SUPPORTING INFORMATION TO

Consistenty in trophic magnification factors of cyclic methyl siloxanes in pelagic freshwater food webs leading to brown trout

Katrine Borgå[1]*, Eirik Fjeld[1], Amelie Kierkegaard[2], Michael S. McLachlan[2]

[1] Norwegian Institute for Water Research (NIVA), Gaustadallèen 21, N-0349 Oslo, Norway
[2] Department of Applied Environmental Science (ITM), Stockholm University, SE-106 91 Stockholm, Sweden.

Corresponding author: katrine.borga@niva.no

CHAPTERs

FIGURES

TABLES

S1. Lake description

The lakes included in this study (Lake Mjøsa, Lake Randsfjorden and Lake Femunden) (Table S1, Figure S1), are deep lakes with a well-defined pelagic food web leading to brown trout (*Salma trutta*) as the top predator. According to dietary information available, trout feed predominantly on smaller smelt (*Osmerus eperlanus*) and some vendace (*Coregonus albula*)[1]. Smelt feed predominantly on Mysis and zooplankton (*Daphina galeata* and *Limnocalanus macrurus*)[2] with an increased degree of cannibalism when the fish are larger than 10 cm[3]. Vendace feed on zooplankton (*D. galeata* and *L. macrurus*)[4]. Among the invertebrates, Mysis feed predominantly on water fleas (e.g. *D. galeata*)[5], whereas *D. galeata* (epilimnic cladoceran) feed predominantly on algae[6], and *L. macrurus* (hypolimnic calanoid copepod) is omnivorous, feeding on algae and zooplankton[7]. In Randsfjorden and Femunden, also arctic char (*Salvelinus alpinus*) is a as top predators, with whitefish (*Coregonus lavaretus*) and smelt as planktivorous prey.

Table S1. Information on lakes included in the present study.

Lake	Mjøsa	Randsfjorden	Femunden
Coordinates	60°53′N 10°41E	60°23′N 10°23′E	62°21′N 11°57′E
Length (km)	117	75	60
Volume (km^3)	65	7,3	6
Area (km^2)	362	134	203
Maximum depth (m)	453	120	153
Person equivalents[a]	206000	28500	200

[a] Estimated from maps with pollution load (person equivalents) and wastewater treatment plants for the different regions

S2. Sampling description

In Mjøsa, zooplankton from the epilimnion (Cladocerans *Daphnia galeata, Bosmina longispina*) and hypolimnion (Copepods *Limnocalanus macrurus*), *Mysis relicta*, vendace, and smelt were collected mid-lake south of Helgøya, while trout were collected close to Gjøvik. In Randsfjorden, zooplankton from the epilimnion (*D. galeata,* Copepods *Eudiaptomus gracilis*) and hypolimnion (*D. galeata* and Copepods *L. macrurus, Heterocope appendiculata*), whitefish, smelt and trout were collected mid-lake, south of Brandbu. In Femunden, Arctic char and trout were collected in the southern basin (Figure S1, Table S2).

Zooplankton from the epilimnion and from the hypolimnion were collected by horizontal trawling at separate depths above and below the thermocline (zooplankton net 250 µm Nylon single strand, custom made at NIVA, with brass cup and brass mesh). In Mjøsa, *Mysis relicta* was picked with tweezers from the hypolimnion trawls. Mysis and zooplankton samples for contaminant analysis were kept in preheated glass jars, and material for stable isotopes was wrapped in aluminum foil. Some of the zooplankton material was difficult to concentrate (i.e. filter off all water), and thus some samples contained more water, leading to a higher estimate of water content (Table S3).

In Lake Mjøsa, vendace and small smelt were collected with gill nets in the surface waters. In Randsfjorden, smelt were collected with gill nets in the surface waters, and whitefish were collected from large traps used for commercial fishing. Brown trout from Mjøsa and

Randsfjorden, and arctic char from Femunden, were fished by angling by local fishermen according to a specific protocol and following instruction by NIVA staff. In Femunden, whitefish and brown trout were collected with pelagic gill nets by local fishermen according to a specific protocol and following instruction by NIVA staff. Only brown trout larger than 30 cm were included to ensure fish-feeding specimens.

Each sample of fish consisted of skinless filets from one individual fish, with the exception of small smelt from Mjøsa and Randsfjorden, where 5-6 skinless filets were pooled. Brown trout from Mjøsa were stored frozen whole until sample preparation (dissection of skinless filet) at NIVA, whereas fish from Femunden and Randsfjorden were dissected fresh. The dissected samples were stored frozen in preheated glass jars.

