How to read the results

Results of Fish oil, Salmon and Lamb for PCDDs, PCDFs and dioxin-like PCBs

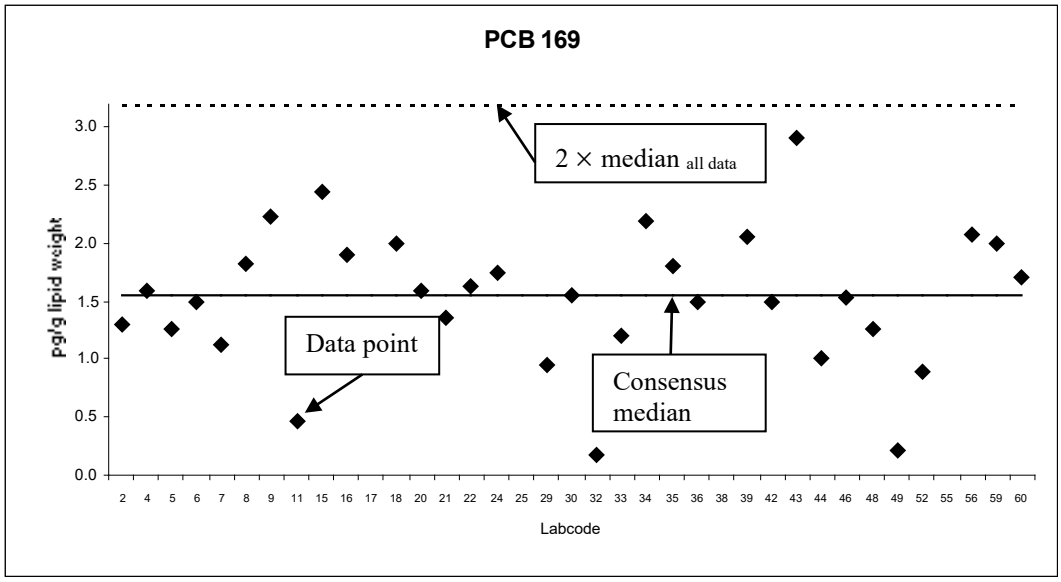
For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. Congener-by-congener medians were calculated from the data reported by all laboratories using the reported detection limit as the concentrations for non-detected congeners (NDs).

2. Values exceeding twice the calculated medians were then 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.

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



Z-Scores of individual congeners

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

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

where x = reported value, X = assigned value (consensus median), σ = target value for standard deviation. A σ-value of 0.2 was chosen, i.e. Z-scores of +1 and -1 reflect deviations of 20 % from the consensus value.

Results of Fish oil, Salmon and Lamb for PBDEs, indicator PCBs and HBCD

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

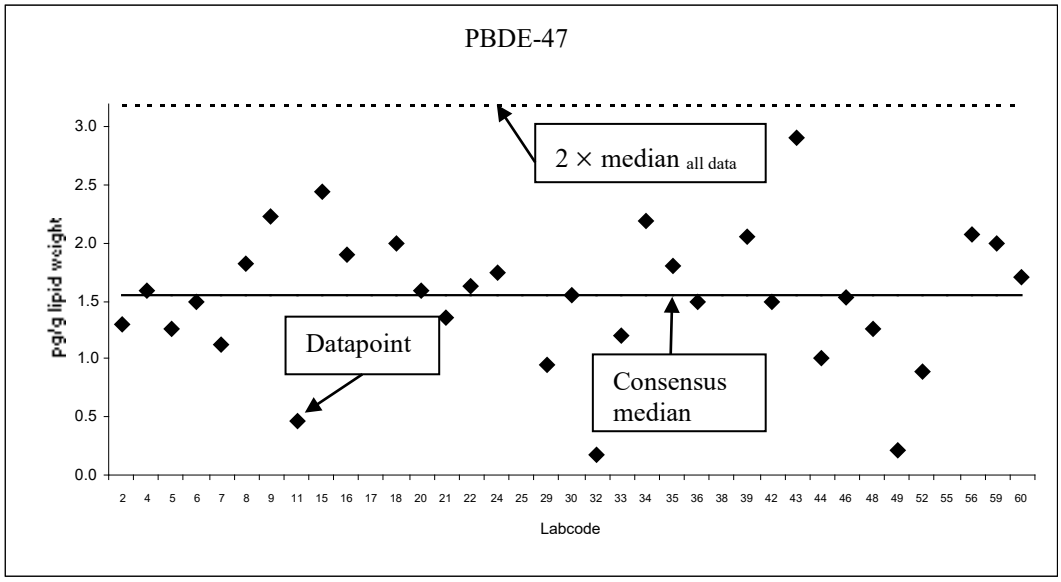
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).

