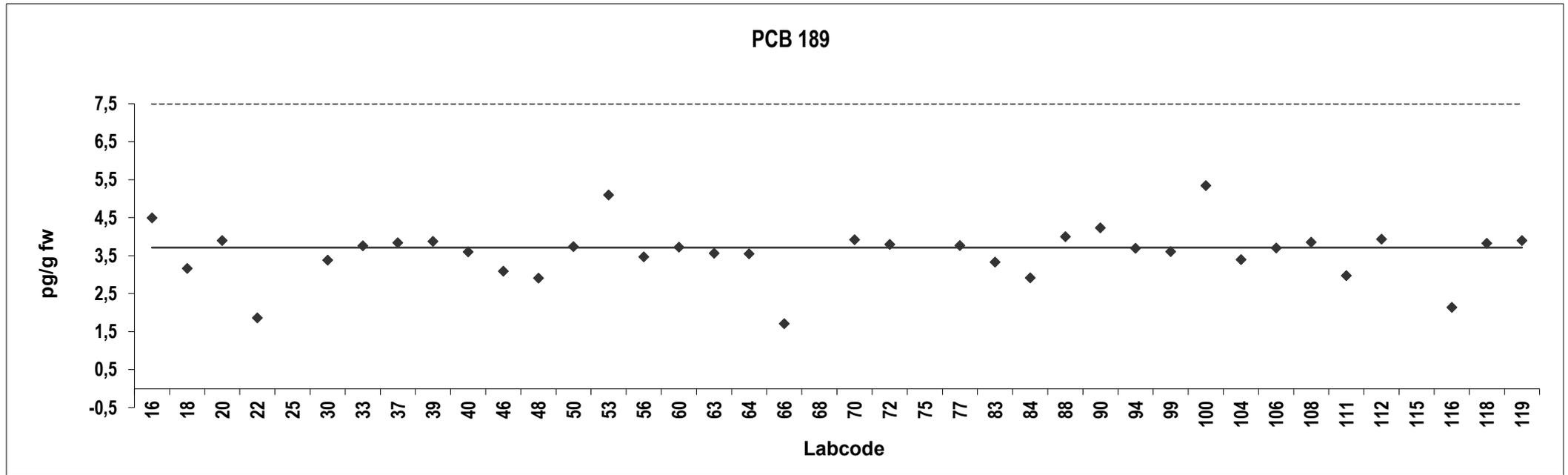
Consensus statistics	
Consensus median, pg/g	8,9
Median all values pg/g	9,0
Consensus mean, pg/g	9,2
Standard deviation, pg/g	1,5
Relative standard deviation, %	16
No. of values reported	40
No. of values removed	4
No. of reported non-detects	0



**Egg yolk**  
**Congener: PCB 189**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	4,5	1,0				
18	3,2	-0,74				
20	3,9	0,25				
22	1,9	-2,5				
25	15	15	Outlier			
30	3,4	-0,45				
33	3,8	0,059				
37	3,8	0,17				
39	3,9	0,22				
40	3,6	-0,16				
46	3,1	-0,83				
48	2,9	-1,1				
50	3,7	0,037				
53	5,1	1,9				
56	3,5	-0,33				
60	3,7	0,018				
63	3,6	-0,20				
64	3,6	-0,22				
66	1,7	-2,7				
68	16	16	Outlier			
70	3,9	0,27				
72	3,8	0,11				
75	10	8,8	Outlier,ND			
77	3,8	0,073				
83	3,3	-0,51				
84	2,9	-1,1				
88	4,0	0,38	ND			
90	4,2	0,70				
94	3,7	-0,022				
99	3,6	-0,14				
100	5,4	2,2				
104	3,4	-0,43				
106	3,7	-0,018				
108	3,9	0,19				
111	3,0	-0,99				
112	3,9	0,30				
115	9,8	8,1	Outlier			
116	2,1	-2,1				
118	3,8	0,15				
119	3,9	0,25				

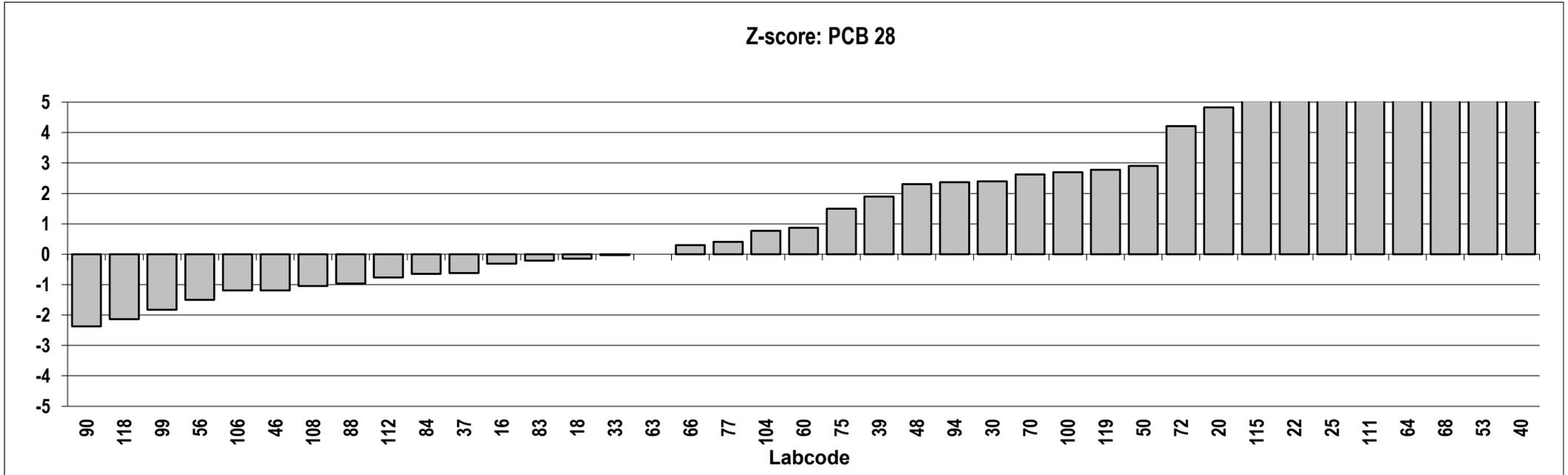
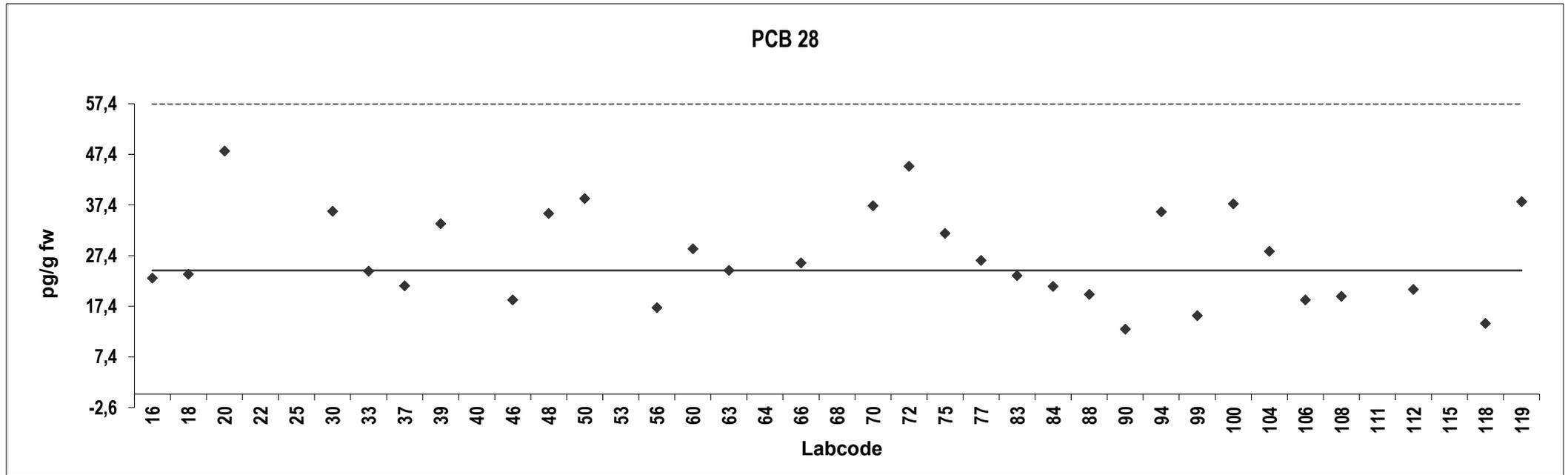
Consensus statistics	
Consensus median, pg/g	3,7
Median all values pg/g	3,8
Consensus mean, pg/g	3,6
Standard deviation, pg/g	0,72
Relative standard deviation, %	20
No. of values reported	40
No. of values removed	4
No. of reported non-detects	2



**Egg yolk**  
**Congener: PCB 28**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	23	-0,31				
18	24	-0,15				
20	48	4,8				
22	87	13	Outlier			
25	100	15	Outlier,ND			
30	36	2,4				
33	24	-0,027				
37	21	-0,62				
39	34	1,9				
40	200	36	Outlier,ND			
46	19	-1,2				
48	36	2,3				
50	39	2,9				
53	170	30	Outlier,ND			
56	17	-1,5				
60	29	0,87				
63	24	0,00000				
64	107	17	Outlier			
66	26	0,30				
68	114	18	Outlier			
70	37	2,6				
72	45	4,2				
75	32	1,5				
77	26	0,41				
83	23	-0,21				
84	21	-0,64				
88	20	-0,97				
90	13	-2,4				
94	36	2,4				
99	15	-1,8				
100	38	2,7				
104	28	0,77				
106	19	-1,2				
108	19	-1,0				
111	100	15	Outlier,ND			
112	21	-0,76				
115	63	7,8	Outlier			
118	14	-2,1				
119	38	2,8				

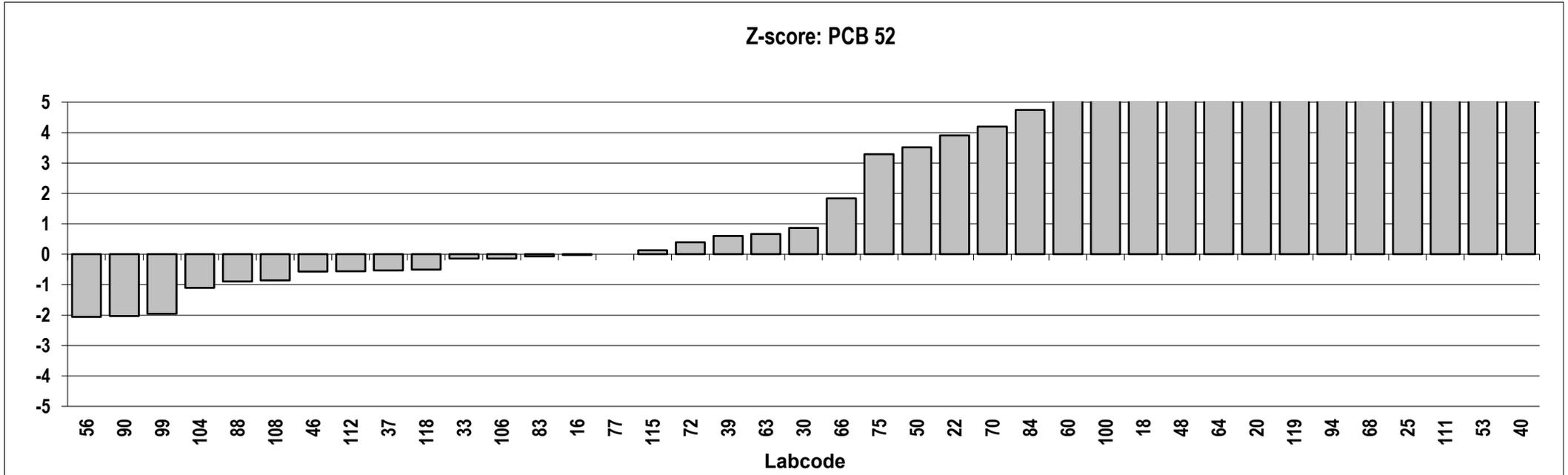
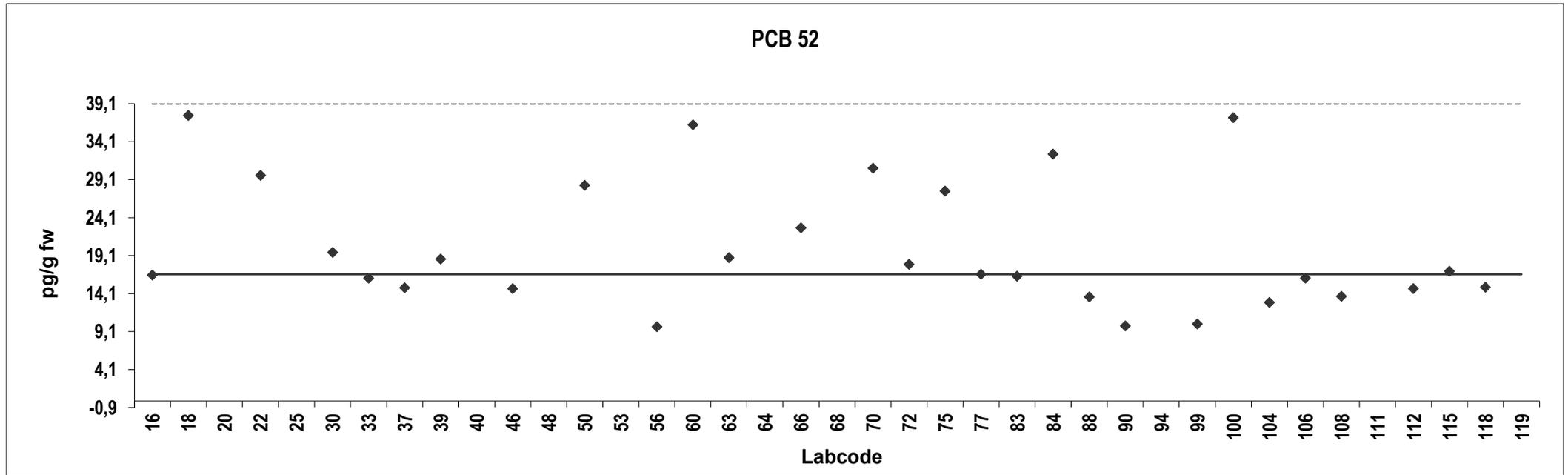
Consensus statistics	
Consensus median, pg/g	24
Median all values pg/g	29
Consensus mean, pg/g	27
Standard deviation, pg/g	9,2
Relative standard deviation, %	34
No. of values reported	39
No. of values removed	8
No. of reported non-detects	4



**Egg yolk**  
Congener: PCB 52

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	17	-0,026				
18	38	6,3				
20	42	7,6	Outlier			
22	30	3,9				
25	100	25	Outlier,ND			
30	20	0,87				
33	16	-0,14				
37	15	-0,53				
39	19	0,60				
40	200	55	Outlier,ND			
46	15	-0,57				
48	40	6,9	Outlier			
50	28	3,5				
53	170	46	Outlier,ND			
56	9,8	-2,1				
60	36	5,9				
63	19	0,66				
64	42	7,5	Outlier			
66	23	1,8				
68	51	10	Outlier			
70	31	4,2				
72	18	0,40				
75	28	3,3				
77	17	0,00000				
83	16	-0,073				
84	32	4,7				
88	14	-0,89				
90	9,9	-2,0				
94	43	7,9	Outlier			
99	10	-2,0				
100	37	6,2				
104	13	-1,1				
106	16	-0,14				
108	14	-0,86				
111	100	25	Outlier,ND			
112	15	-0,56				
115	17	0,13				
118	15	-0,50				
119	42	7,6	Outlier			

Consensus statistics	
Consensus median, pg/g	17
Median all values pg/g	20
Consensus mean, pg/g	20
Standard deviation, pg/g	8,4
Relative standard deviation, %	42
No. of values reported	39
No. of values removed	10
No. of reported non-detects	4

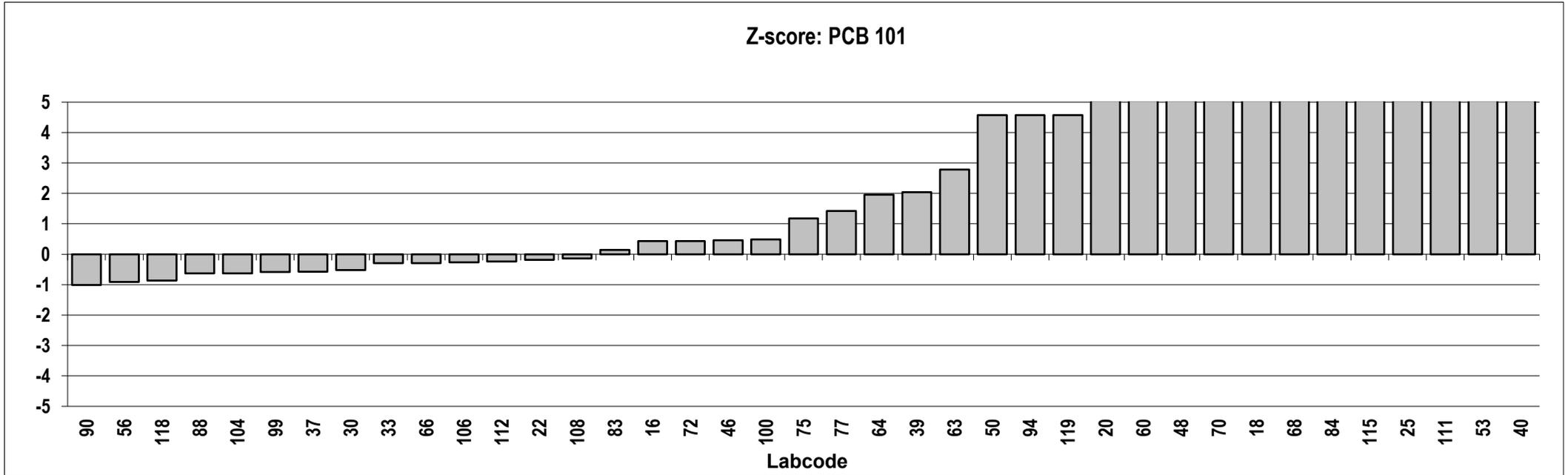
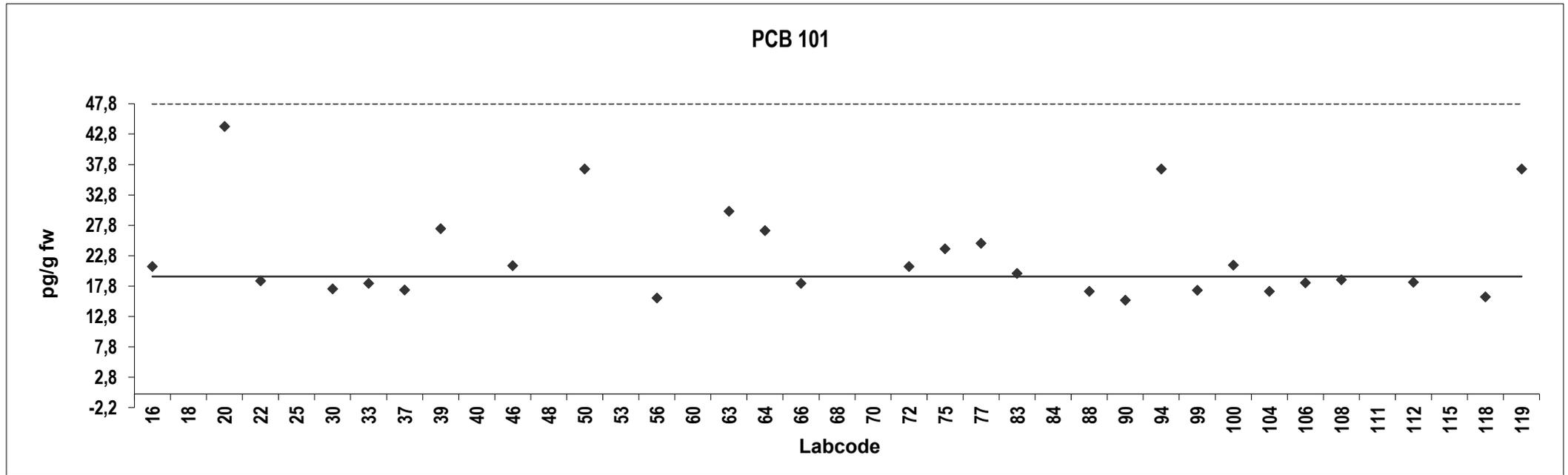


**Egg yolk**  
**Congener: PCB 101**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	21	0,43				
18	58	10	Outlier			
20	44	6,4				
22	19	-0,18				
25	100	21	Outlier,ND			
30	17	-0,52				
33	18	-0,29				
37	17	-0,58				
39	27	2,0				
40	200	47	Outlier,ND			
46	21	0,46				
48	52	8,4	Outlier			
50	37	4,6				
53	170	39	Outlier,ND			
56	16	-0,91				
60	50	8,0	Outlier			
63	30	2,8				
64	27	2,0				
66	18	-0,29				
68	64	12	Outlier			
70	55	9,3	Outlier			
72	21	0,43				
75	24	1,2				
77	25	1,4				
83	20	0,14				
84	64	12	Outlier			
88	17	-0,63				
90	15	-1,0				
94	37	4,6				
99	17	-0,58				
100	21	0,48				
104	17	-0,63				
106	18	-0,27				
108	19	-0,14				
111	100	21	Outlier,ND			
112	18	-0,24				
115	77	15	Outlier			
118	16	-0,86				
119	37	4,6				