Precleaned field blanks (passive samplers: polyester pouches containing ~60 mg ENV+) were exposed to air and handled in the same manner as the biotic samples, as described previously[8]. After exposure the field blanks were wrapped in aluminum foil and kept frozen in sealed PE bags until analysis.

To reduce the risk of contamination during sampling, all sample preparation was conducted outdoors, i.e., the material was outdoors from the time of sampling until it was freezer-ready for storage until shipment to the Department of Applied Environmental Science (ITM, Stockholm University, Sweden) and analysis of cVMS in October-November 2012. NIVA personnel and the local fishermen who helped with sampling avoided personal care products at least 24 h prior to field work. All large surfaces (e.g. tubs for gill nets, gill nets after retrieval before the fish were collected, the chopping board for sample preparation and fish dissection) were covered in aluminium foil. All sampling equipment in contact with any sampling matrix was cleaned with solvents (acetone/methanol) between samples. Contact with plastics was avoided. The samples were only in contact with clean utensils of stainless steel (tweezers, knife, scalpel). The samples were stored in pre-heated glass jars sealed with aluminium foil under the lid. All samples were stored frozen until chemical analysis.

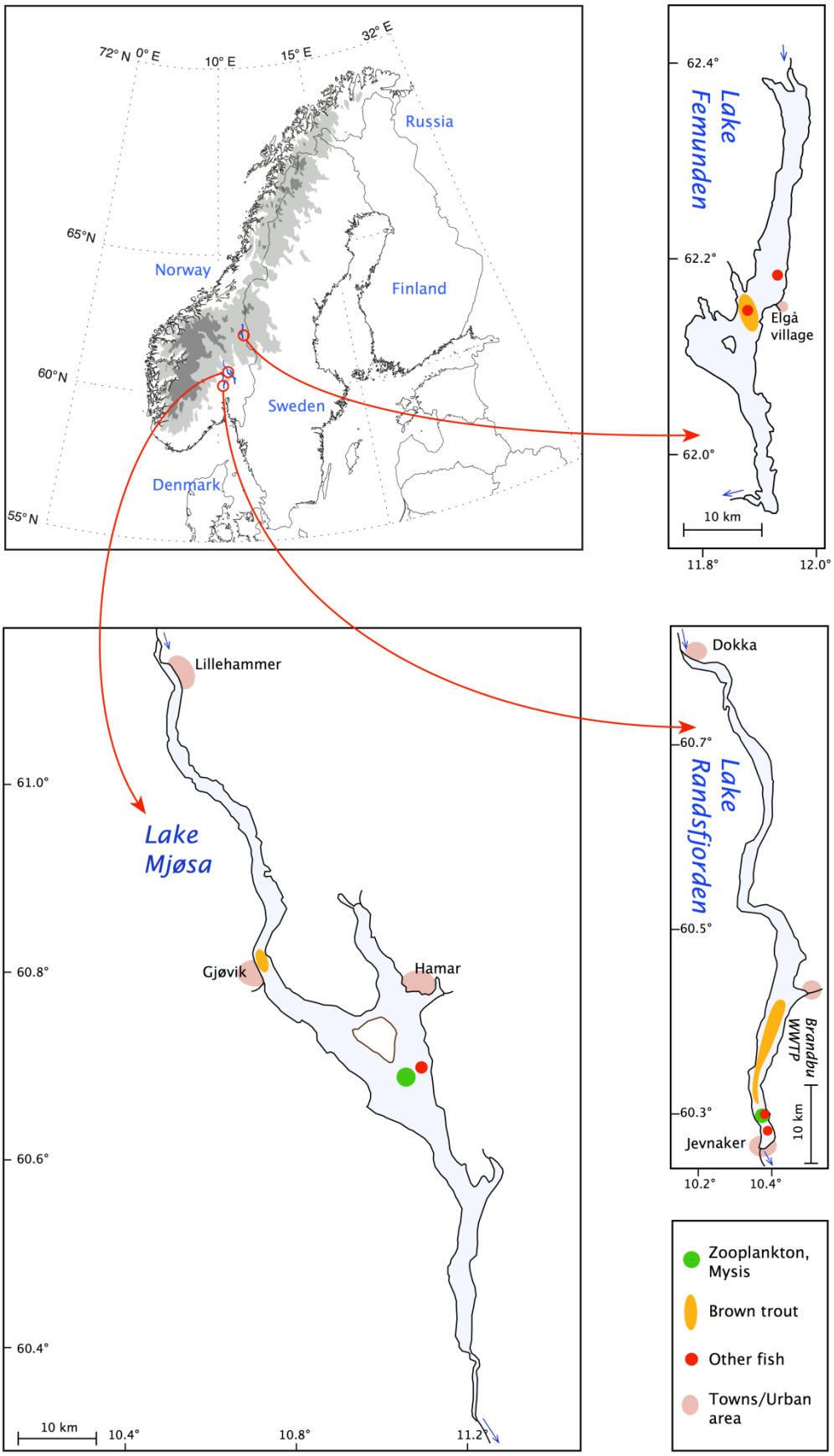

Figure S1. Map of Lake Mjøsa, Lake Randsfjorden, and Lake Femunden with sampling sites, major urban areas and waste water treatment plants.

Table S2. Sampling information from Lake Mjøsa, Lake Randsfjorden and Lake Femunden in 2012.