2. Values exceeding two 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 × 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 median); σ = target value for standard deviation. A σ-value of 0.2 was chosen, i.e. Z-scores of +1 and -1 reflect deviations of 20% from the consensus value.

Analyte solution

The analyte solution contained

- PCDDs/PCDFs at concentrations 2:5:10 pg/µl for tetra:penta-hexa-hepta:octa chlorinated dibenzodioxins/furans respectively
- non-ortho PCBs at concentration 10 pg/µl
- mono-ortho PCBs at concentration 100 pg/µl
- indicator PCBs at concentration 100 pg/µl
- PBDE at concentration 25 pg/µl, except BDE-209 at 100 pg/µl
- α-HBCD at concentration 500 pg/µl

These concentrations are called the congeners' target value.

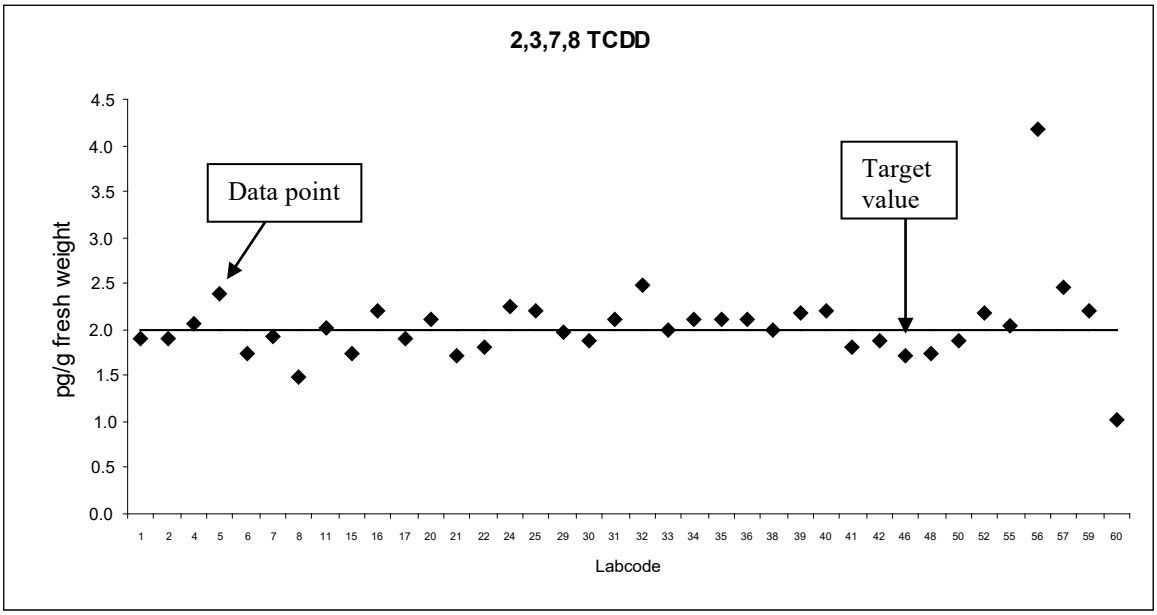
For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. The median was calculated from all the reported data.

2. Values outside a range of 50 % to 150 % of this median, were defined as outliers and removed from the data set.

3. Median, mean and standard deviation were re-calculated from the remaining data. This median and mean were called consensus median and mean.