**Consensus statistics**

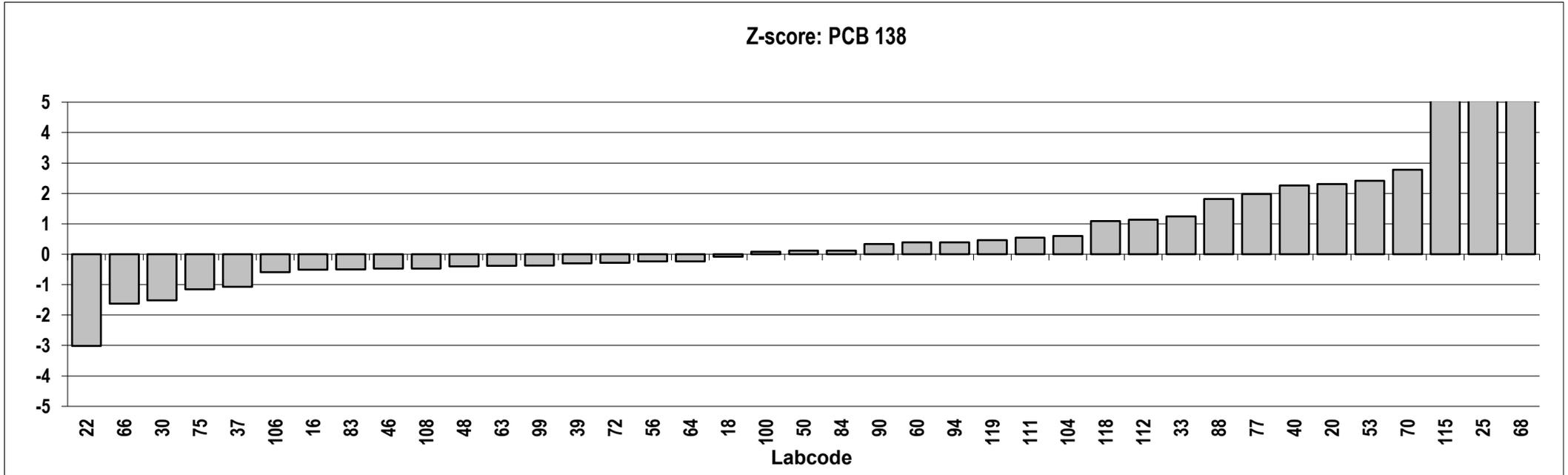
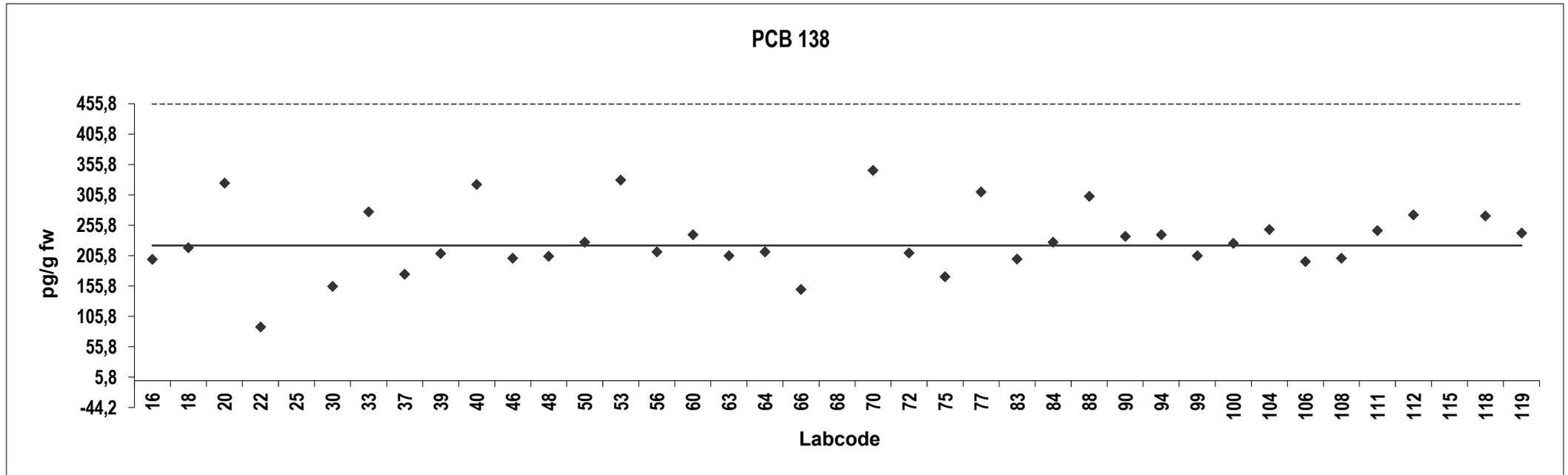
Consensus median, pg/g	19
Median all values pg/g	24
Consensus mean, pg/g	23
Standard deviation, pg/g	7,7
Relative standard deviation, %	34
No. of values reported	39
No. of values removed	11
No. of reported non-detects	4



**Egg yolk**  
**Congener: PCB 138**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	200	-0,51				
18	219	-0,079				
20	325	2,3				
22	88	-3,0				
25	940	16	Outlier			
30	155	-1,5				
33	278	1,2				
37	175	-1,1				
39	209	-0,30				
40	323	2,3				
46	201	-0,47				
48	205	-0,40				
50	228	0,12				
53	330	2,4				
56	212	-0,24				
60	240	0,39				
63	206	-0,38				
64	212	-0,24				
66	150	-1,6				
68	1102	20	Outlier			
70	346	2,8				
72	210	-0,28				
75	171	-1,2				
77	311	2,0				
83	200	-0,50				
84	228	0,12				
88	303	1,8				
90	237	0,33				
94	240	0,39				
99	206	-0,38				
100	226	0,079				
104	249	0,60				
106	196	-0,59				
108	201	-0,47				
111	247	0,55				
112	273	1,1				
115	621	9,0	Outlier			
118	271	1,1				
119	243	0,46				

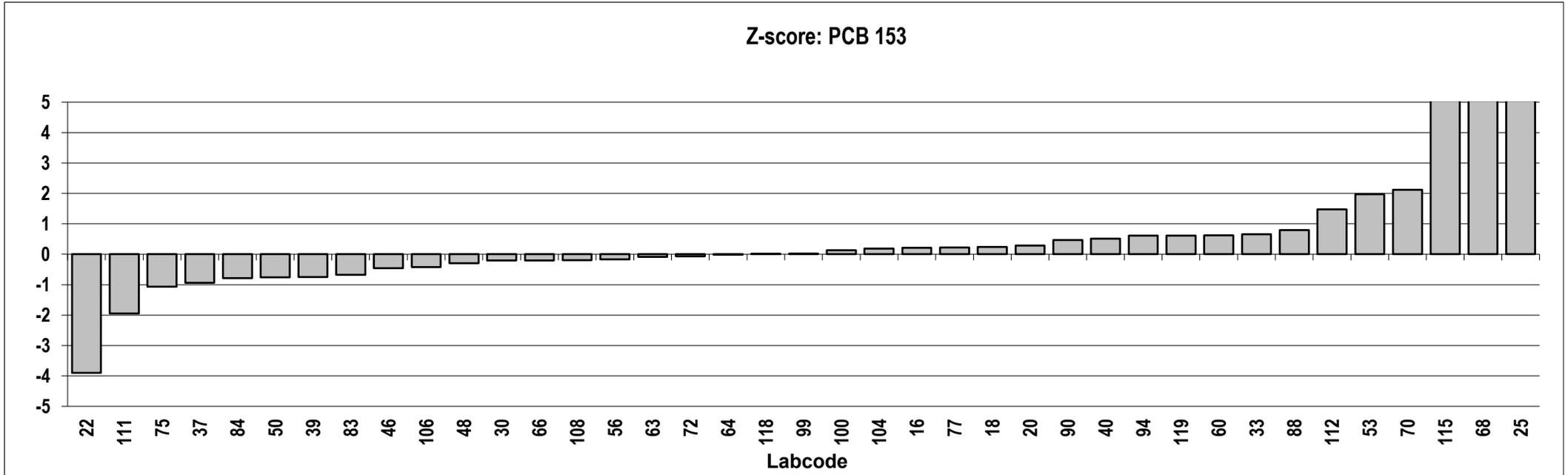
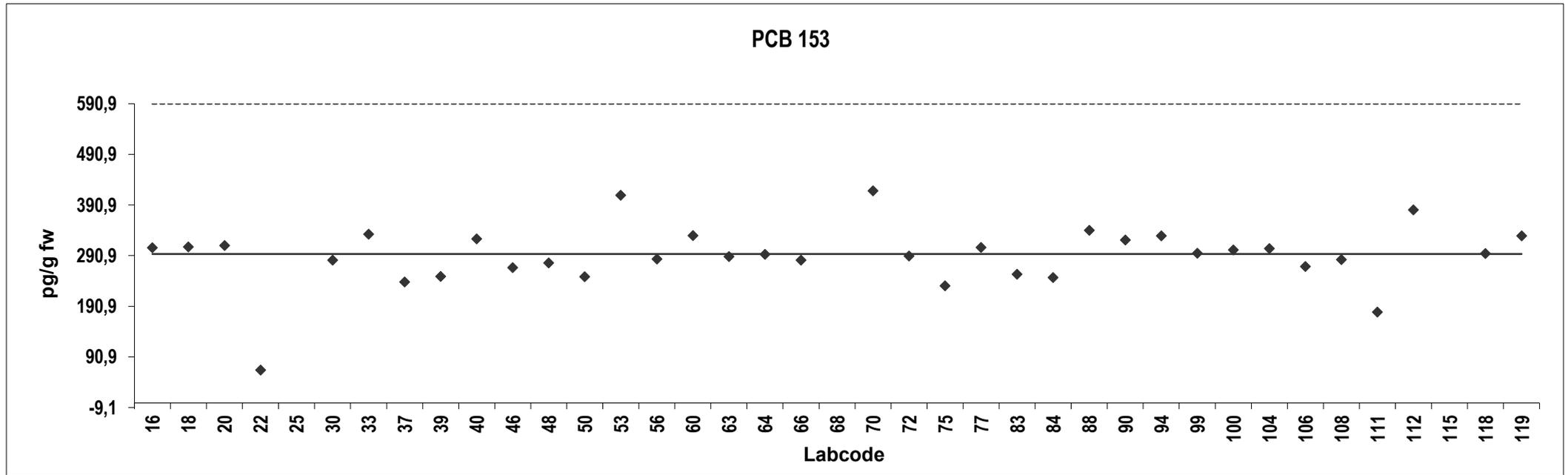
<b>Consensus statistics</b>	
Consensus median, pg/g	223
Median all values pg/g	228
Consensus mean, pg/g	231
Standard deviation, pg/g	55
Relative standard deviation, %	24
No. of values reported	39
No. of values removed	3
No. of reported non-detects	0



**Egg yolk**  
Congener: PCB 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	306	0,21				
18	308	0,24				
20	311	0,29				
22	65	-3,9				
25	1010	12	Outlier			
30	282	-0,21				
33	333	0,66				
37	239	-0,94				
39	250	-0,75				
40	324	0,51				
46	267	-0,46				
48	277	-0,30				
50	249	-0,76				
53	410	2,0				
56	284	-0,17				
60	330	0,62				
63	289	-0,087				
64	293	-0,015				
66	282	-0,21				
68	809	8,7	Outlier			
70	419	2,1				
72	290	-0,070				
75	232	-1,1				
77	307	0,22				
83	254	-0,68				
84	248	-0,79				
88	341	0,79				
90	322	0,47				
94	330	0,61				
99	295	0,022				
100	302	0,13				
104	305	0,18				
106	269	-0,42				
108	283	-0,19				
111	179	-2,0				
112	381	1,5				
115	760	7,9	Outlier			
118	295	0,015				
119	330	0,61				

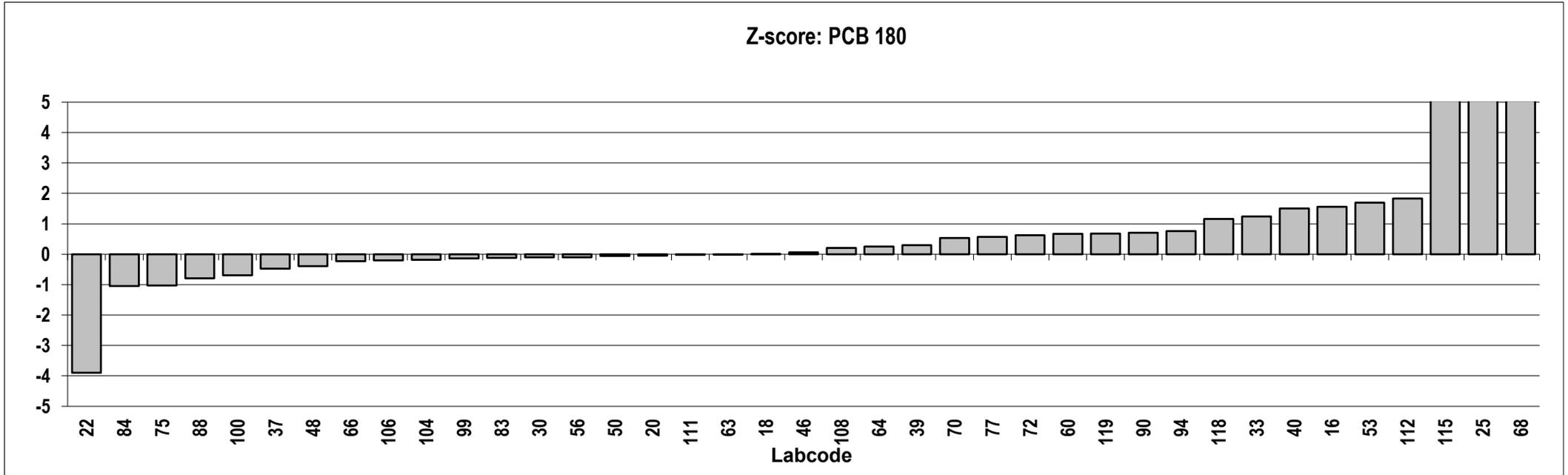
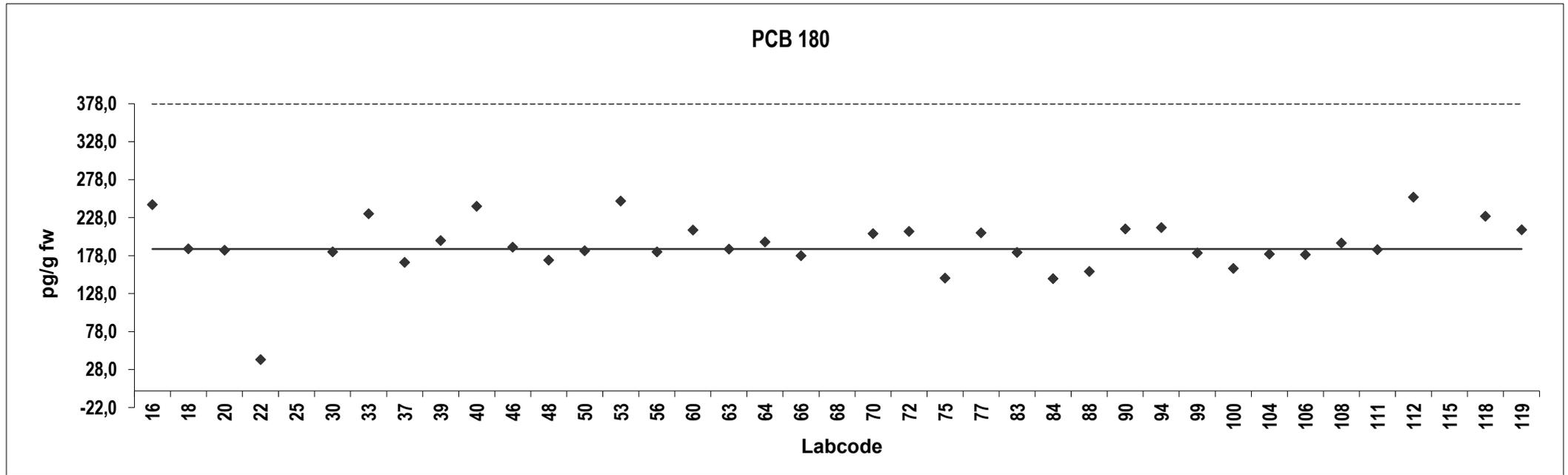
Consensus statistics	
Consensus median, pg/g	294
Median all values pg/g	295
Consensus mean, pg/g	291
Standard deviation, pg/g	61
Relative standard deviation, %	21
No. of values reported	39
No. of values removed	3
No. of reported non-detects	0



**Egg yolk**  
**Congener: PCB 180**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	245	1,6				
18	187	0,0078				
20	185	-0,046				
22	41	-3,9				
25	760	15	Outlier			
30	183	-0,10				
33	233	1,2				
37	169	-0,47				
39	198	0,30				
40	243	1,5				
46	189	0,061				
48	172	-0,39				
50	185	-0,059				
53	250	1,7				
56	183	-0,10				
60	212	0,67				
63	186	-0,0078				
64	196	0,25				
66	178	-0,23				
68	792	16	Outlier			
70	207	0,54				
72	210	0,62				
75	148	-1,0				
77	208	0,57				
83	182	-0,12				
84	148	-1,0				
88	157	-0,79				
90	213	0,70				
94	215	0,76				
99	182	-0,14				
100	161	-0,69				
104	180	-0,18				
106	179	-0,20				
108	195	0,21				
111	186	-0,020				
112	255	1,8				
115	693	14	Outlier			
118	230	1,2				
119	212	0,68				

Consensus statistics	
Consensus median, pg/g	187
Median all values pg/g	189
Consensus mean, pg/g	192
Standard deviation, pg/g	38
Relative standard deviation, %	20
No. of values reported	39
No. of values removed	3
No. of reported non-detects	0

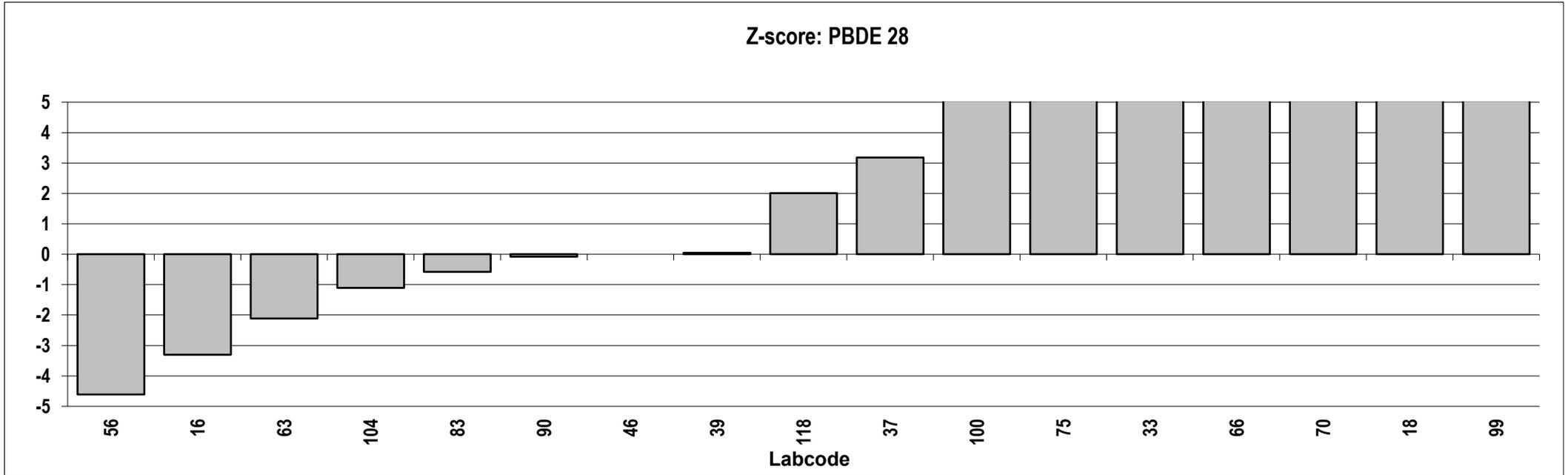
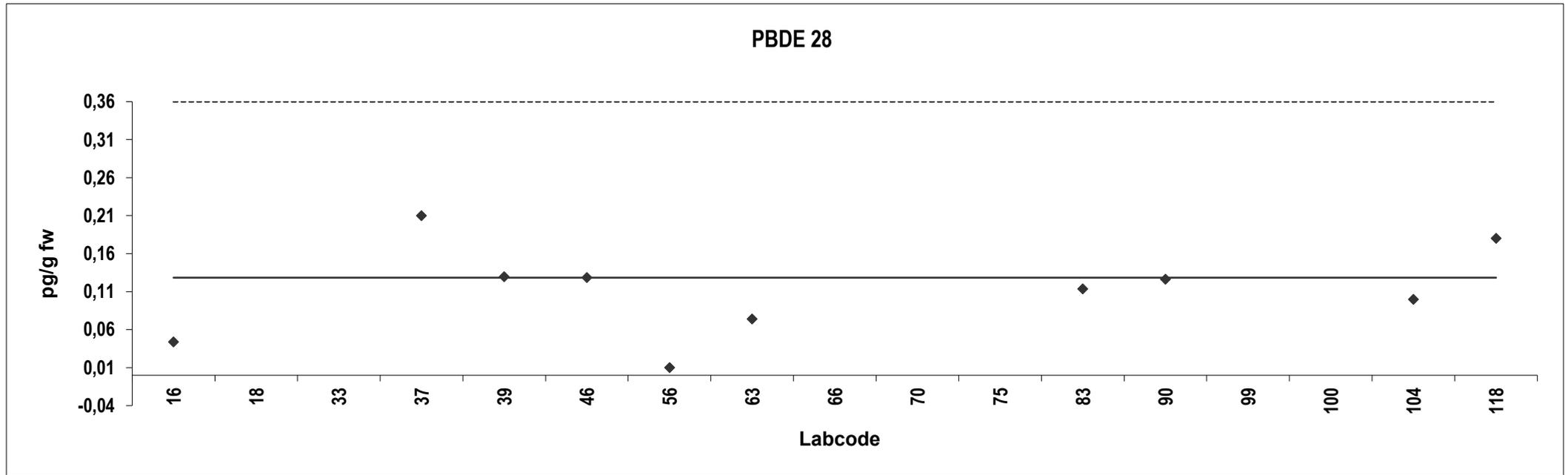