Vial ID	Species	Tissue/Matrix	Date	Notes
MJØSA				
S-1	Mysis	whole body, pooled ind.	2 Aug.	Gillundstranda
S-2	Mysis	whole body, pooled ind.	2 Aug.	Gillundstranda
S-3	Mysis	whole body, pooled ind.	2 Aug.	Gillundstranda
S-4	Zooplankton hypo	whole body, pooled ind.	2 Aug.	Gillundstranda
S-5	Zooplankton hypo	whole body, pooled ind.	2 Aug.	Gillundstranda
S-6	Zooplankton hypo	whole body, pooled ind.	2 Aug.	Gillundstranda
S-7	Zooplankton hypo	whole body, pooled ind.	2 Aug.	Gillundstranda
S-8	Zooplankton hypo	whole body, pooled ind.	2 Aug.	Gillundstranda
S-9	Zooplankton epi	whole body, pooled ind.	3 Aug.	Gillundstranda
S-10	Zooplankton epi	whole body, pooled ind.	3 Aug.	Gillundstranda
S-11	Zooplankton epi	whole body, pooled ind.	3 Aug.	Gillundstranda
S-12	Zooplankton epi	whole body, pooled ind.	3 Aug.	Gillundstranda
S-13	Zooplankton epi	whole body, pooled ind.	3 Aug.	Gillundstranda
B-1	Mysis	whole body, pooled ind.	21 Aug.	Gillundstranda
B-2	Zooplankton hypo	whole body, pooled ind.	21 Aug.	Gillundstranda
B-3	Mysis	whole body, pooled ind.	21 Aug.	Gillundstranda
B-4	Zooplankton hypo	whole body, pooled ind.	21 Aug.	Gillundstranda
B-5	Zooplankton epi	whole body, pooled ind.	21 Aug.	Gillundstranda
M-14	Mysis-1	whole body, pooled ind.	6 July	Gillundstranda
L-1	Vendace	skin free filet	3 July	Gillundstranda
L-2	Vendace	skin free filet	3 July	Gillundstranda
L-3	Vendace	skin free filet	3 July	Gillundstranda
L-4	Vendace	skin free filet	3 July	Gillundstranda
L-6	Vendace	skin free filet	3 July	Gillundstranda
L-7	Vendace	skin free filet	3 July	Gillundstranda
L-8	Vendace	skin free filet	3 July	Gillundstranda
K-1	Smelt	skin free filet, homogenate 6 ind.	6 July	Gillundstranda