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



Presentation of results for lipid determination

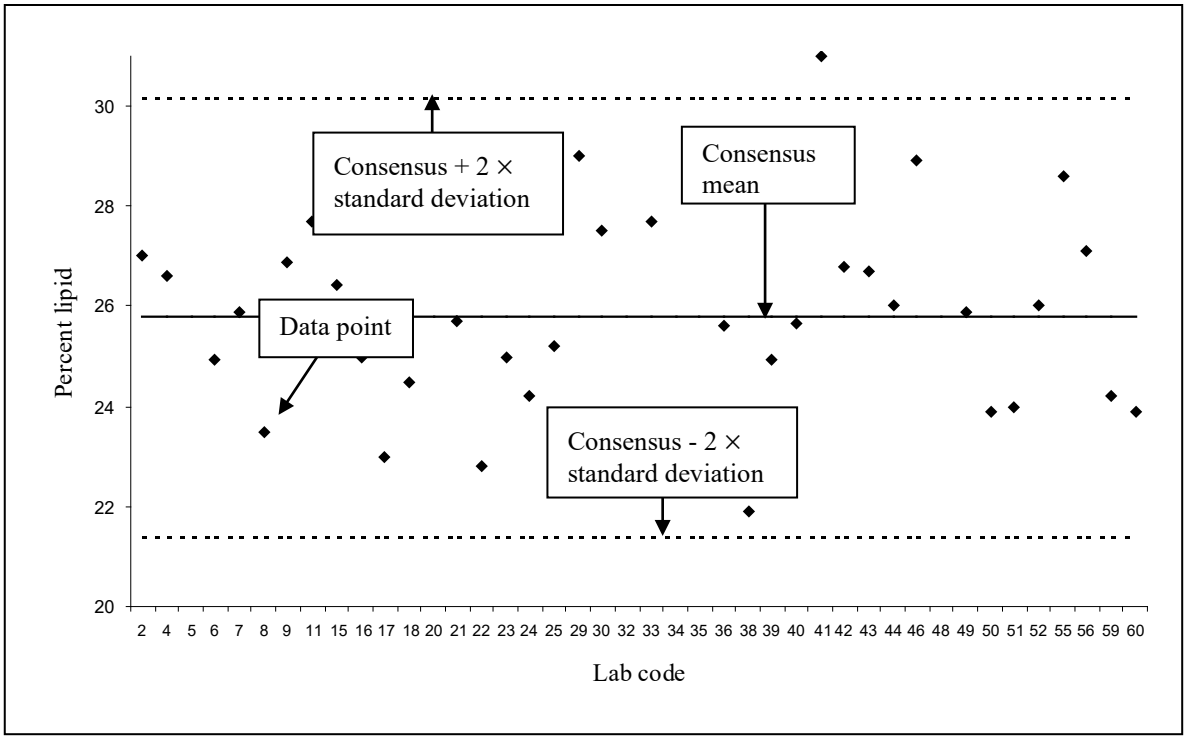
Removal of outliers and calculation of consensus were done by the following procedure:

1. The mean was calculated from all the reported data.

2. Values outside a range of ± 2 × 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 ± the new standard deviation × 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 mean); σ = target value for standard deviation. A σ-value of 0.2 was chosen, i.e. Z-scores of +1 and -1 reflect deviations of 20% from the consensus value.

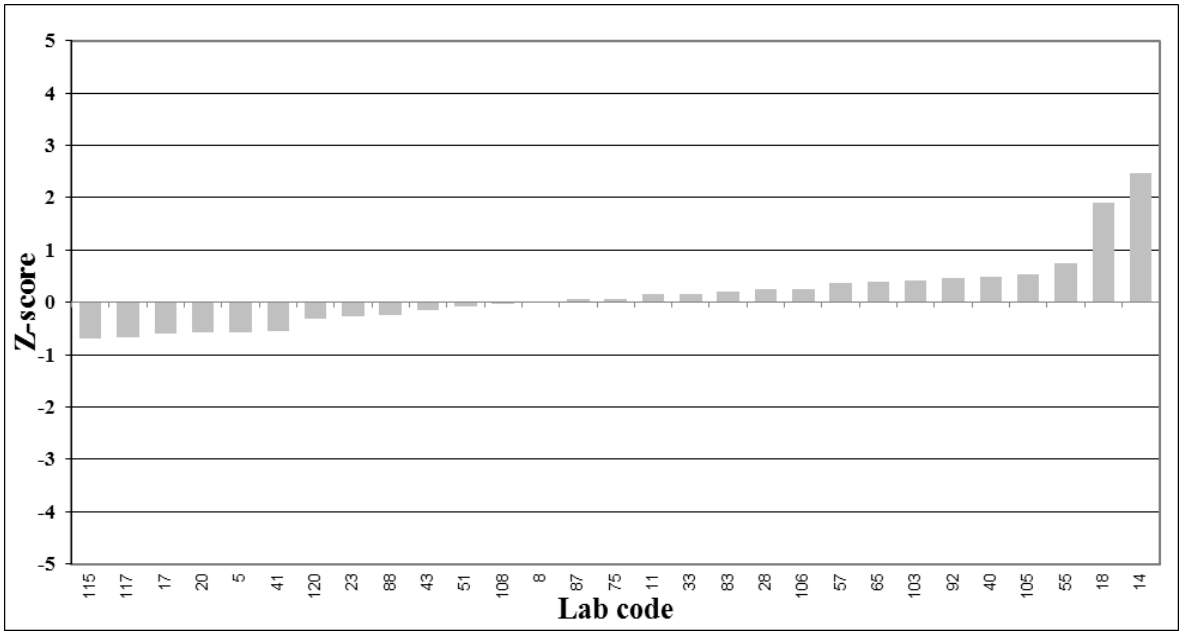
Z-Scores of TEQ, sum indicator PCB and sum PBDE without BDE 209