**Egg yolk**  
**Congener: PBDE 28**

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	0,044	-3,3	ND			
18	4,7	178	Outlier			
33	1,9	69	Outlier,ND			
37	0,21	3,2				
39	0,13	0,047				
46	0,13	0,00000				
56	0,010	-4,6	ND			
63	0,074	-2,1				
66	2,4	87	Outlier			
70	2,8	103	Outlier			
75	0,52	15	Outlier,ND			
83	0,11	-0,58				
90	0,13	-0,078				
99	6,3	242	Outlier,ND			
100	0,50	14	Outlier,ND			
104	0,10	-1,1	ND			
118	0,18	2,0				

**Consensus statistics**

Consensus median, pg/g	0,13
Median all values pg/g	0,18
Consensus mean, pg/g	0,11
Standard deviation, pg/g	0,059
Relative standard deviation, %	53
No. of values reported	17
No. of values removed	7
No. of reported non-detects	7

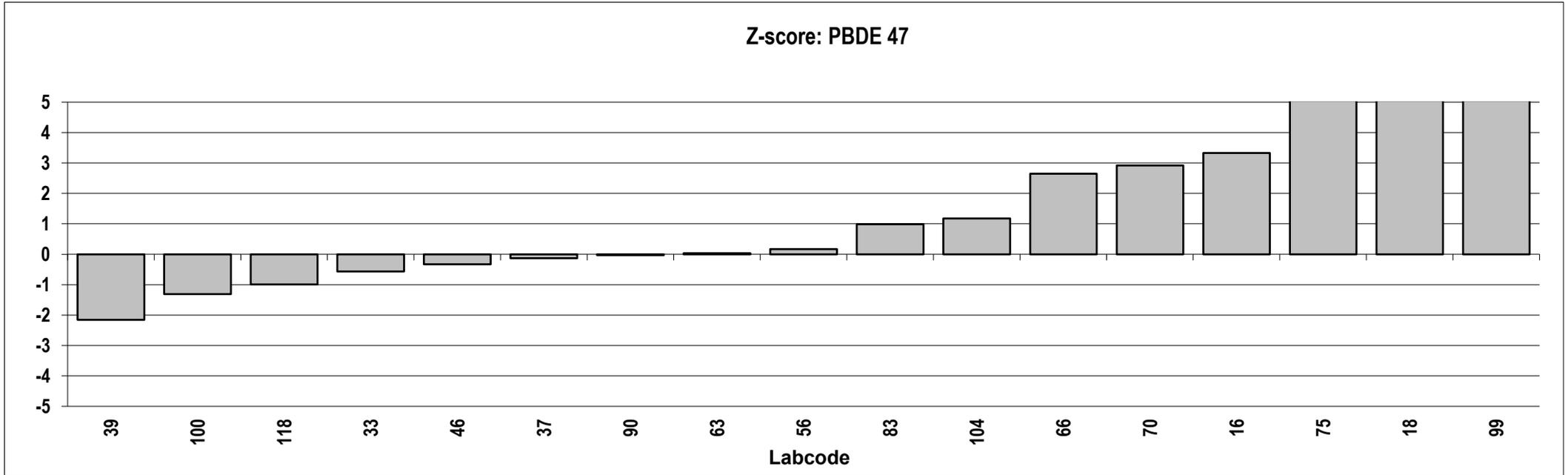
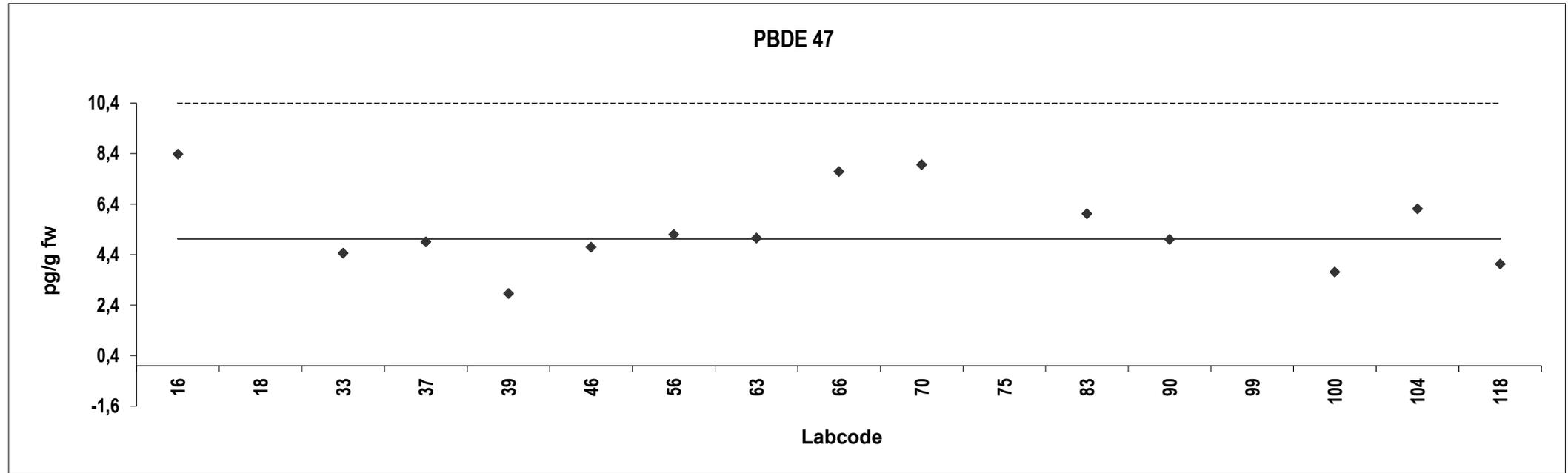


**Egg yolk**  
Congener: PBDE 47

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	8,4	3,3				
18	42	36	Outlier			
33	4,5	-0,57				
37	4,9	-0,13				
39	2,9	-2,2				
46	4,7	-0,33				
56	5,2	0,17				
63	5,1	0,030				
66	7,7	2,6				
70	8,0	2,9				
75	19	14	Outlier			
83	6,0	1,0				
90	5,0	-0,030				
99	127	121	Outlier,ND			
100	3,7	-1,3				
104	6,2	1,2				
118	4,0	-1,0				

**Consensus statistics**

Consensus median, pg/g	5,0
Median all values pg/g	5,2
Consensus mean, pg/g	5,4
Standard deviation, pg/g	1,6
Relative standard deviation, %	30
No. of values reported	17
No. of values removed	3
No. of reported non-detects	1

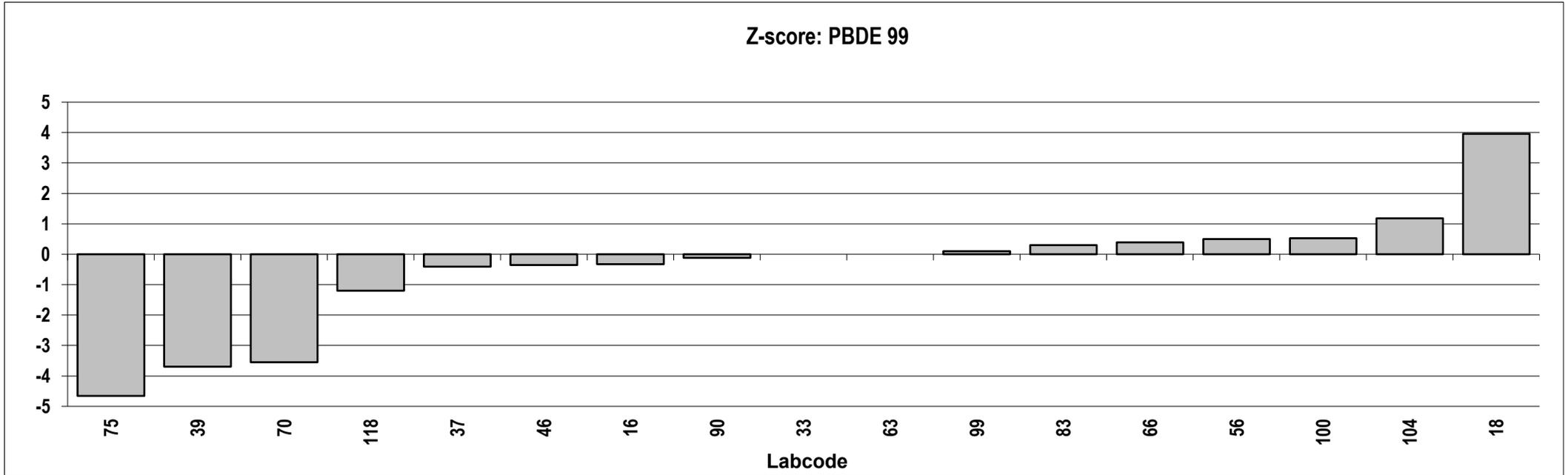
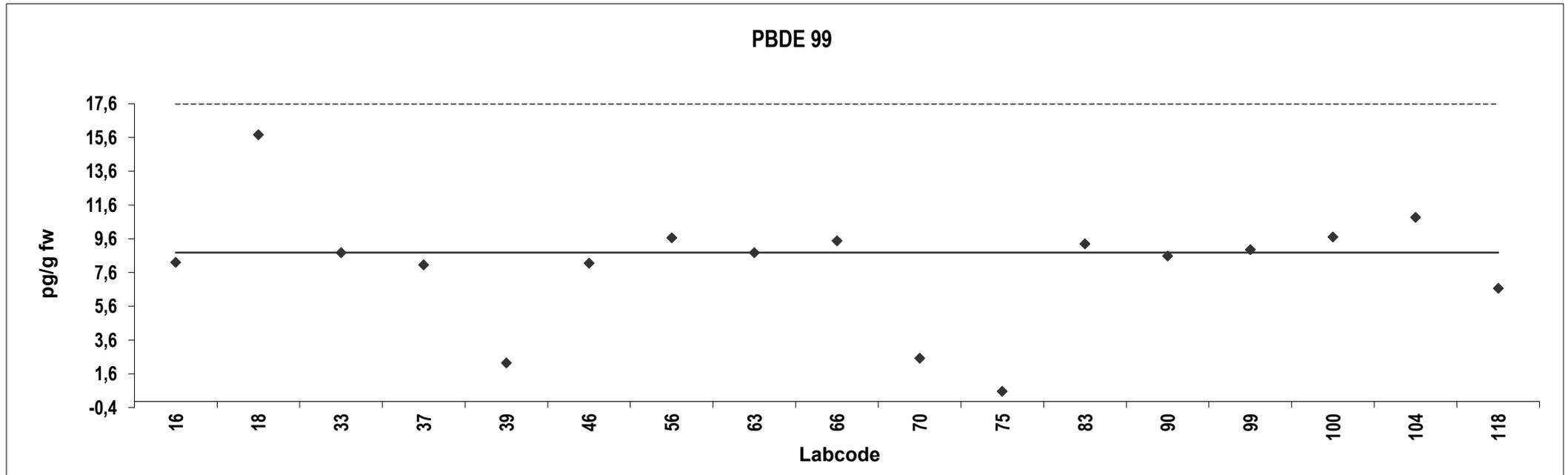


**Egg yolk**  
Congener: PBDE 99

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	8,2	-0,33				
18	16	4,0				
33	8,8	0,00000				
37	8,1	-0,41				
39	2,3	-3,7				
46	8,2	-0,35				
56	9,7	0,50				
63	8,8	0,00000				
66	9,5	0,39				
70	2,6	-3,5				
75	0,60	-4,7	ND			
83	9,3	0,30				
90	8,6	-0,12				
99	9,0	0,10				
100	9,7	0,52				
104	11	1,2				
118	6,7	-1,2				

**Consensus statistics**

Consensus median, pg/g	8,8
Median all values pg/g	8,8
Consensus mean, pg/g	8,1
Standard deviation, pg/g	3,5
Relative standard deviation, %	44
No. of values reported	17
No. of values removed	0
No. of reported non-detects	1

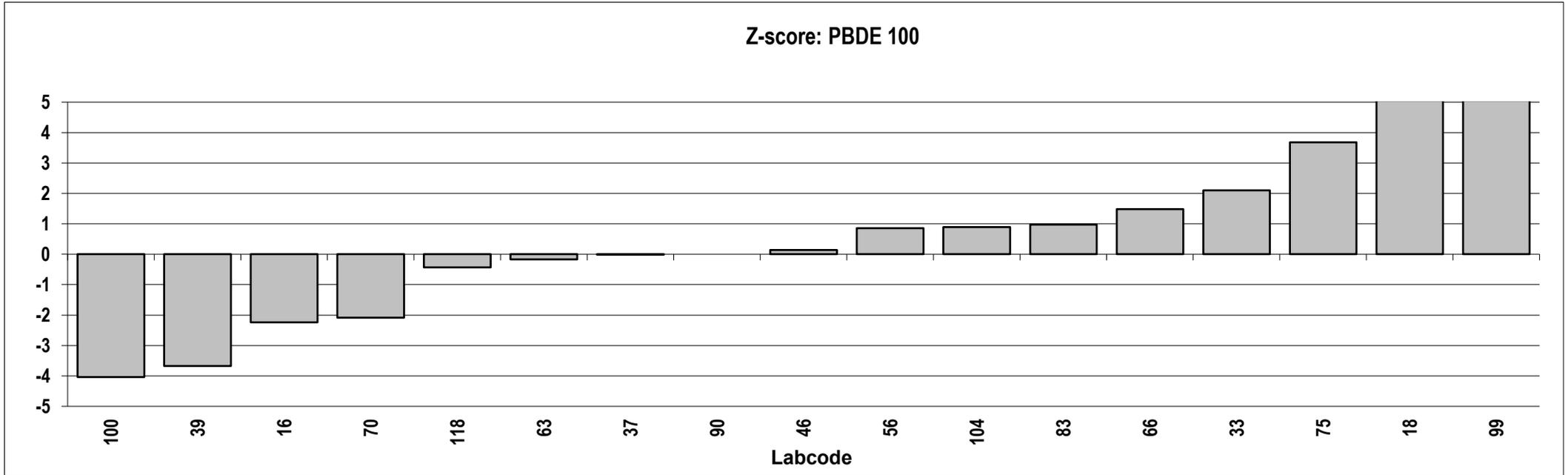
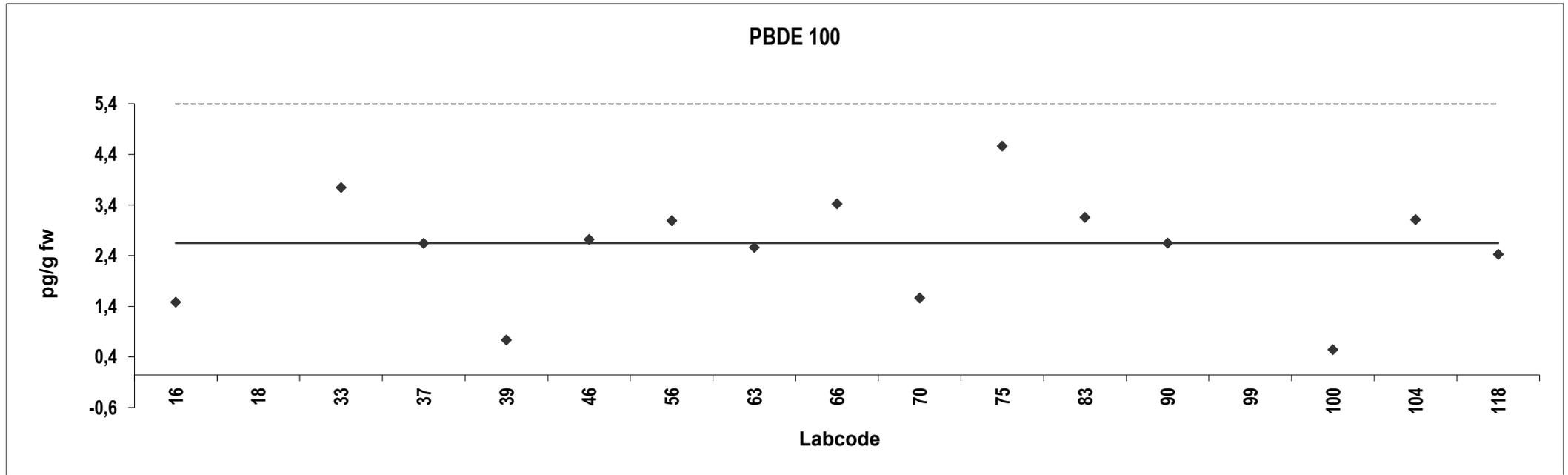


**Egg yolk**  
Congener: PBDE 100

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	1,4	-2,2				
18	6,2	6,8	Outlier			
33	3,7	2,1	ND			
37	2,6	-0,012				
39	0,69	-3,7				
46	2,7	0,14				
56	3,1	0,85				
63	2,5	-0,17				
66	3,4	1,5				
70	1,5	-2,1				
75	4,5	3,7				
83	3,1	0,97				
90	2,6	0,00000				
99	13	19	Outlier,ND			
100	0,50	-4,0	ND			
104	3,1	0,89				
118	2,4	-0,43				

**Consensus statistics**

Consensus median, pg/g	2,6
Median all values pg/g	2,7
Consensus mean, pg/g	2,5
Standard deviation, pg/g	1,1
Relative standard deviation, %	43
No. of values reported	17
No. of values removed	2
No. of reported non-detects	3

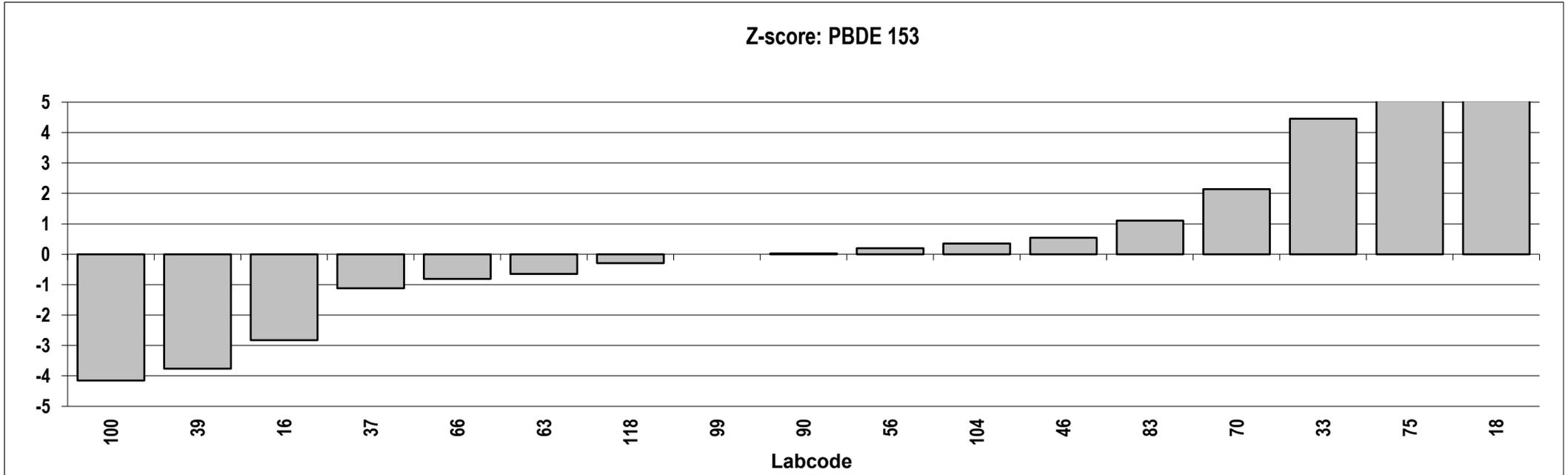
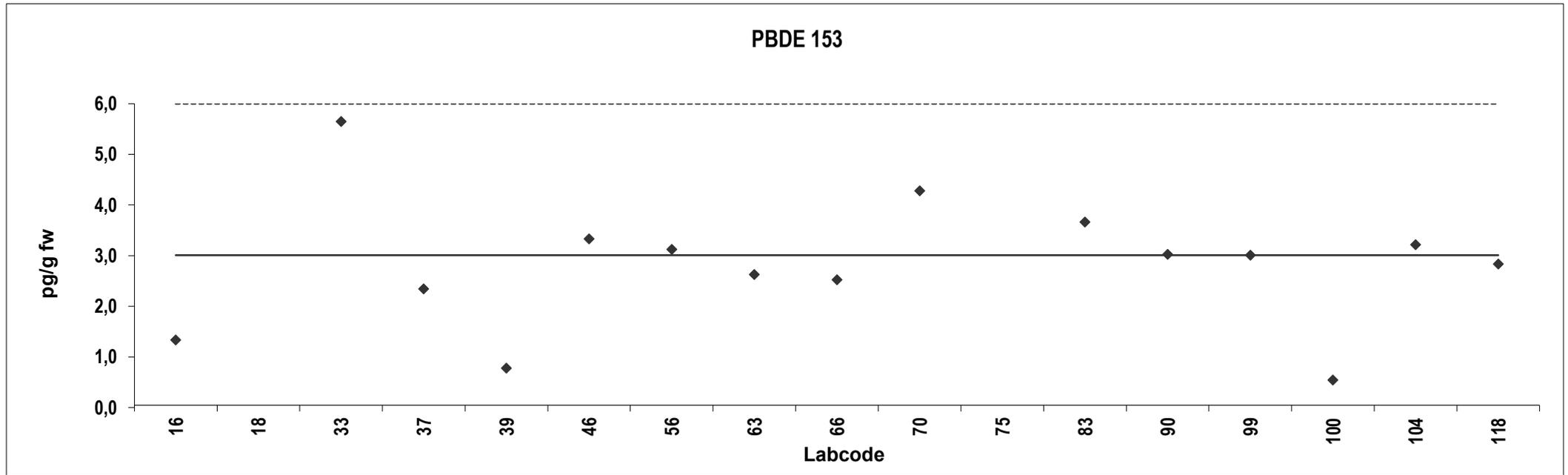


**Egg yolk**  
Congener: PBDE 153

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	1,3	-2,8				
18	14	18	Outlier			
33	5,6	4,5	ND			
37	2,3	-1,1				
39	0,74	-3,8				
46	3,3	0,55				
56	3,1	0,20				
63	2,6	-0,65				
66	2,5	-0,81				
70	4,2	2,1				
75	6,9	6,6	Outlier			
83	3,6	1,1				
90	3,0	0,024				
99	3,0	0,00000				
100	0,50	-4,2	ND			
104	3,2	0,35				
118	2,8	-0,29				