K-2	Smelt	skin free filet, homogenate 6 ind.	6 July	Gillundstranda
K-3	Smelt	skin free filet, homogenate 6 ind.	6 July	Gillundstranda
K-4	Smelt	skin free filet, homogenate 6 ind.	6 July	Gillundstranda
K-5	Smelt	skin free filet, homogenate 6 ind.	6 July	Gillundstranda
K-7	Smelt	skin free filet	7 Sept.	Ottestad
K-8	Smelt	skin free filet	7 Sept.	Ottestad
K-9	Smelt	skin free filet	13 Sept.	Ottestad
K-10	Smelt	skin free filet	13 Sept.	Ottestad
K-11	Smelt	skin free filet	13 Sept.	Ottestad
MS-1	Whitefish	skin free filet	3 July	Gillundstranda
MS-2	Whitefish	skin free filet	3 July	Gillundstranda
MS-3	Whitefish	skin free filet	3 July	Gillundstranda
MS-4	Whitefish	skin free filet	3 July	Gillundstranda
MS-6	Whitefish	skin free filet	3 July	Gillundstranda
MT-1	Brown trout	skin free filet	29 Aug.	Gjøvik
MT-2	Brown trout	skin free filet	29 Aug.	Gjøvik
MT-3	Brown trout	skin free filet	29 Aug.	Gjøvik
MT-4	Brown trout	skin free filet	29 Aug.	Gjøvik
MT-5	Brown trout	skin free filet	29 Aug.	Gjøvik
RANDSFJORDEN				
R1	zooplankton epi	whole body, pooled ind.	27-29 Aug.	
R3	zooplankton epi	whole body, pooled ind.	27-29 Aug.	
R4	zooplankton epi	whole body, pooled ind.	27-29 Aug.	
R5	zooplankton epi	whole body, pooled ind.	27-29 Aug.	
R6	zooplankton hypo	whole body, pooled ind.	27-29 Aug.	
R7	zooplankton hypo	whole body, pooled ind.	27-29 Aug.	
R8	zooplankton hypo	whole body, pooled ind.	27-29 Aug.	
R9	zooplankton hypo	whole body, pooled ind.	27-29 Aug.	
R11	Smelt	skin free filet	27-29 Aug.	
R12	Smelt	skin free filet	27-29 Aug.	
R14	Smelt	skin free filet	27-29 Aug.	

R15	Smelt	skin free filet	27-29 Aug.
R16	Smelt	skin free filet	27-29 Aug.
R17	Whitefish	skin free filet	27-29 Aug.
R18	Whitefish	skin free filet	27-29 Aug.
R19	Whitefish	skin free filet	27-29 Aug.
R20	Whitefish	skin free filet	27-29 Aug.
R21	Whitefish	skin free filet	27-29 Aug.
R22	Whitefish	skin free filet	27-29 Aug.
R23	Whitefish	skin free filet	27-29 Aug.
R24	Whitefish	skin free filet	27-29 Aug.
R25	Whitefish	skin free filet	27-29 Aug.
R36	Brown trout	skin free filet	27-29 Aug.
R37	Brown trout	skin free filet	27-29 Aug.
R38	Brown trout	skin free filet	27-29 Aug.
R39	Brown trout	skin free filet	27-29 Aug.
R40	Brown trout	skin free filet	27-29 Aug.
FEMUNDEN			
F19	Arctic char	skin free filet	8-9 Aug.
F26	Brown trout	skin free filet	8-9 Aug.
F27	Brown trout	skin free filet	8-9 Aug.
F28	Brown trout	skin free filet	8-9 Aug.
F29	Brown trout	skin free filet	8-9 Aug.
F30	Brown trout	skin free filet	8-9 Aug.
F31	Brown trout	skin free filet	8-9 Aug.

Table S3. Water content and lipid content of zooplankton samples.

Species	Vial ID	Sample weight (g)	Dry weight %	Lipid %
MJØSA				
Zooplankton epilimnion	S-13	5.2	6.2	0.76
Zooplankton epilimnion	B-5	54.7	4.9	0.59
Zooplankton hypolimnion	B-2	16.8	13	6.2
Zooplankton hypolimnion	S-8	5.8	5.7	1.3
Zooplankton hypolimnion	B-4	24.4	14	7.4
Mysis relicta	S-3	2.4	11	2.1
Mysis relicta	B-1	18.2	13	3.4
Mysis relicta	B-3	21.0	13	4.1
Mysis relicta	M-14	7.3	6.6	0.99
RANDSFJORDEN				
Zooplankton epilimnion	R1	27.0	6.0	0.76
Zooplankton epilimnion	R3	44.0	4.8	0.67
Zooplankton epilimnion	R4	19.9	6.75	0.80
Zooplankton epilimnion	R5	33.1	6.0	0.67
Zooplankton hypolimnion	R6	13.3	2.4	0.73
Zooplankton hypolimnion	R7	16.0	3.6	1.85
Zooplankton hypolimnion	R8	27.2	1.28	0.23
Zooplankton hypolimnion	R9	29.7	4.33	2.37