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

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

where x = reported value; X = assigned value (consensus median); σ = target value for standard deviation. A σ-value of 0.2 was chosen, i.e. Z-scores of +1 and -1 reflect deviations of 20% from the consensus value.

Z score plot:



Results Halibut for PFAS 2025

For PFAS we have used the same approach as we did for PBDEs, indicator PCBs and HBCDs when calculating the results. For each congener, the outliers were removed and the consensus calculated according to the following procedure:

4. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).

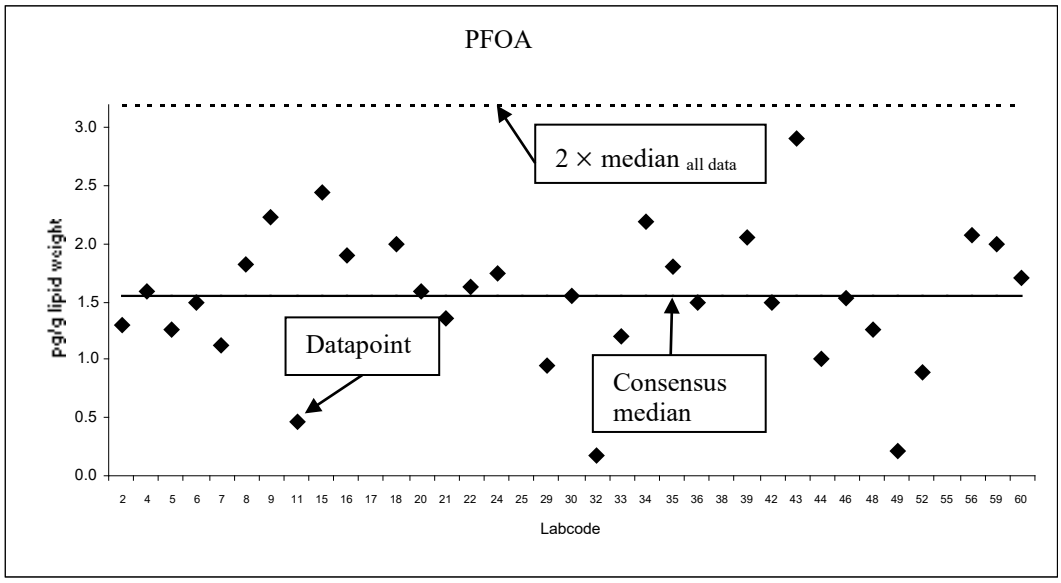
5. Values exceeding two times this median were defined as outliers and removed from the data set. The NDs were also removed.

6. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

5. For comparison, median, mean and standard deviation were also calculated without removing NDs.

6. As the set of data was considerably smaller than the other set of data, we have also chosen to define a very low reported value as outlier, and thus removed this value before calculating the consensus values

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



Z-Scores of individual congeners

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

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

where x = reported value; X = assigned value (consensus median); σ = target value for standard deviation. A σ-value of 0.2 was chosen, i.e. Z-scores of +1 and -1 reflect deviations of 20% from the consensus value.