**Consensus statistics**

Consensus median, pg/g	3,0
Median all values pg/g	3,0
Consensus mean, pg/g	2,8
Standard deviation, pg/g	1,3
Relative standard deviation, %	47
No. of values reported	17
No. of values removed	2
No. of reported non-detects	2

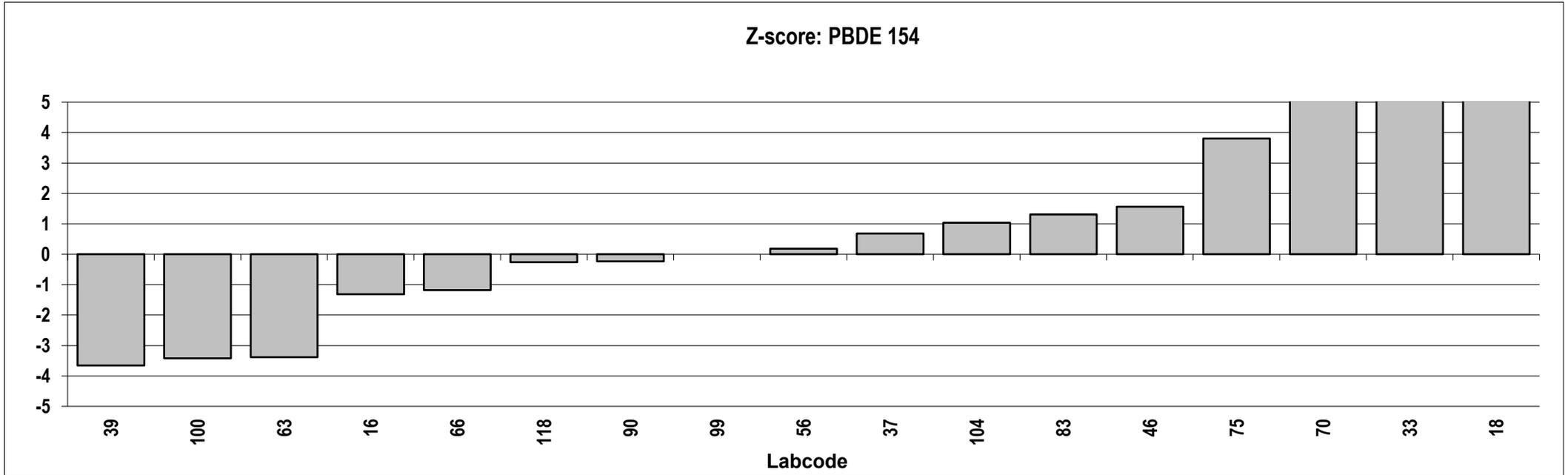
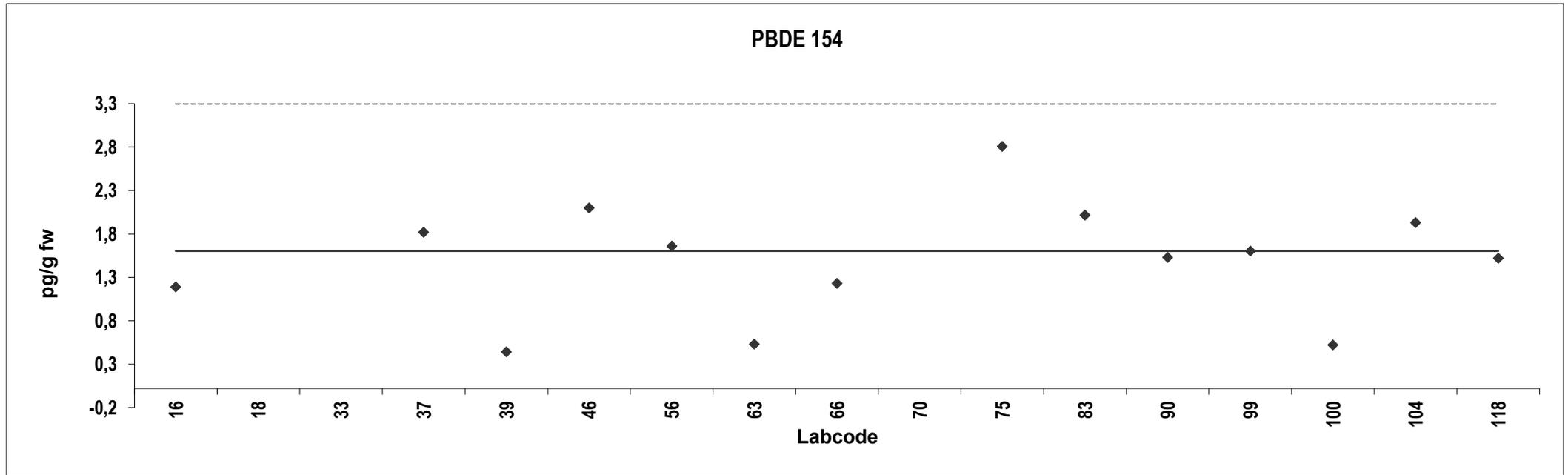


**Egg yolk**  
Congener: PBDE 154

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	1,2	-1,3				
18	7,6	19	Outlier			
33	5,6	13	Outlier,ND			
37	1,8	0,68				
39	0,42	-3,7				
46	2,1	1,6				
56	1,6	0,18				
63	0,51	-3,4				
66	1,2	-1,2				
70	4,2	8,2	Outlier			
75	2,8	3,8				
83	2,0	1,3				
90	1,5	-0,24				
99	1,6	0,00000				
100	0,50	-3,4	ND			
104	1,9	1,0				
118	1,5	-0,26				

**Consensus statistics**

Consensus median, pg/g	1,6
Median all values pg/g	1,6
Consensus mean, pg/g	1,5
Standard deviation, pg/g	0,67
Relative standard deviation, %	46
No. of values reported	17
No. of values removed	3
No. of reported non-detects	2

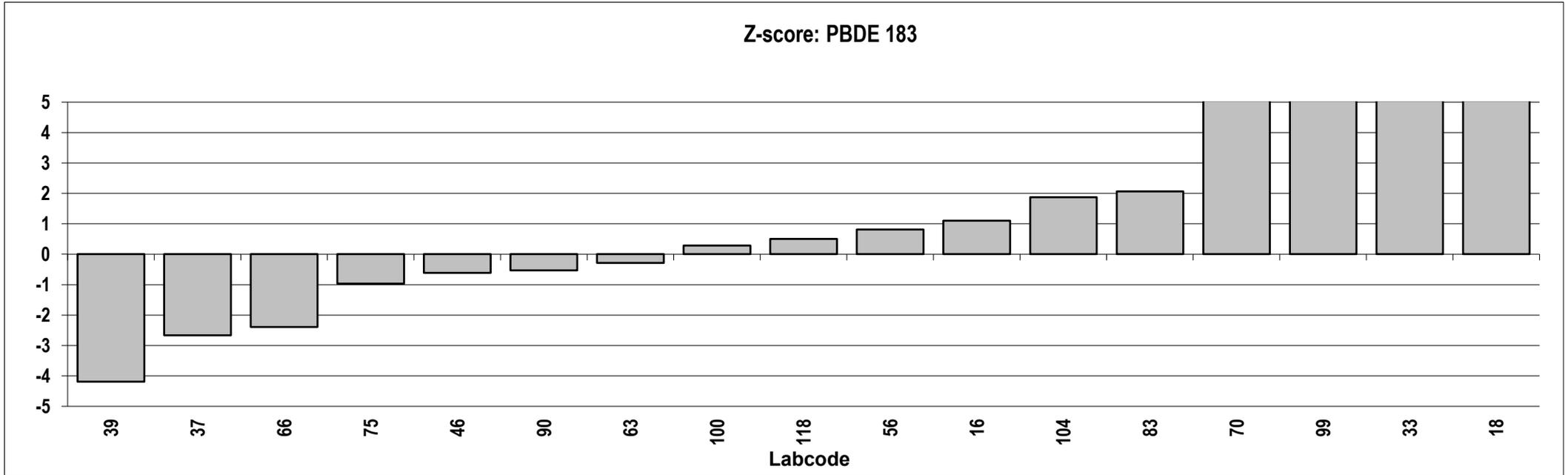
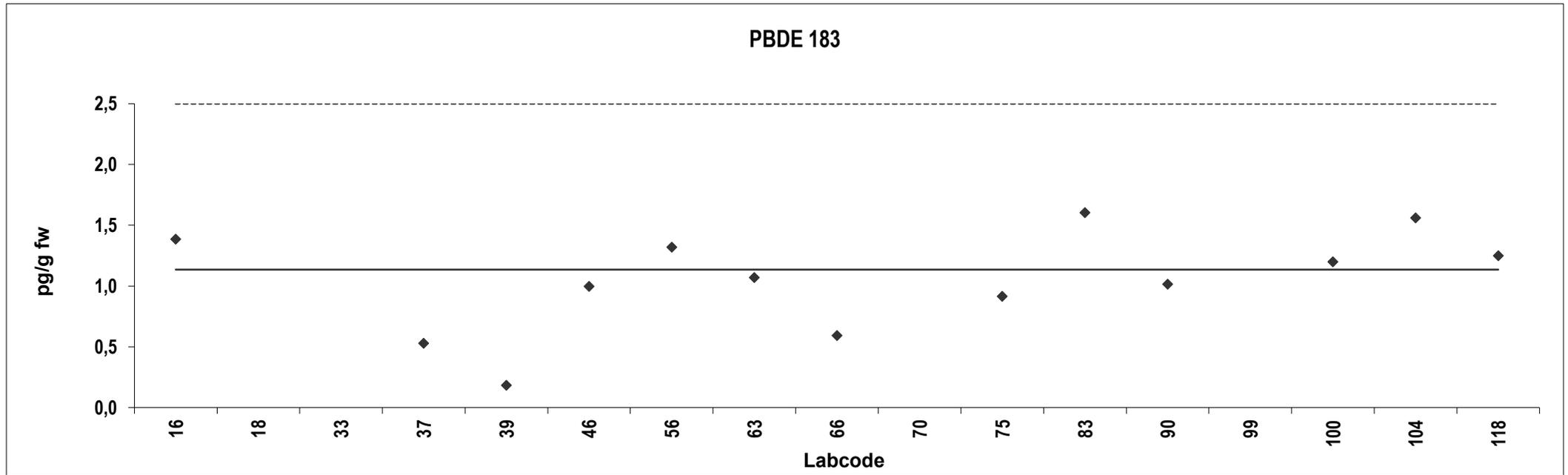


**Egg yolk**  
Congener: PBDE 183

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
16	1,4	1,1				
18	15	61	Outlier			
33	9,4	36	Outlier,ND			
37	0,53	-2,7	ND			
39	0,18	-4,2				
46	1,00	-0,61				
56	1,3	0,81				
63	1,1	-0,29				
66	0,59	-2,4				
70	2,7	7,0	Outlier			
75	0,92	-1,0				
83	1,6	2,1				
90	1,0	-0,53				
99	6,3	23	Outlier,ND			
100	1,2	0,29				
104	1,6	1,9				
118	1,3	0,51				

**Consensus statistics**

Consensus median, pg/g	1,1
Median all values pg/g	1,3
Consensus mean, pg/g	1,0
Standard deviation, pg/g	0,41
Relative standard deviation, %	40
No. of values reported	17
No. of values removed	4
No. of reported non-detects	3

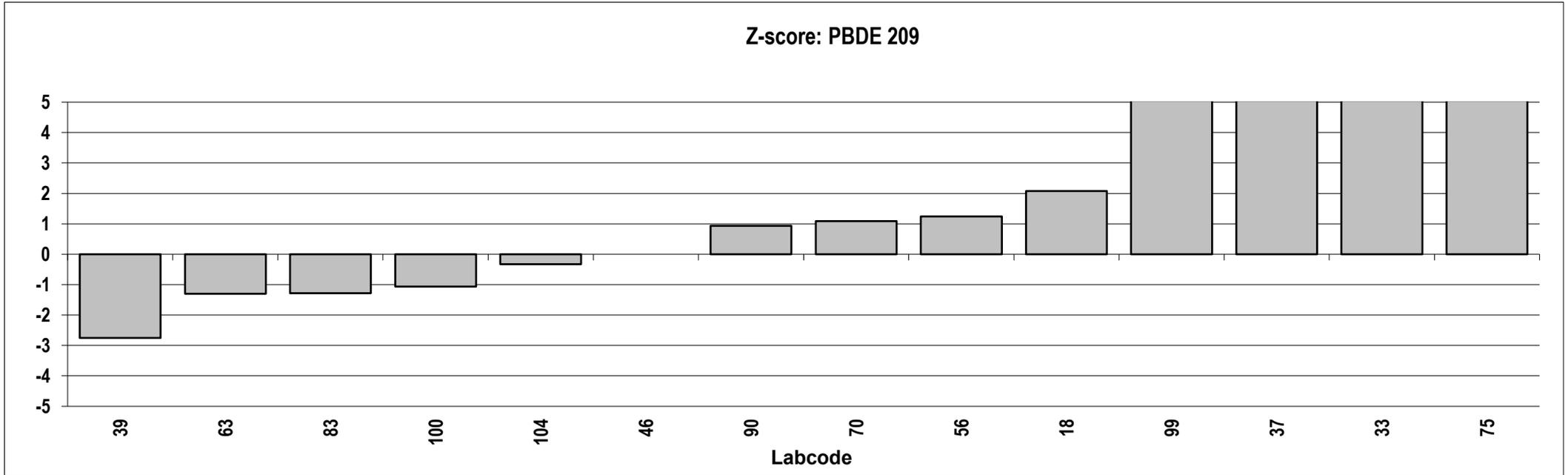
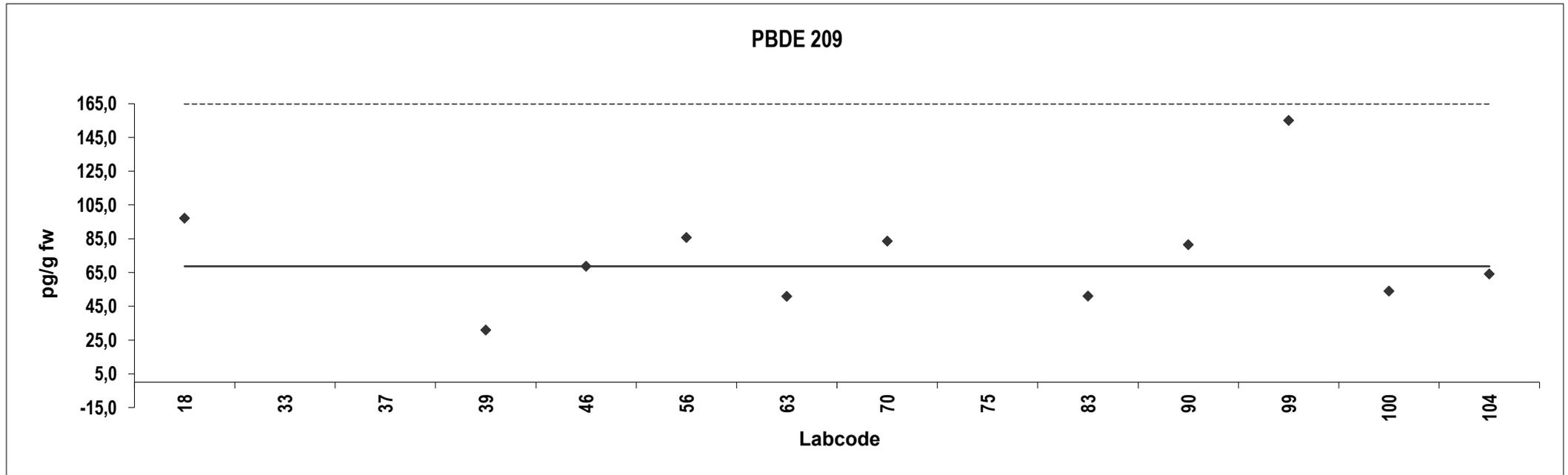


**Egg yolk**  
Congener: PBDE 209

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
18	97	2,1				
33	187	8,6	Outlier,ND			
37	168	7,2	Outlier,ND			
39	31	-2,8				
46	69	0,00000				
56	86	1,2				
63	51	-1,3				
70	84	1,1				
75	763	51	Outlier			
83	51	-1,3				
90	81	0,93				
99	155	6,3				
100	54	-1,1				
104	64	-0,32				

**Consensus statistics**

Consensus median, pg/g	69
Median all values pg/g	82
Consensus mean, pg/g	75
Standard deviation, pg/g	33
Relative standard deviation, %	44
No. of values reported	14
No. of values removed	3
No. of reported non-detects	2

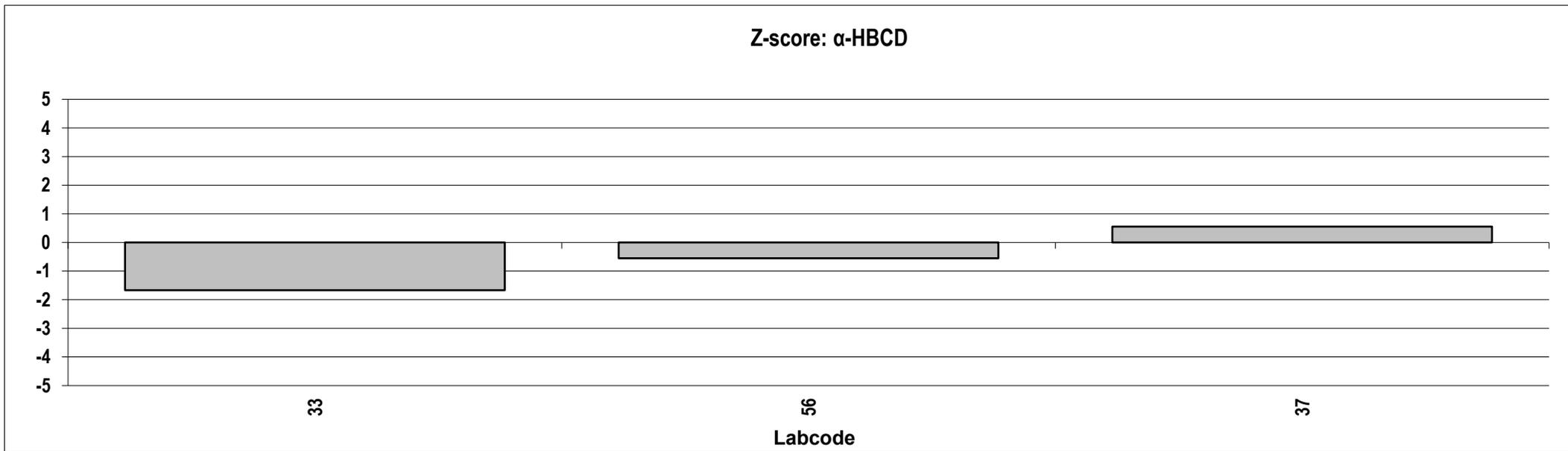
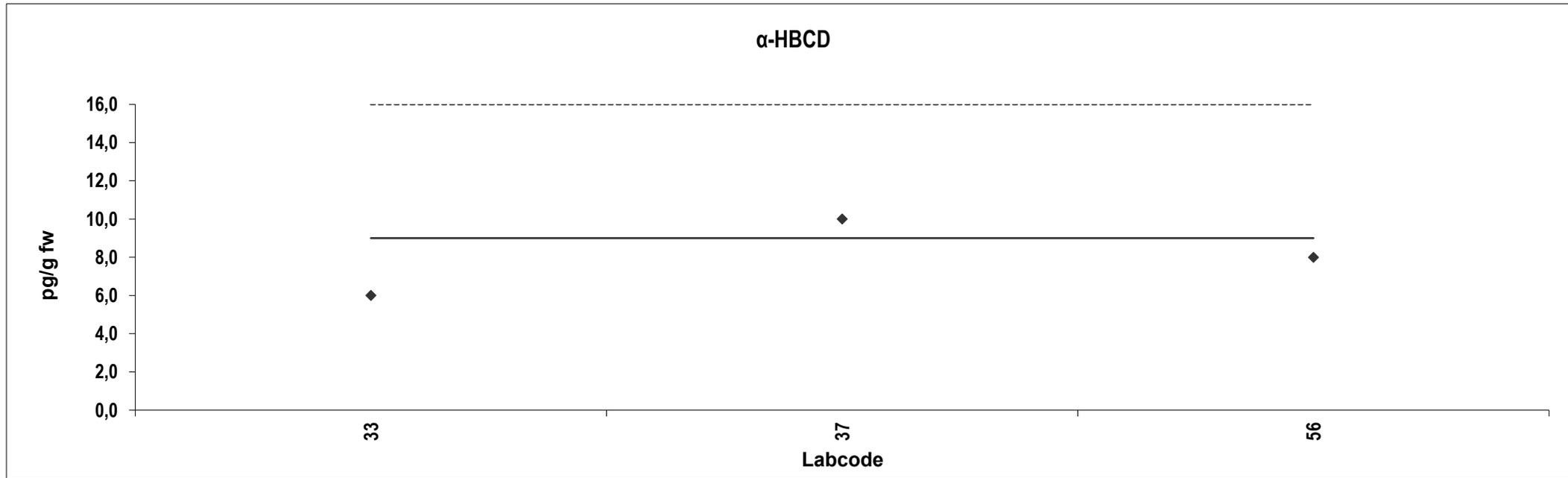


**Egg yolk**  
Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
33	6,0	-1,7	ND			
37	10	0,56				
56	8,0	-0,56				

**Consensus statistics**

Consensus median, pg/g	9,0
Median all values pg/g	8,0
Consensus mean, pg/g	8,0
Standard deviation, pg/g	2,0
Relative standard deviation, %	25
No. of values reported	3
No. of values removed	0
No. of reported non-detects	1

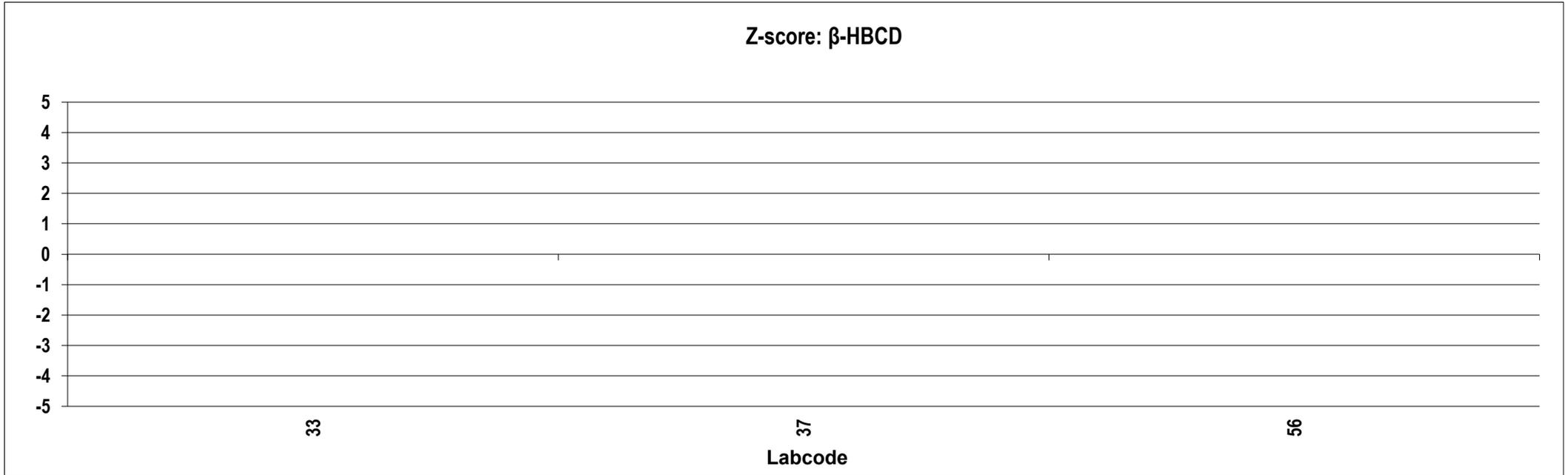
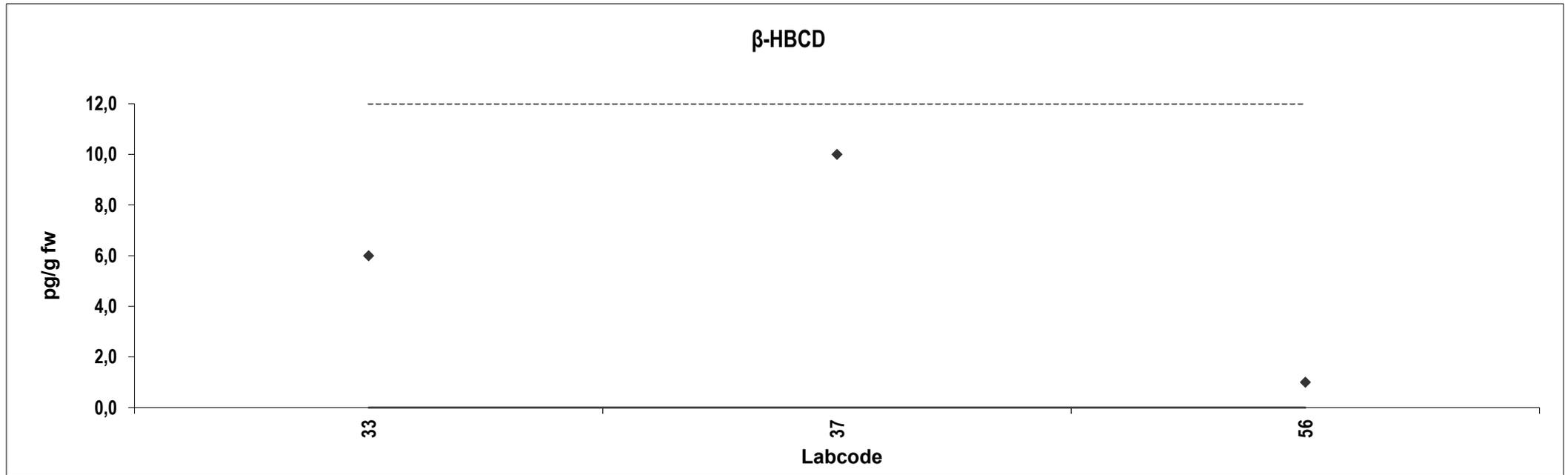


**Egg yolk**  
Congener:  $\beta$ -HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
33	6,0	**	ND			
37	10	**	ND			
56	1,0	**	ND			

**Consensus statistics**

Consensus median, pg/g	**
Median all values pg/g	6,0
Consensus mean, pg/g	5,7
Standard deviation, pg/g	4,5
Relative standard deviation, %	80
No. of values reported	3
No. of values removed	0
No. of reported non-detects	3

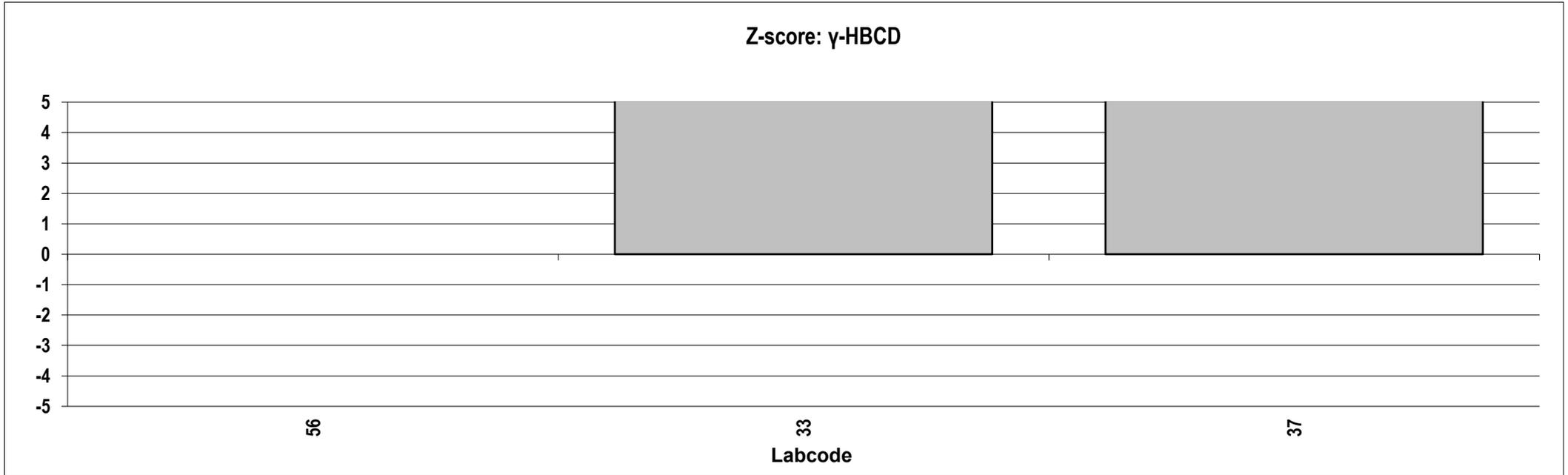
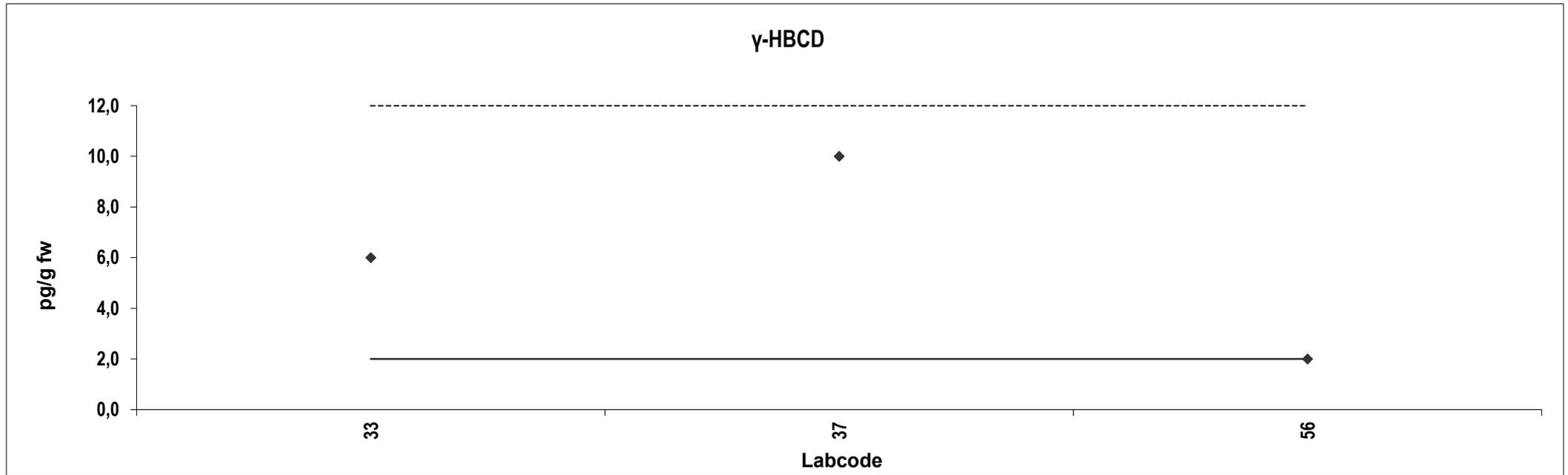


**Egg yolk**  
Congener:  $\gamma$ -HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
33	6,0	10	ND			
37	10	20	ND			
56	2,0	0,00000				

**Consensus statistics**

Consensus median, pg/g	2,0
Median all values pg/g	6,0
Consensus mean, pg/g	6,0
Standard deviation, pg/g	4,0
Relative standard deviation, %	67
No. of values reported	3
No. of values removed	0
No. of reported non-detects	2

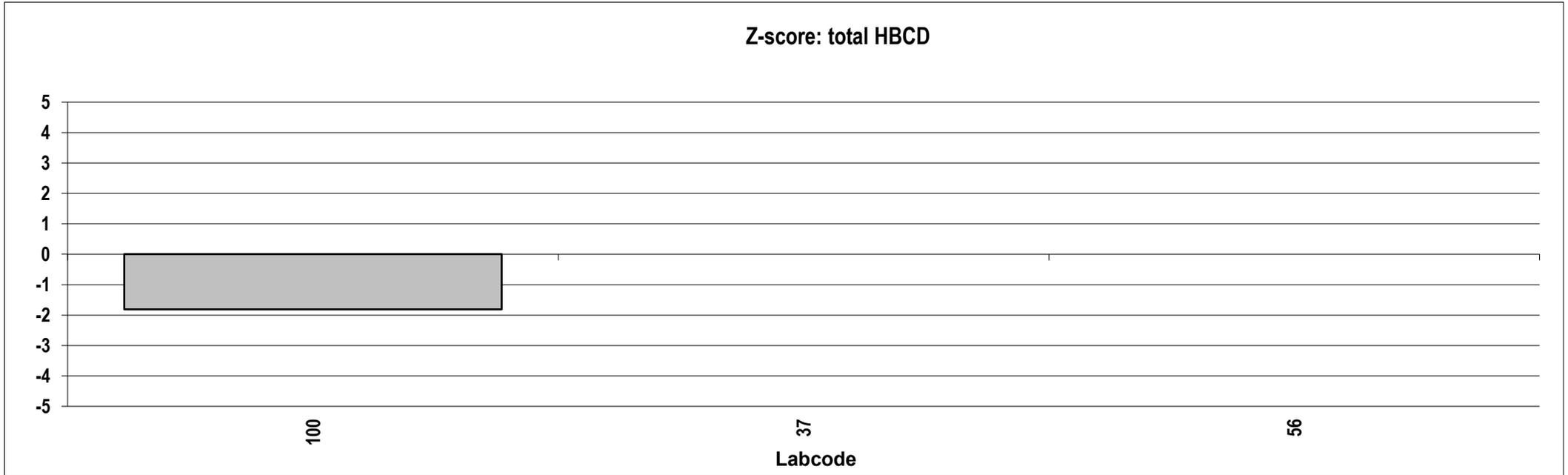
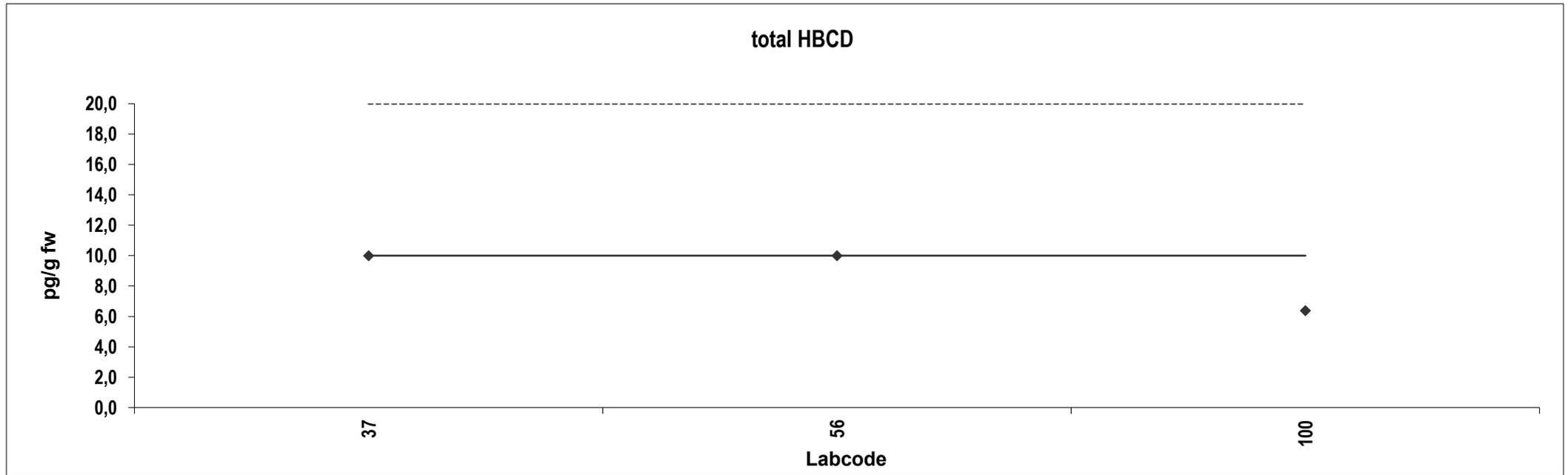


**Egg yolk**  
Congener: total HBCD

Lab code	Conc. pg/g fw.	Z-score	Notes	Lab code	Conc. pg/g fw.	Notes
37	10	0,00000				
56	10	0,00000				
100	6,4	-1,8				

**Consensus statistics**

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	8,8
Standard deviation, pg/g	2,1
Relative standard deviation, %	24
No. of values reported	3
No. of values removed	0
No. of reported non-detects	0





## **Appendix 5:**



Presentation of results for  
PFAS Mackerel 2024



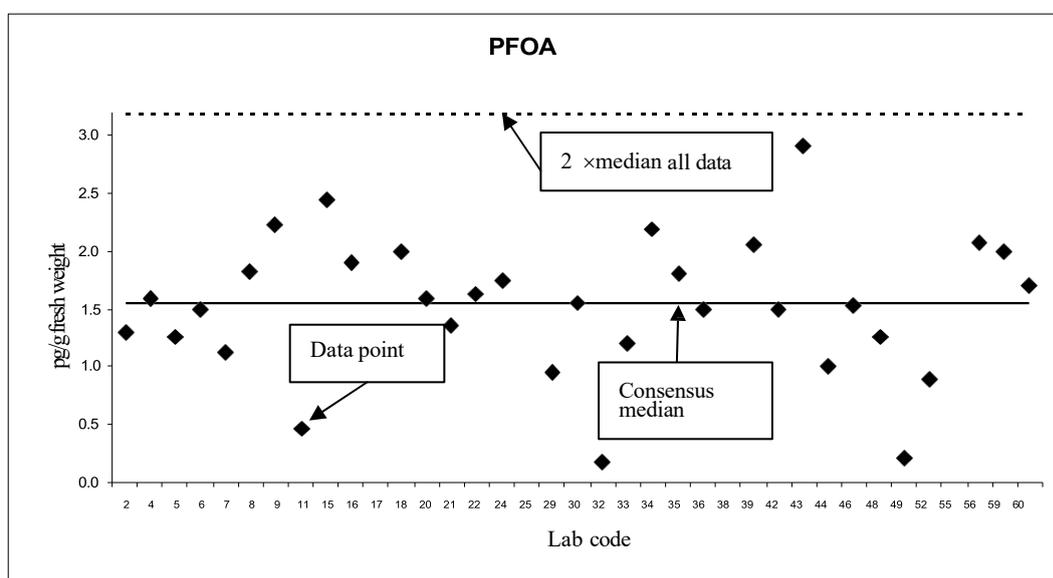
## Appendix 5: Presentation of results: PFAS Mackerel 2024

### 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  $2 \times$  this median were defined as outliers and removed from the data set. The NDs were also removed.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

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



### Z-Scores of individual congeners

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

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

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



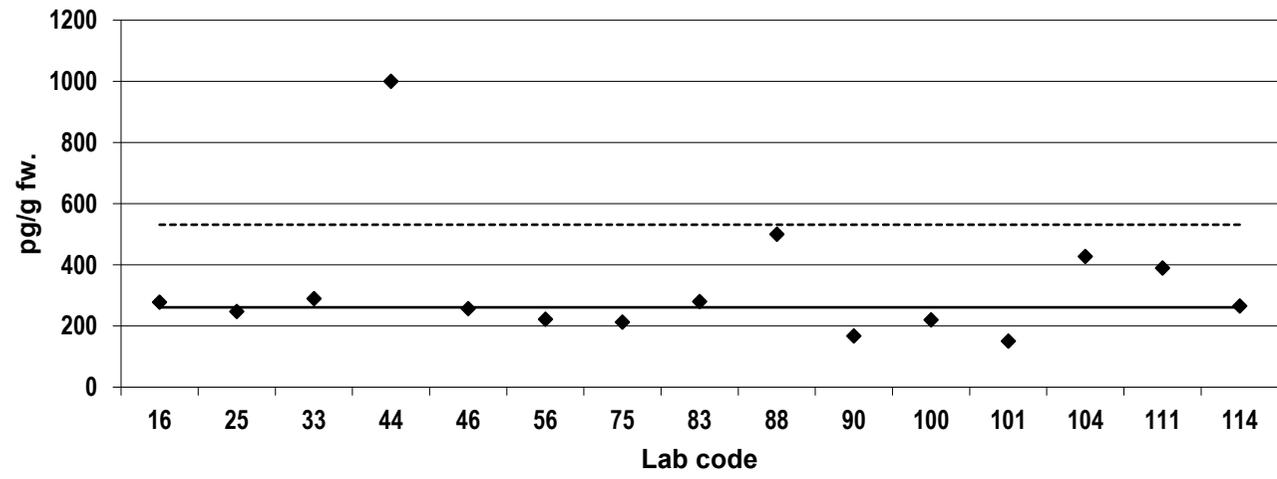
**Mackerel**  
**PFOS - All reported**

Lab code	pg/g fw.	Z-score	Notes
16	278	0,33	
25	247	-0,27	
33	289	0,54	
44	1000	14	ND, outlier
46	256	-0,088	
56	222	-0,75	
75	213	-0,92	
83	280	0,36	
88	500	4,6	ND
90	167	-1,8	ND
100	220	-0,79	
101	151	-2,1	
104	427	3,2	
111	390	2,5	
114	266	0,088	

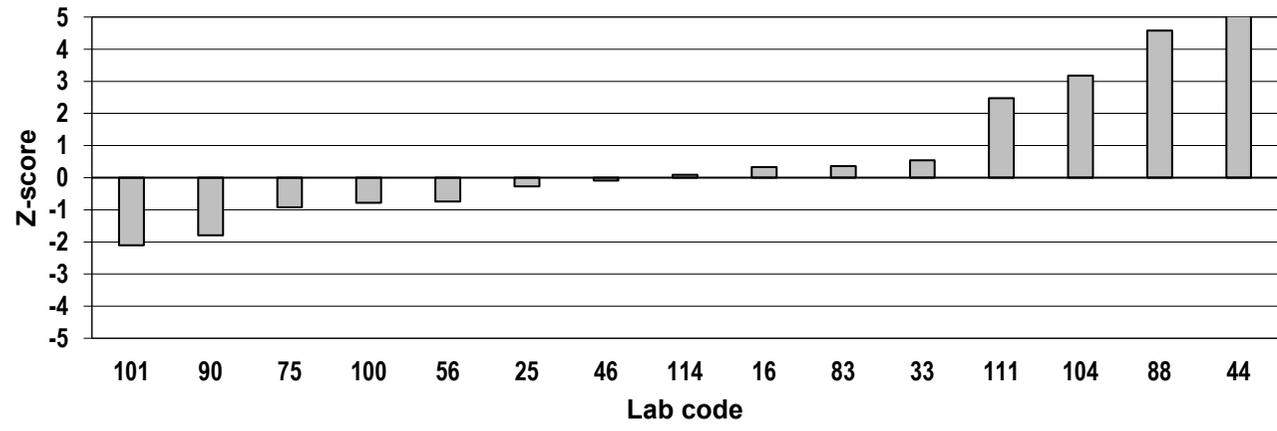
**Consensus statistics**

Consensus median, pg/g	261
Median all values pg/g	266
Consensus mean, pg/g	270
Standard deviation, pg/g	75
Relative standard deviation, %	28
No. of values reported	15
No. of values removed	3
No. of reported non-detects	3

PFOS - All reported



Z-score: PFOS - All reported

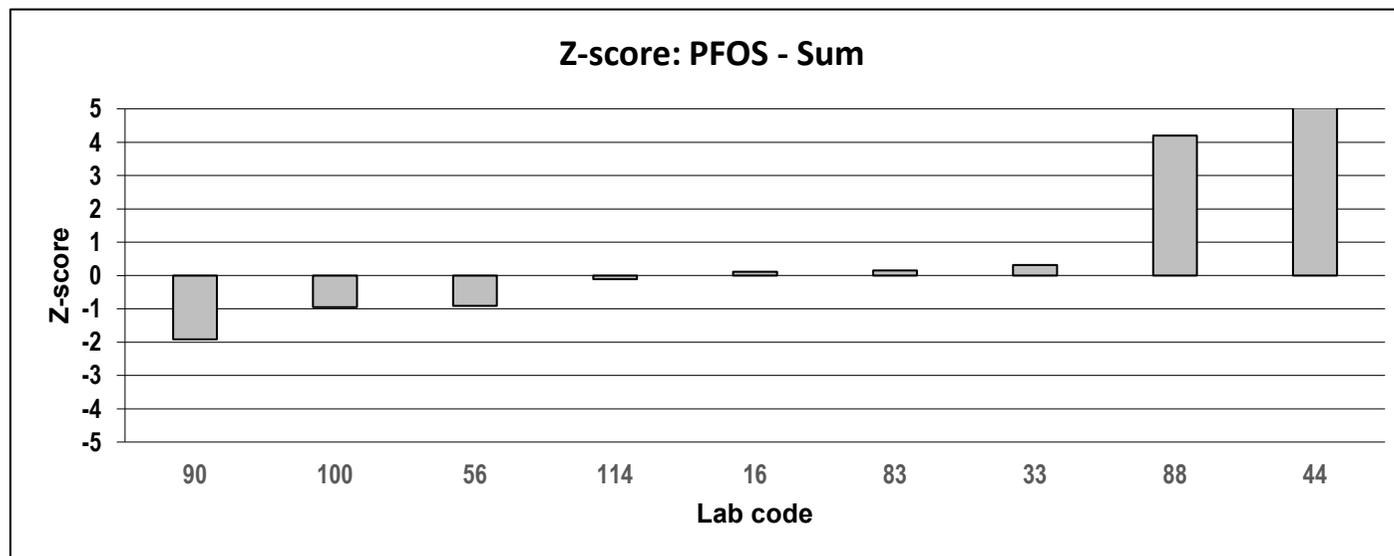
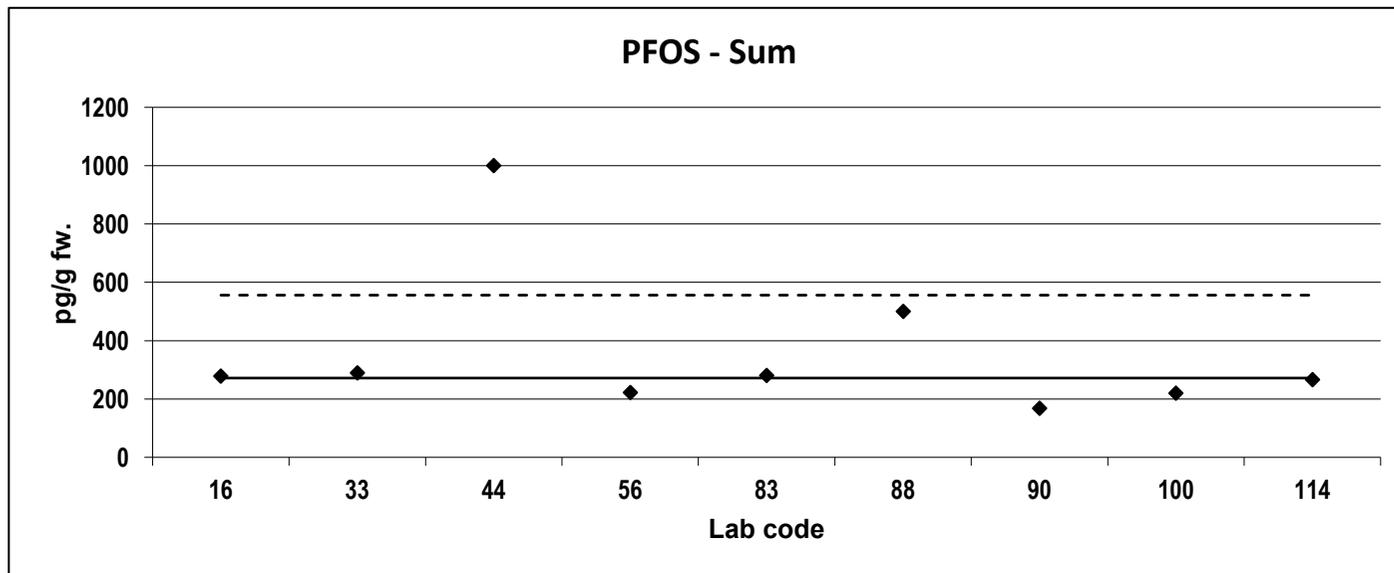


**Mackerel**  
**PFOS - Sum**

Lab code	pg/g fw.	Z-score	Notes
16	278	0,11	
33	289	0,32	
44	1000	13	ND, outlier
56	222	-0,92	
83	280	0,15	
88	500	4,2	ND
90	167	-1,9	ND
100	220	-0,95	
114	266	-0,11	

**Consensus statistics**

Consensus median, pg/g	272
Median all values pg/g	278
Consensus mean, pg/g	259
Standard deviation, pg/g	30
Relative standard deviation, %	12
No. of values reported	9
No. of values removed	3
No. of reported non-detects	3

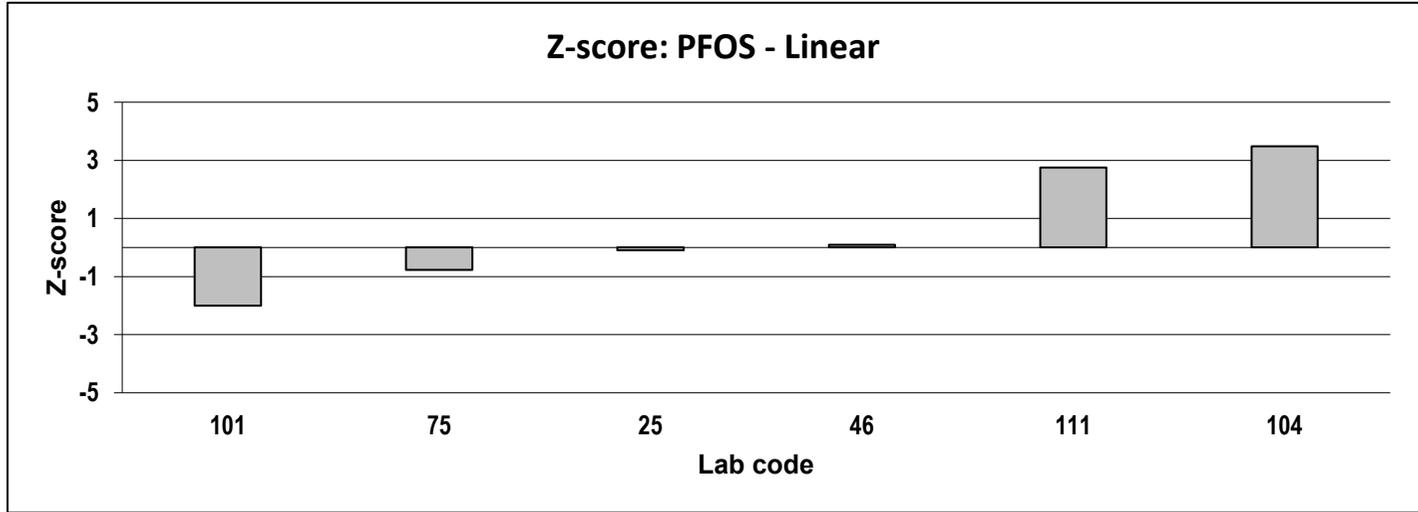
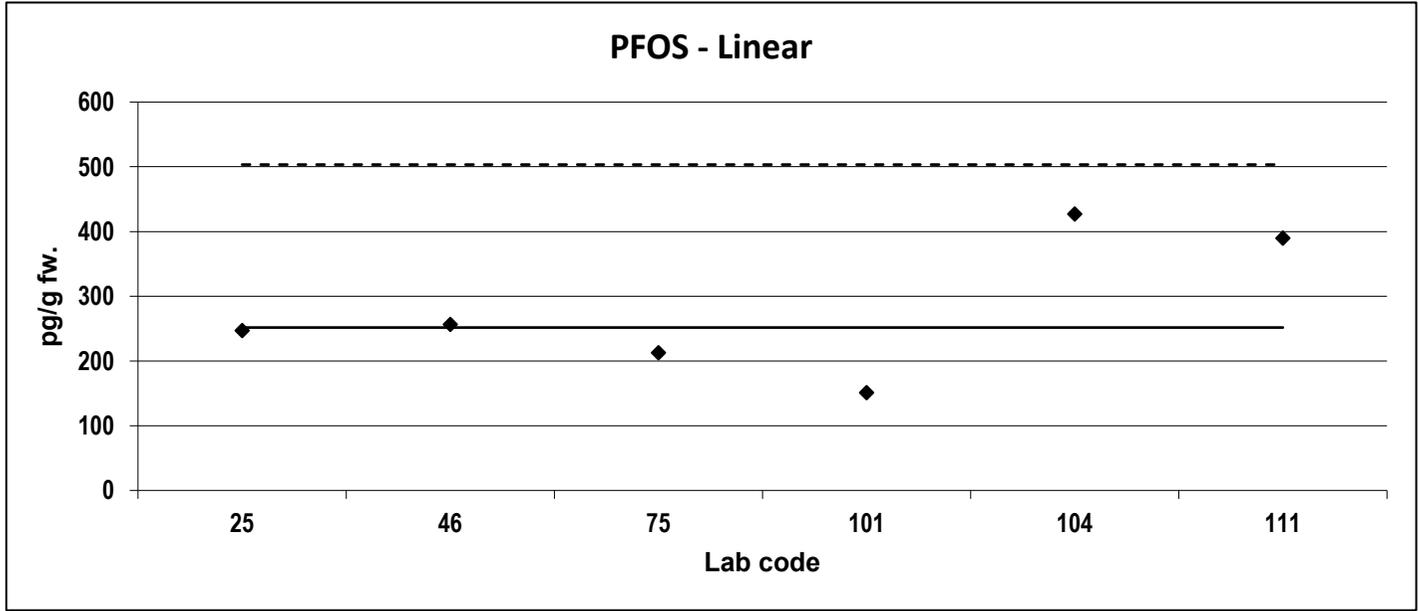


**Mackerel**  
**PFOS - Linear**

Lab code	pg/g fw.	Z-score	Notes
25	247	-0,093	
46	256	0,093	
75	213	-0,77	
101	151	-2,0	
104	427	3,5	
111	390	2,7	

**Consensus statistics**

Consensus median, pg/g	252
Median all values pg/g	252
Consensus mean, pg/g	281
Standard deviation, pg/g	106
Relative standard deviation, %	38
No. of values reported	6
No. of values removed	0
No. of reported non-detects	0

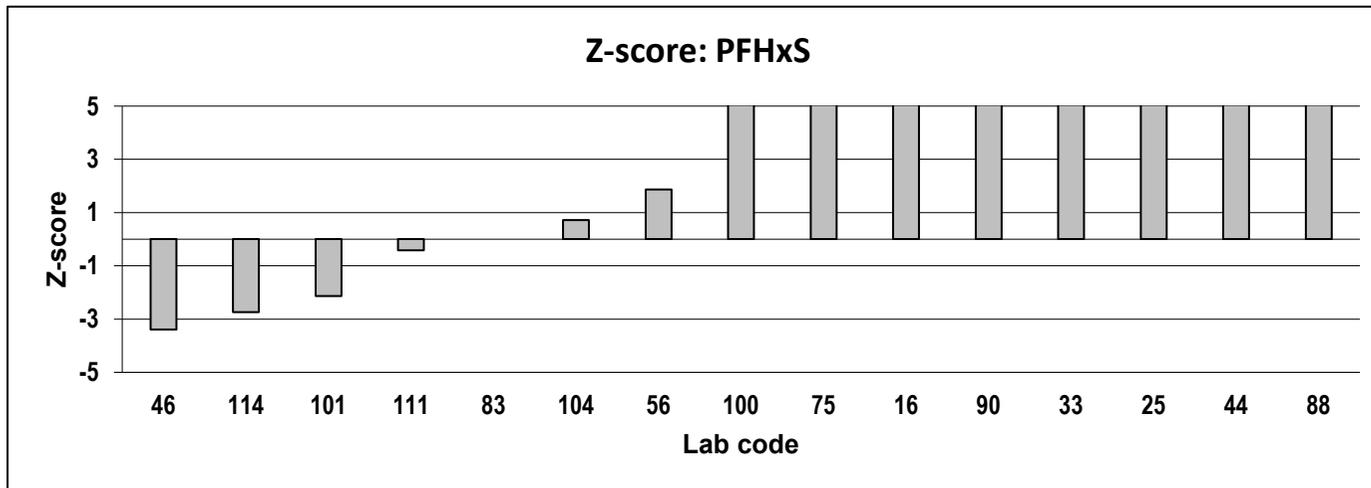
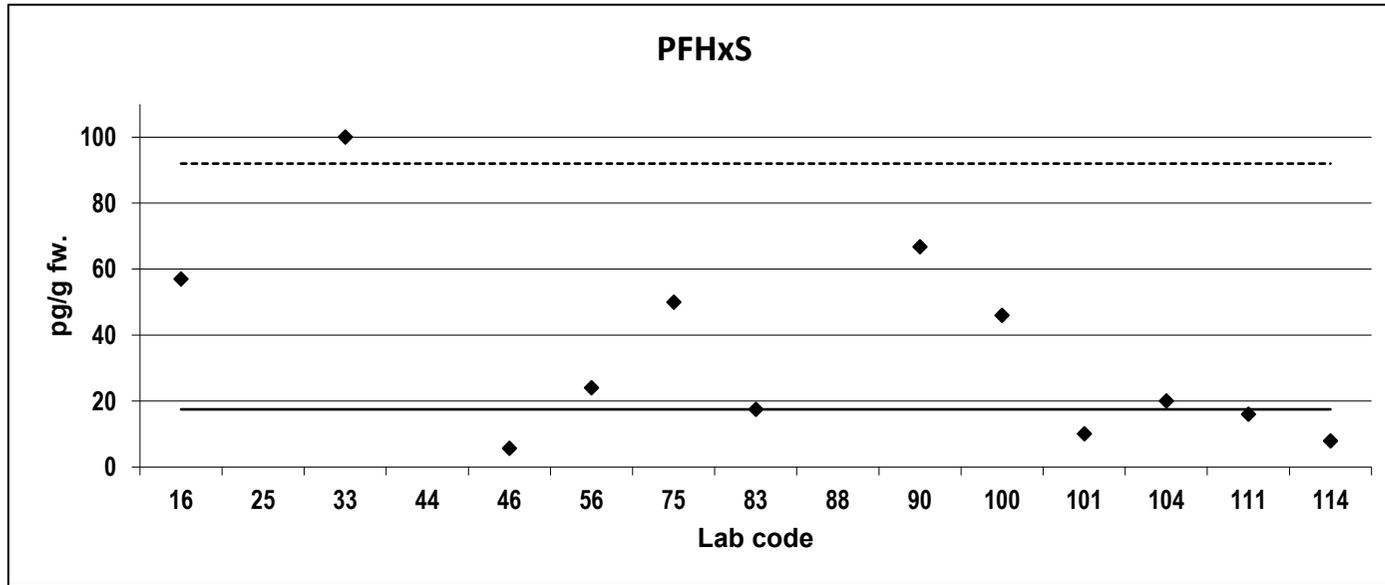


**Mackerel**  
**PFHxS**

Lab code	pg/g fw.	Z-score	Notes
16	57	11	
25	250	67	Outlier
33	100	24	ND
44	300	81	ND, outlier
46	6	-3,4	
56	24	1,9	
75	50	9,3	ND
83	17	0,00000	
88	500	138	ND, outlier
90	67	14	ND
100	46	8,2	ND
101	10	-2,1	ND
104	20	0,72	
111	16	-0,42	
114	8	-2,7	

**Consensus statistics**

Consensus median, pg/g	17
Median all values pg/g	46
Consensus mean, pg/g	21
Standard deviation, pg/g	17
Relative standard deviation, %	81
No. of values reported	15
No. of values removed	8
No. of reported non-detects	7

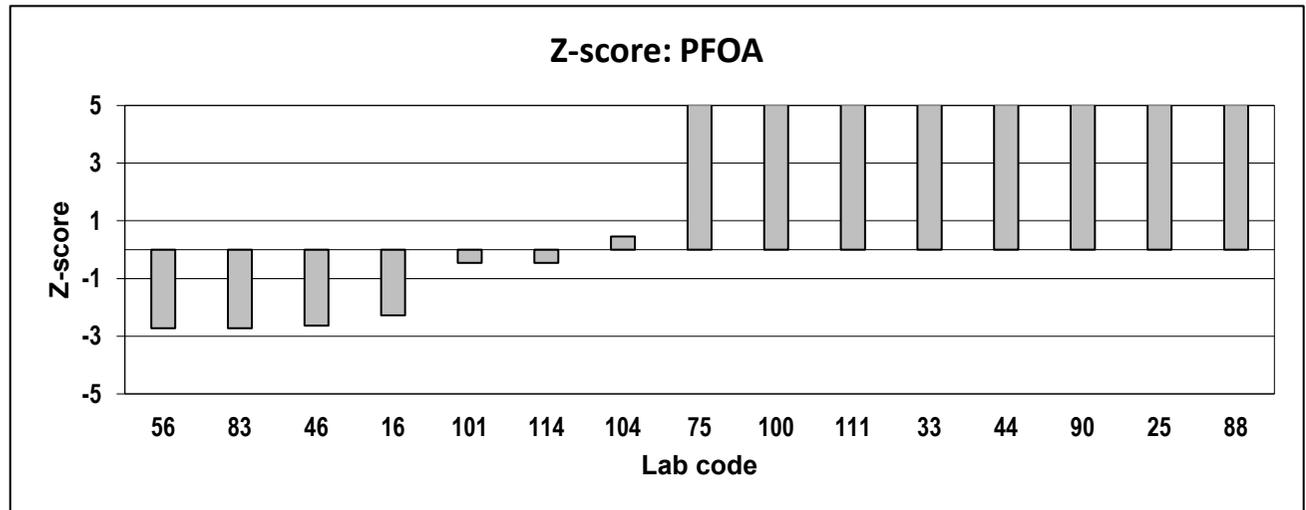
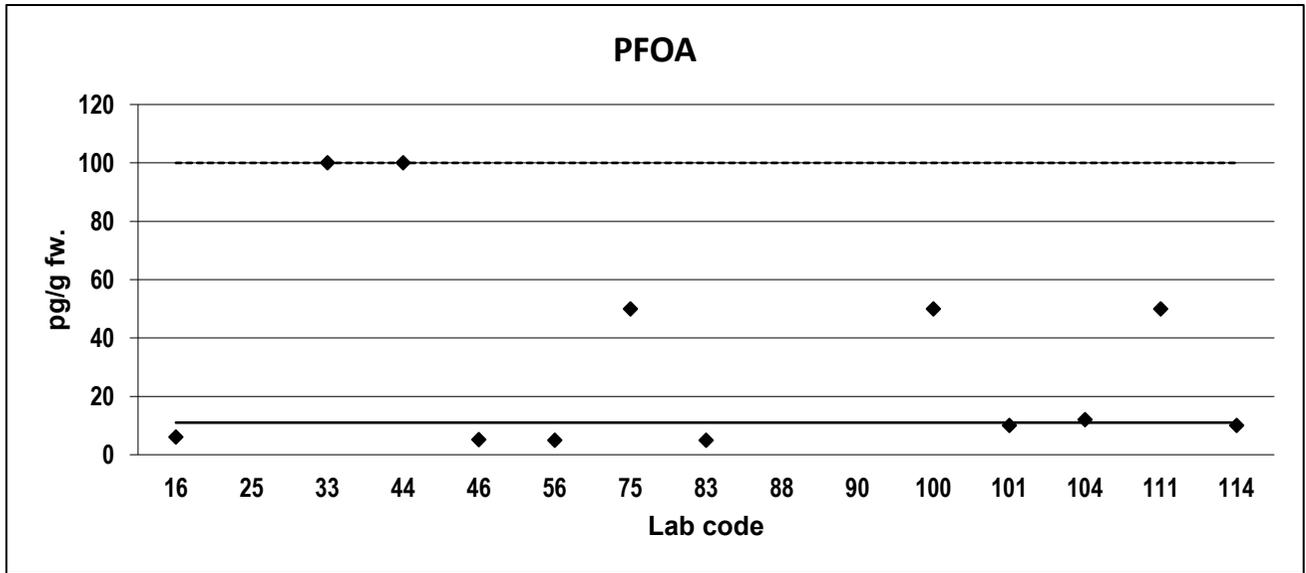


**Mackerel**  
**PFOA**

Lab code	pg/g fw.	Z-score	Notes
16	6	-2,3	ND
25	250	109	Outlier
33	100	40	ND
44	100	40	ND
46	5	-2,6	
56	5	-2,7	ND
75	50	18	ND
83	5	-2,7	ND
88	500	222	ND, outlier
90	213	92	ND, outlier
100	50	18	ND
101	10	-0,45	ND
104	12	0,45	
111	50	18	
114	10	-0,45	

**Consensus statistics**

Consensus median, pg/g	11
Median all values pg/g	50
Consensus mean, pg/g	19
Standard deviation, pg/g	21
Relative standard deviation, %	107
No. of values reported	15
No. of values removed	11
No. of reported non-detects	10



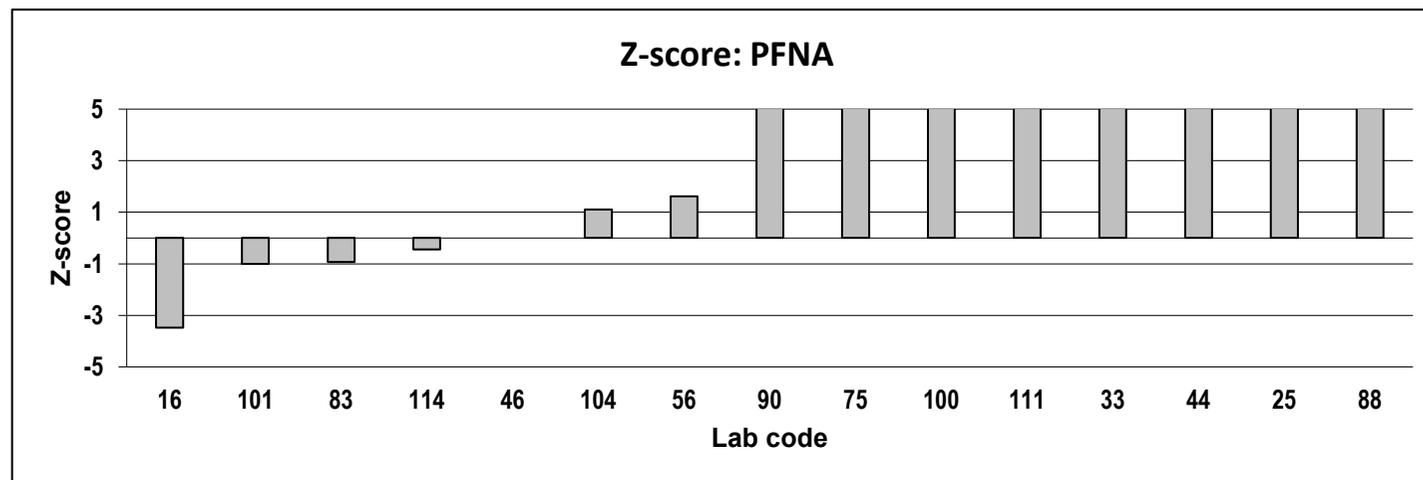
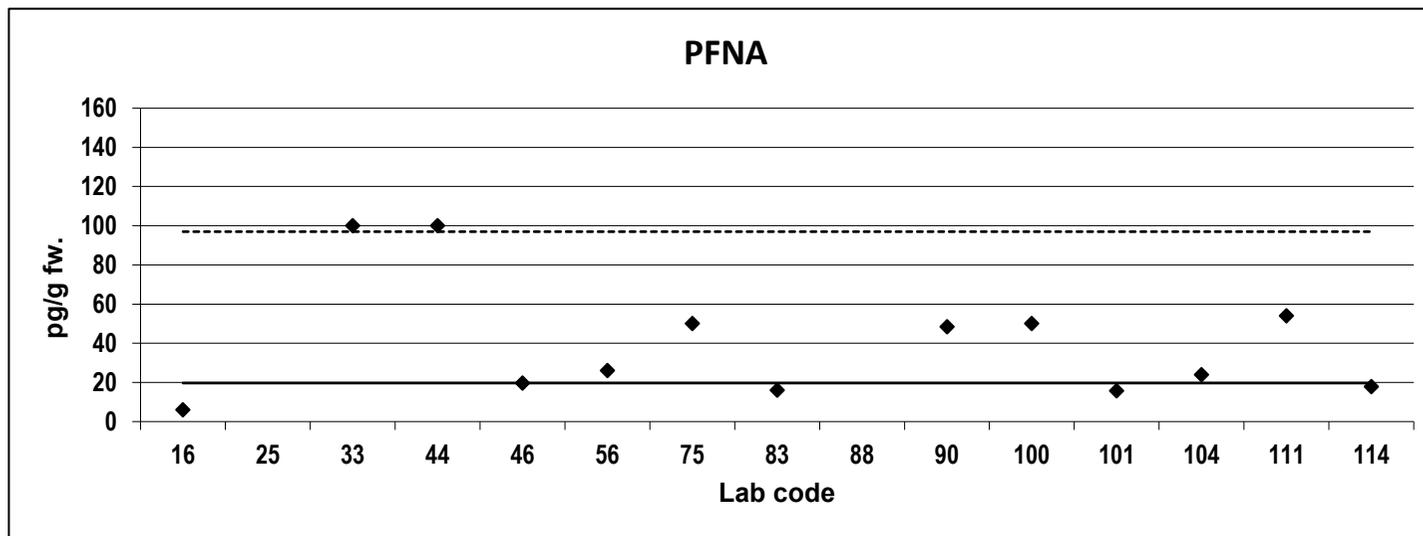
## Mackerel PFNA

Lab code	pg/g fw.	Z-score	Notes
16	6	-3,5	ND
25	250	59	Outlier
33	100	20	ND, outlier
44	100	20	ND, outlier
46	20	0,00000	
56	26	1,6	
75	50	7,7	ND
83	16	-0,93	
88	500	122	ND, outlier
90	48	7,3	ND
100	50	7,7	ND
101	16	-1,0	
104	24	1,1	
111	54	8,7	
114	18	-0,45	

r

### Consensus statistics

Consensus median, pg/g	20
Median all values pg/g	48
Consensus mean, pg/g	25
Standard deviation, pg/g	13
Relative standard deviation, %	54
No. of values reported	15
No. of values removed	8
No. of reported non-detects	7

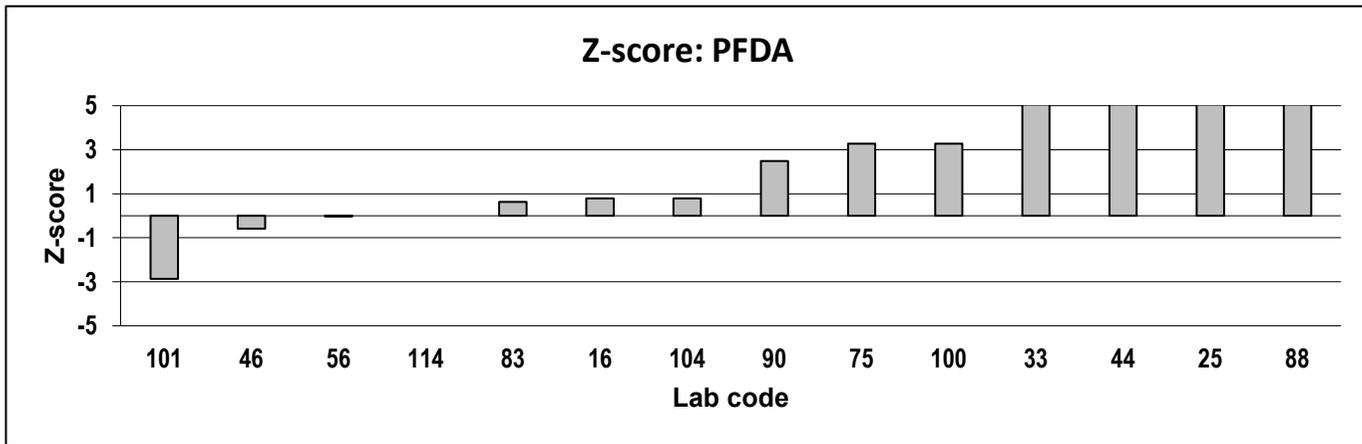
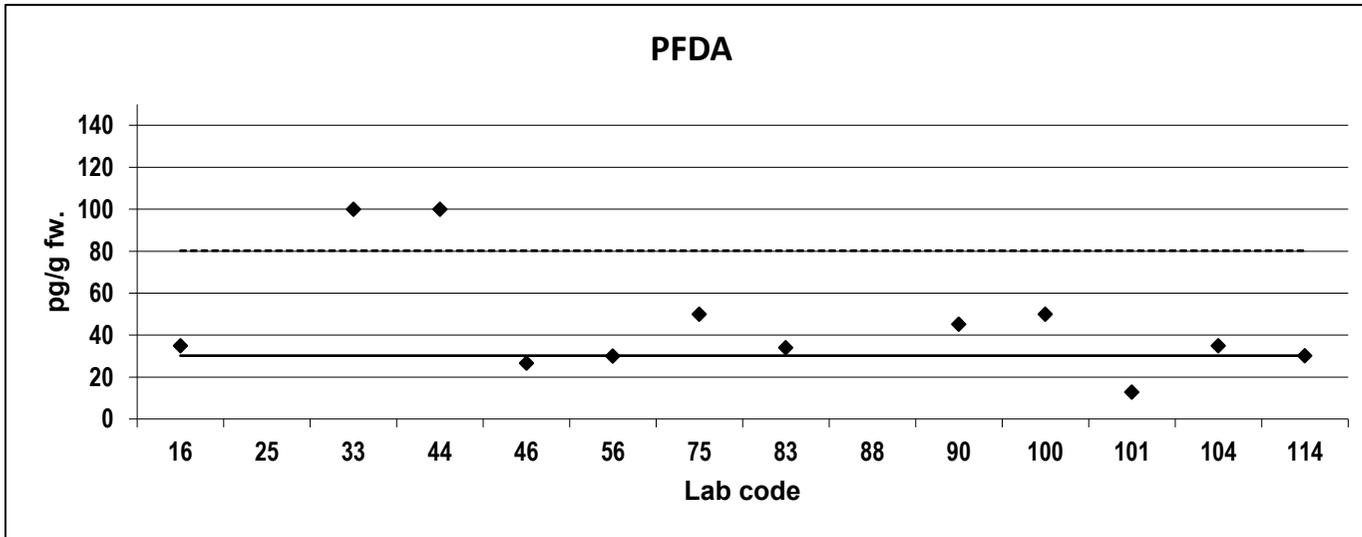


**Mackerel**  
**PFDA**

Lab code	pg/g fw.	Z-score	Notes
16	35	0,79	
25	250	36	Outlier
33	100	12	ND, outlier
44	100	12	ND, outlier
46	27	-0,58	
56	30	-0,033	
75	50	3,3	ND
83	34	0,63	
88	500	78	ND, outlier
90	45	2,5	ND
100	50	3,3	ND
101	13	-2,9	
104	35	0,79	
114	30	0,00000	

**Consensus statistics**

Consensus median, pg/g	30
Median all values pg/g	40
Consensus mean, pg/g	29
Standard deviation, pg/g	7,8
Relative standard deviation, %	27
No. of values reported	14
No. of values removed	7
No. of reported non-detects	6

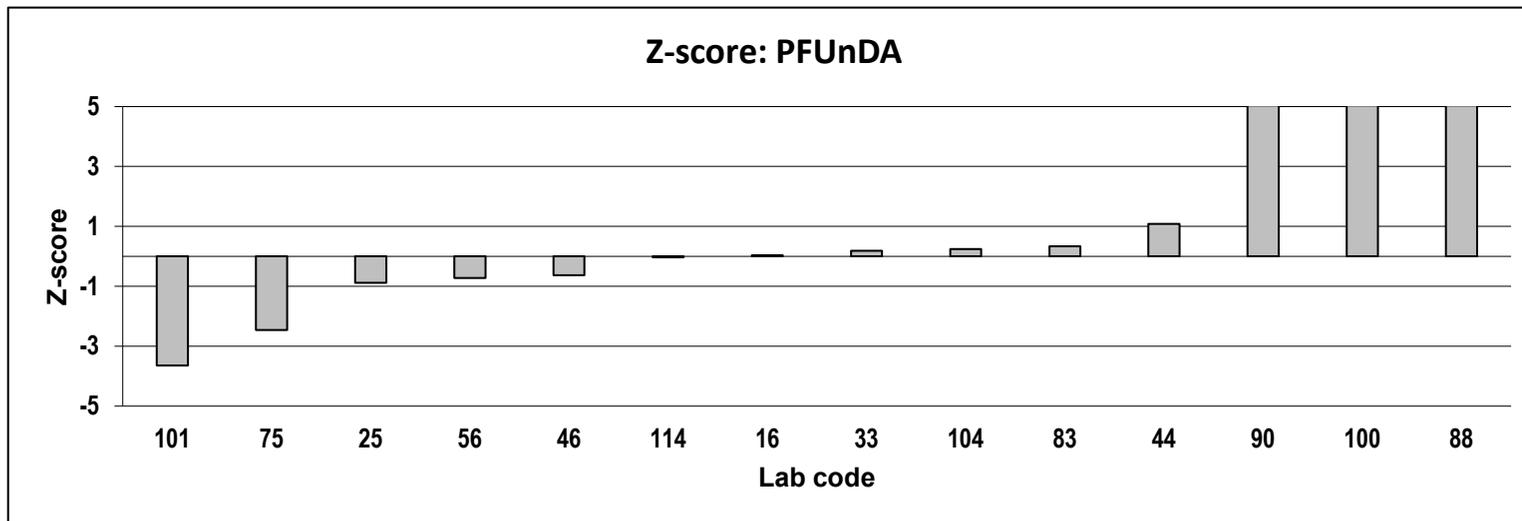
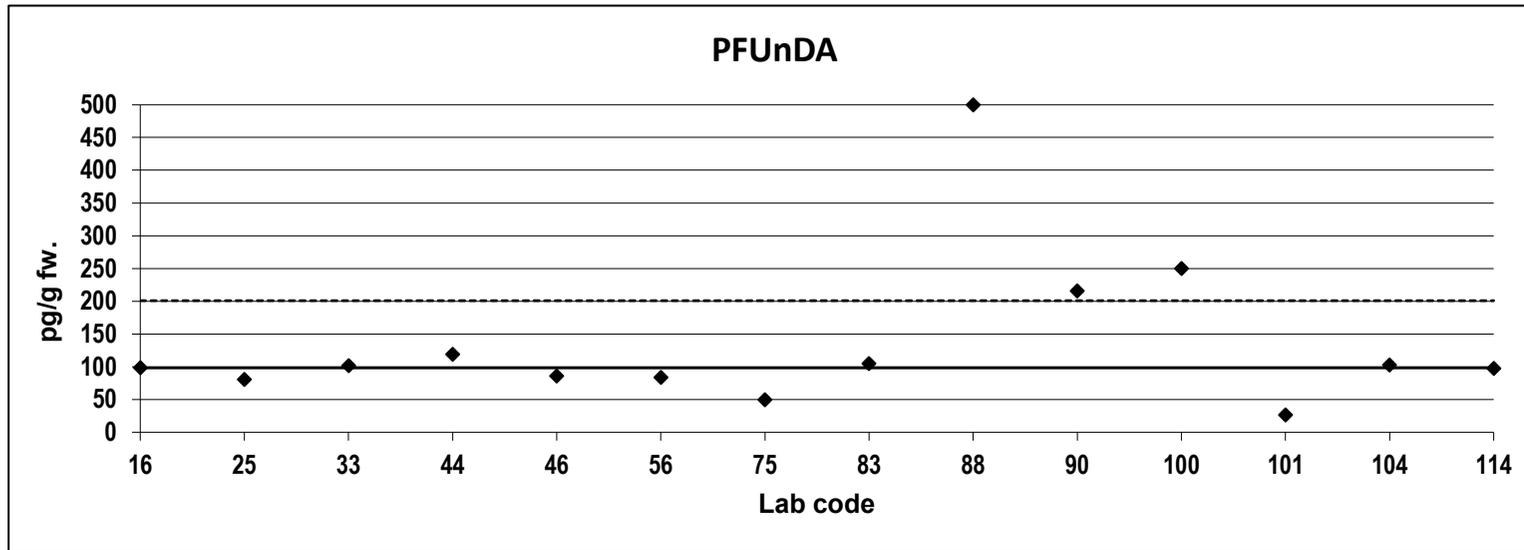


**Mackerel**  
**PFUnDA**

Lab code	pg/g fw.	Z-score	Notes
16	99	0,036	
25	81	-0,88	
33	102	0,19	
44	120	1,1	
46	86	-0,63	
56	84	-0,73	
75	50	-2,5	ND
83	105	0,34	
88	500	20	ND, outlier
90	216	6,0	Outlier
100	250	7,7	ND, outlier
101	27	-3,6	
104	103	0,24	
114	98	-0,036	

**Consensus statistics**

Consensus median, pg/g	98
Median all values pg/g	101
Consensus mean, pg/g	90
Standard deviation, pg/g	25
Relative standard deviation, %	28
No. of values reported	14
No. of values removed	4
No. of reported non-detects	3





## **Appendix 6:**

Presentation of results  
for lipid determination

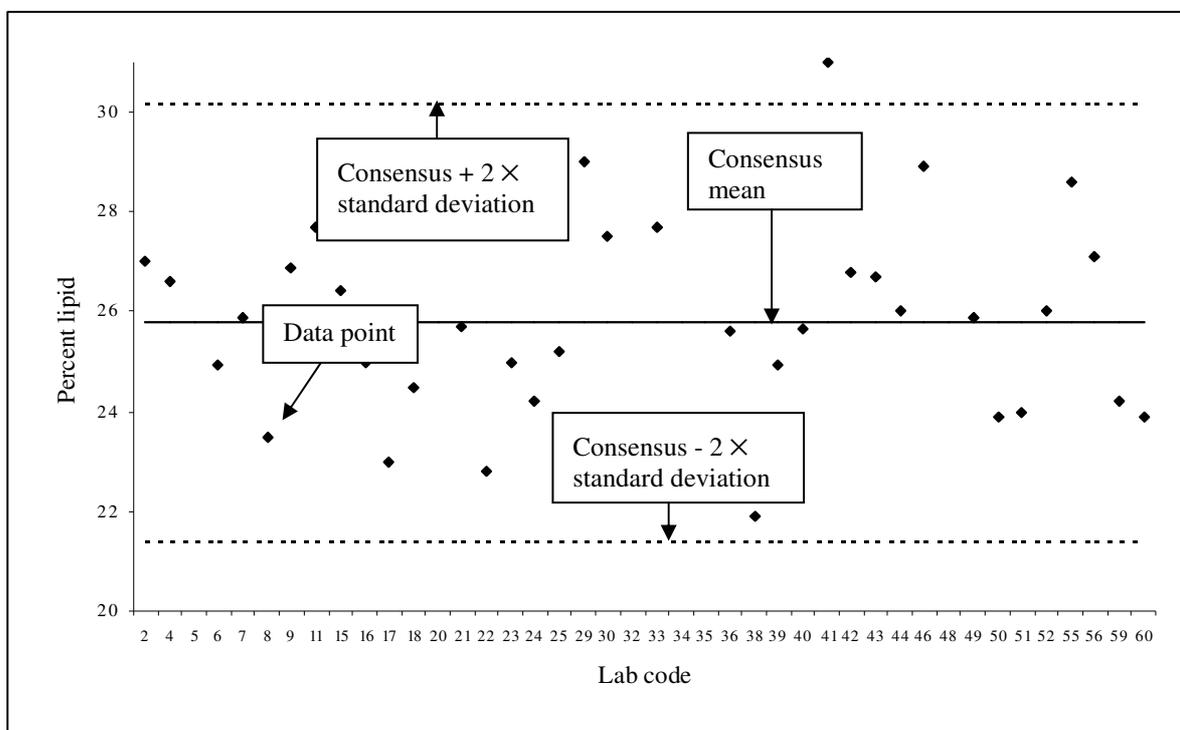


## Presentation of results for lipid determination

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



### Lipid determination for Mackerel

Lab code	% lipid	Z-score	Notes	Lab code	% lipid	Z-score	Notes
15	16	0,0062		106	17	0,10	
16	18	0,44		108	16	0,051	
18	17	0,30		110	19	0,78	
20	20	1,2	Outlier	111	16	0,10	
21	17	0,22		112	16	0,074	
22	12	-1,2		114	17	0,20	
25	16	-0,062		115	22	1,8	Outlier
29	16	-0,15		116	18	0,68	
30	16	0,019		119	15	-0,27	
33	16	0,068					
35	15	-0,22					
37	15	-0,30					
39	17	0,17					
40	16	0,037					
44	17	0,13					
46	15	-0,42					
48	17	0,15					
50	16	0,0062					
53	14	-0,78					
56	16	-0,15					
60	14	-0,80					
63	16	-0,040					
64	17	0,20					
66	16	0,062					
68	11	-1,6	Outlier				
70	16	-0,074					
72	15	-0,21					
75	16	-0,0062					
77	14	-0,55					
80	13	-0,95					
83	15	-0,22					
84	11	-1,7	Outlier				
88	15	-0,24					
90	17	0,33					
94	15	-0,50					
99	16	-0,17					
100	12	-1,2					
104	11	-1,8	Outlier				

Mean	Standard deviation	Relative standard deviation	Median
16	1,4	8,7	16

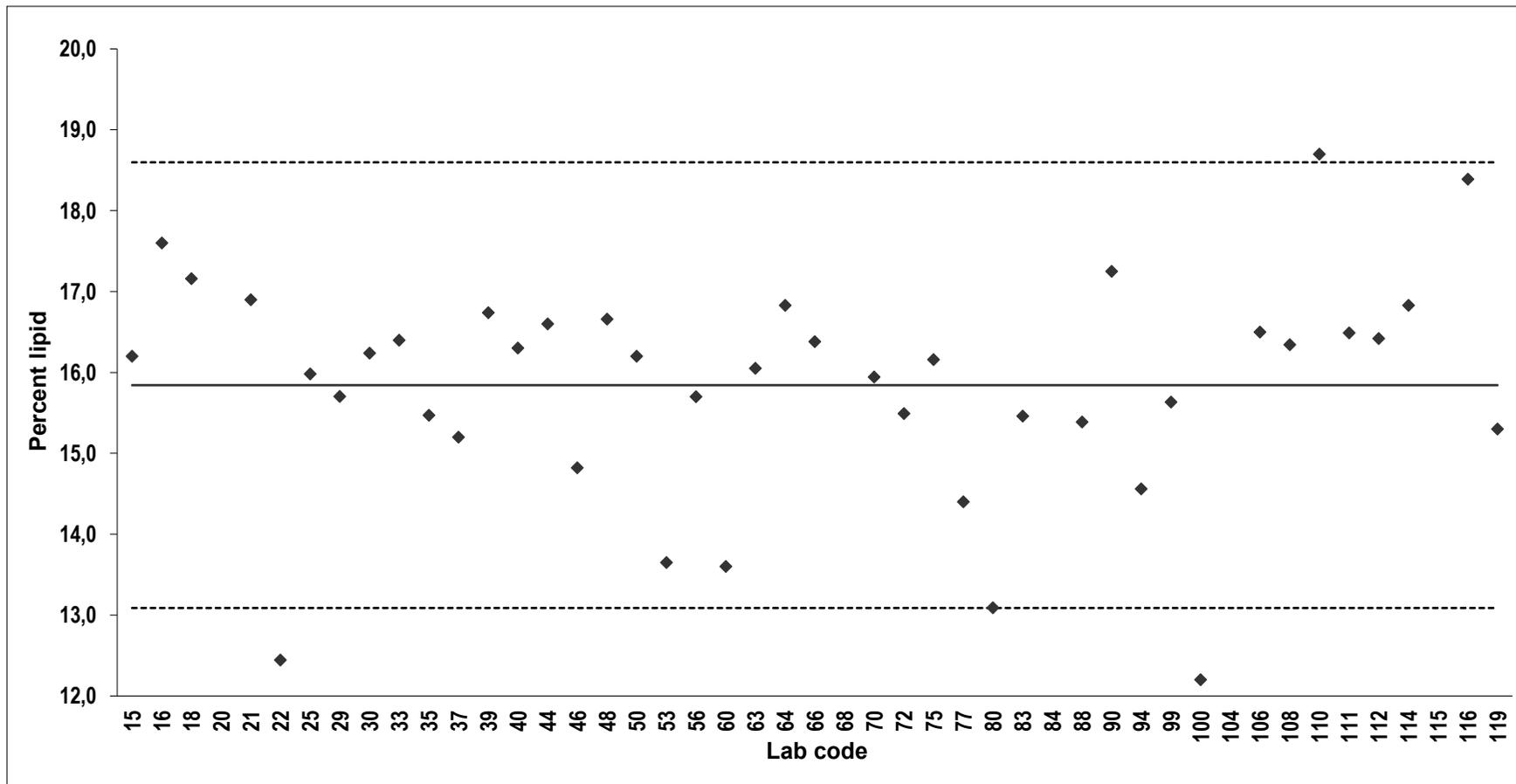


### Lipid determination for Egg yolk

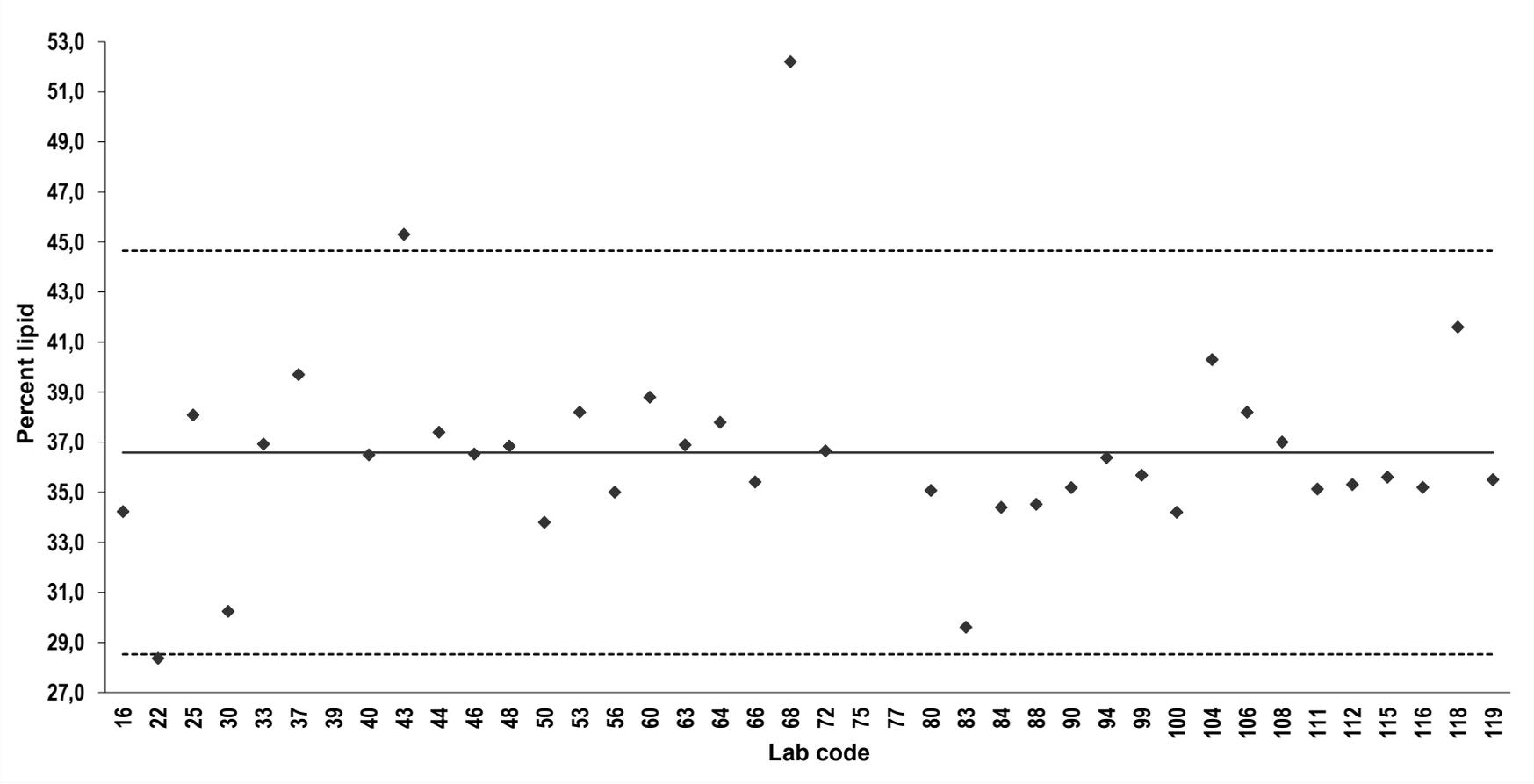
Lab code	% lipid	Z-score	Notes	Lab code	% lipid	Z-score	Notes
16	22	-0,27					
18	23	-0,013					
20	27	0,76					
22	25	0,27					
30	25	0,26					
33	27	0,85					
37	21	-0,43					
39	25	0,32					
40	23	-0,043					
46	21	-0,53					
48	23	-0,14					
50	22	-0,30					
53	34	2,3	Outlier				
56	24	0,19					
60	19	-1,0					
63	23	-0,10					
64	22	-0,31					
66	28	0,90					
68	22	-0,41					
70	20	-0,66					
72	24	0,18					
75	24	0,043					
77	23	0,00000					
83	24	0,13					
84	17	-1,5	Outlier				
88	23	-0,17					
90	21	-0,47					
94	28	1,1					
99	22	-0,35					
100	24	0,17					
104	23	0,00000					
106	24	0,096					
108	20	-0,66					
111	23	-0,17					
112	24	0,13					
115	27	0,68					
116	27	0,73					
119	29	1,1					

Mean	Standard deviation	Relative standard deviation	Median
24	2,4	10	23

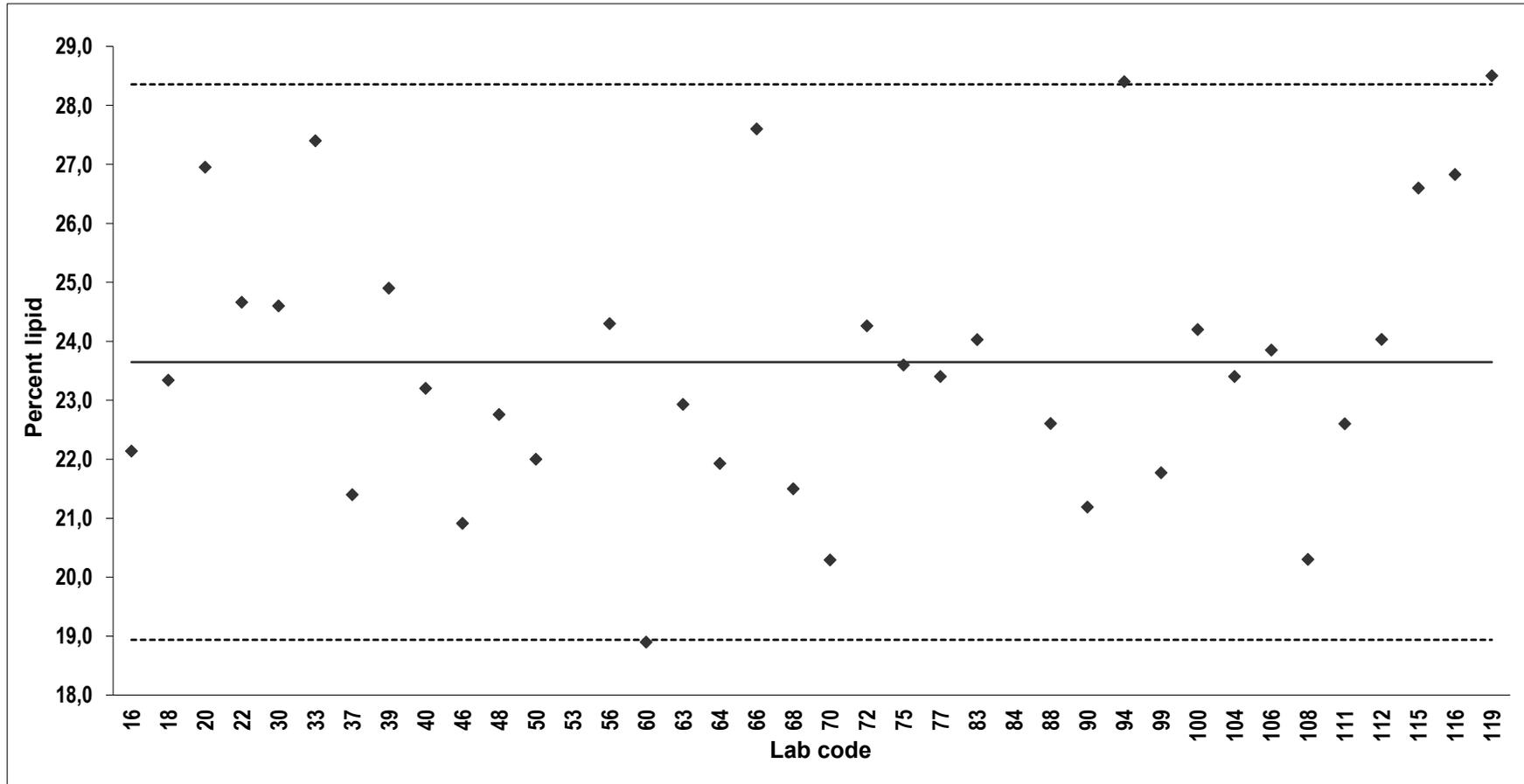
### Lipid determination; Mackerel



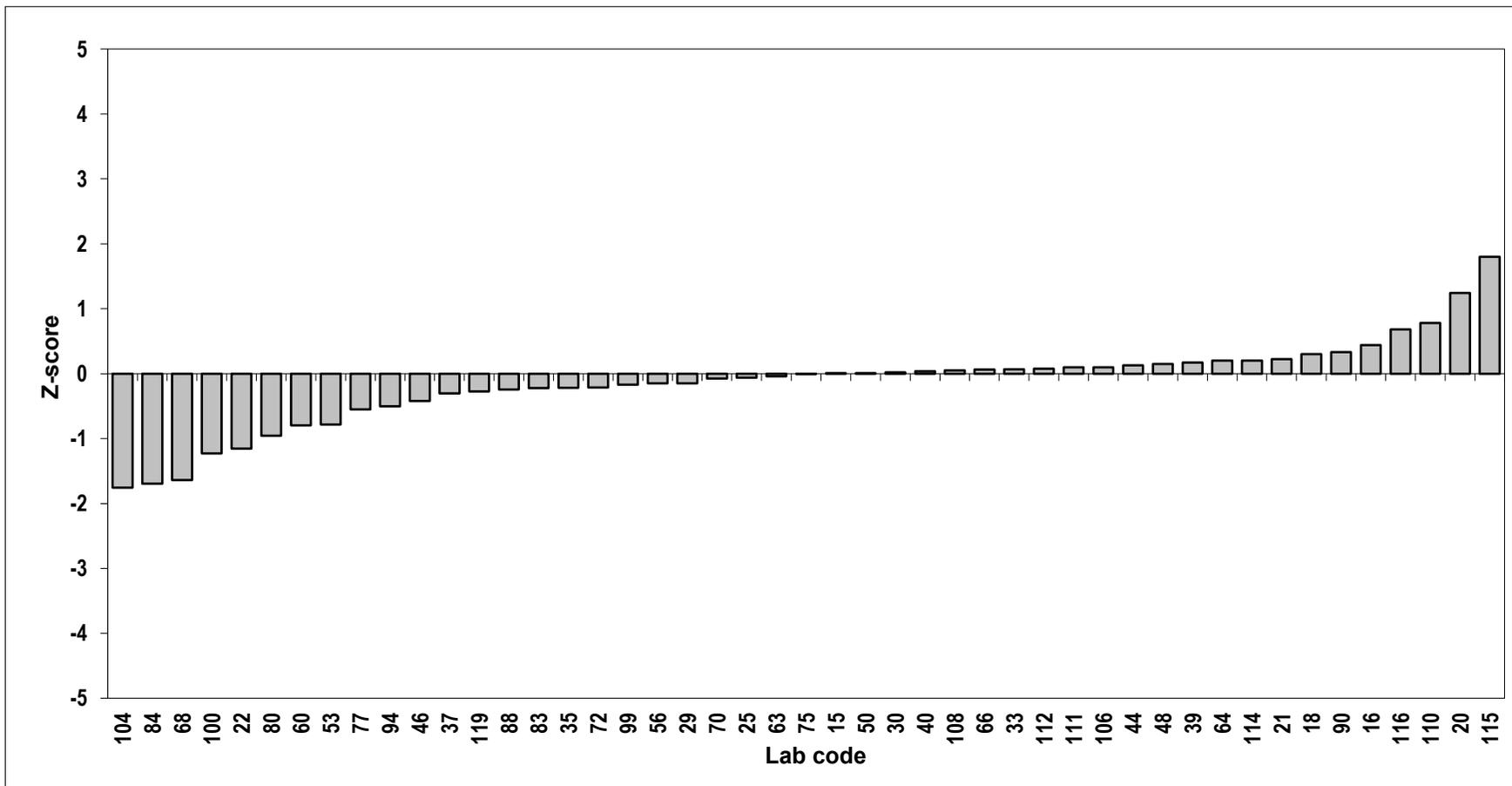
# Lipid determination; Cream



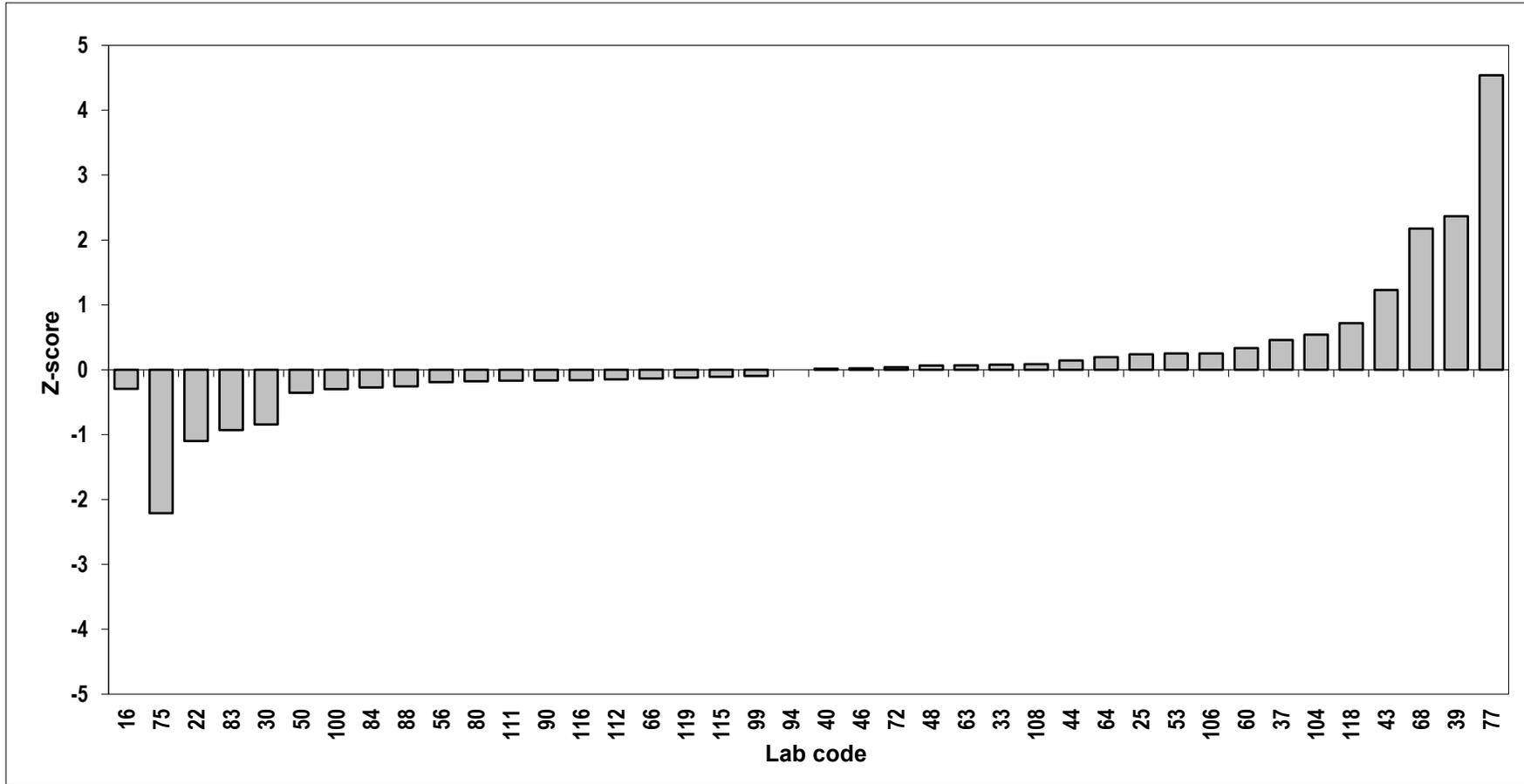
# Lipid determination; Egg yolk



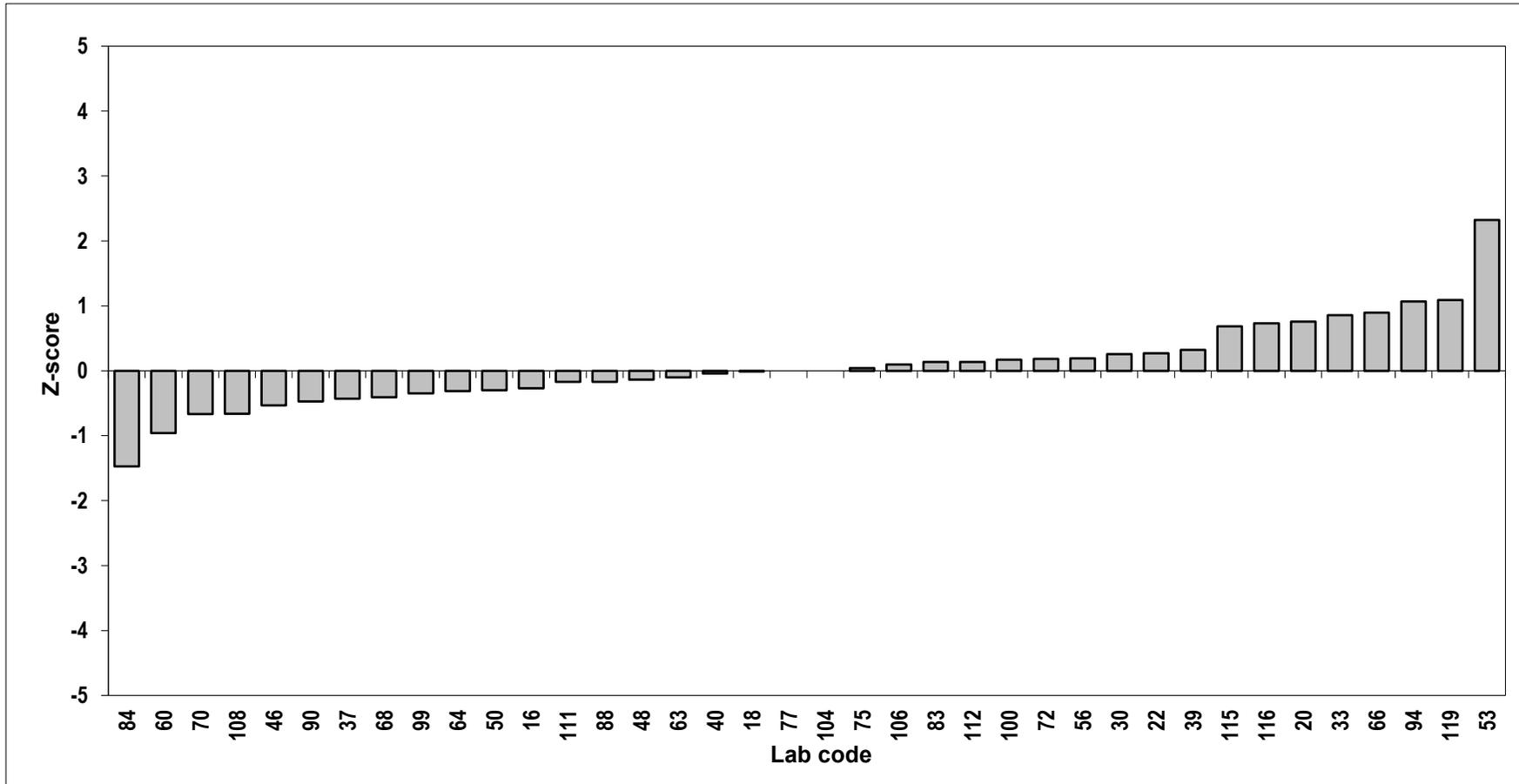
### Z-score lipid determination; Mackerel



### Z-score lipid determination; Cream



### Z-score lipid determination; Egg yolk





Published by the Norwegian Institute of Public Health  
December 2024  
PO Box 222 Skøyen  
N-0213 Oslo  
Tel.: (+47) 21 07 70 00  
The report can be downloaded as a pdf at [www.fhi.no](http://www.fhi.no)