S3. Chemical analyses

cVMS analysis - Method Description

Fish. About 10 g of tissue (1 g for three of the fish liver samples) was weighed into 50 mL centrifuge tubes. After addition of 20 mL of dichloromethane (DCM) (Lichrosolve, Merck, Germany) and 60 µL of the surrogate standard solution (containing ^{13}C labelled D4, D5, and D6), the tubes were closed with aluminium foil under the lid and left to stand overnight in the clean air cabinet. The tissue was homogenized with an ultra turrax and centrifuged for 10 min at 2200 rpm. This resulted in 3 phases, with DCM at the bottom, fish homogenate in the middle, and water on the top. The water phase was decanted and discarded. The homogenate was punctured and the DCM extract was transferred to a 250 mL Erlenmeyer flask containing 16-21 g of glass beads (diameter 4 mm, Marienfeld, Germany) and a magnetic stir bar. For the procedural blanks, 75-200 mg of corn oil was also added to simulate the sample matrix. A gas washing bottle stopper was placed on the flask. The inlet port of the stopper was connected to a nitrogen gas supply, which was equipped with purification cartridges containing ENV+ to remove any traces of cVMS. The outlet port of the stopper was connected to a sorbent cartridge. The 1 mL plastic cartridges were manually filled with 10-15 mg of Isolute ENV+ packed between 2 PE frits (all from Biotage AB, Sweden). After the first 4 extractions the PE frits were identified as a source of D6 contamination. The frits were from that point on stored in DCM and repeatedly ultrasonicated and rinsed with DCM prior to use and the lower frit was replaced with glass wool. The clean-up of the extract was started by turning on the magnetic stirrer and purging the flask with N_2 at a flow rate of 200-300 mL/min until the solvent was fully evaporated (2.5-3 h). Then the heating element of the

magnetic stirrer (5 positions, IKAMAG, Germany) was set to maximum, giving a flask wall temperature of ~72 °C, and purging was continued for a further 2 h. The sorbent cartridge was removed and eluted with 0.8 mL hexane. Tetrakis(trimethylsiloxy)silane, M4Q, was added as a volumetric standard, and the cVMS were analysed by GC/MS as described in Kierkegaard et al.[9].

Zooplankton and Mysis. Sub-samples were transferred from the sample jar to two 50 mL centrifuge tubes using a spoon, stirring the sample jar between each spoonful, and alternating between centrifuge tubes. Surrogate standard solution and 20 mL of DCM were added and the tubes were ultrasonicated for 2*15 min, mixing the tubes between the sonications. The tubes were centrifuged, the water discarded, and the DCM transferred to Erlenmeyer flasks. The extraction was then repeated with another 15 mL of DCM. The extracts were cleaned up and analysed in the same manner as the fish samples.

Field blanks. The pouches were transferred to a glass tube. 1.5 mL of n-hexane and the surrogate standard solution were added. The tube was mixed with a vortex mixer for about 15 s. The n-hexane was transferred to a GC vial and analysed.

Method Evaluation and QA/QC

cVMS formation. It has previously been shown that D5 can be transformed into D4 and D3 during sampling out of the gas phase onto ENV+ [10]. To test whether this was occurring, two blank samples with 100 mg of corn oil were analysed in which the surrogate standard solution of ^{13}C labelled D4, D5 and D6 was replaced with a single ^{13}C labelled cVMS: ^{13}C-D5 for one of the blank samples and ^{13}C-D6 for the other. After these standards were added to the extraction solvent and submitted to the sample clean-up, they were quantified against the volumetric standard M4Q. The results showed that there was a high recovery of the labelled D5 and D6 and no evidence for the formation of ^{13}C labelled D4, D5, or D6 during the sample clean-up procedure (Table S4).

Table S4. Concentrations* of 13C labelled cVMS in standards of 13C labelled D5 and D6 before and after having been submitted to the clean-up procedure.

	^{13}CD4	^{13}CD5	^{13}CD6
^{13}CD5 before clean-up	0.002	1.025	0.000
^{13}CD5 after clean-up	0.001	0.916	0.000
^{13}CD6 before clean-up	0.003	0.002	0.330
^{13}CD6 after clean-up	0.003	0.002	0.310

*Concentration approximated as the peak area of the analyte normalized to that of the volumetric standard (M4Q).

Extraction efficiency. Extraction efficiency was assessed in two manners. First the effect of extending the second (heated) phase of the purge and trap clean-up was studied. Two smelt samples were extracted and subjected to the clean-up. However, instead of using one ENV+ cartridge on the outlet of the Erlenmeyer flask, the cartridge was exchanged, first after the end of the solvent evaporation phase, and then at intervals of 30 min, 40 min, 60 min and 30 min during the heating phase. The recovery of the surrogate standards was quantified in each of the samples. The results showed that no further cVMS were transferred from the extract to the cartridge after the solvent evaporation phase plus 70 min of the heating phase (see Figure S2). On the basis of these results we chose a 2 h duration for the heating phase as more than sufficient to transfer all of the cVMS from the extract.

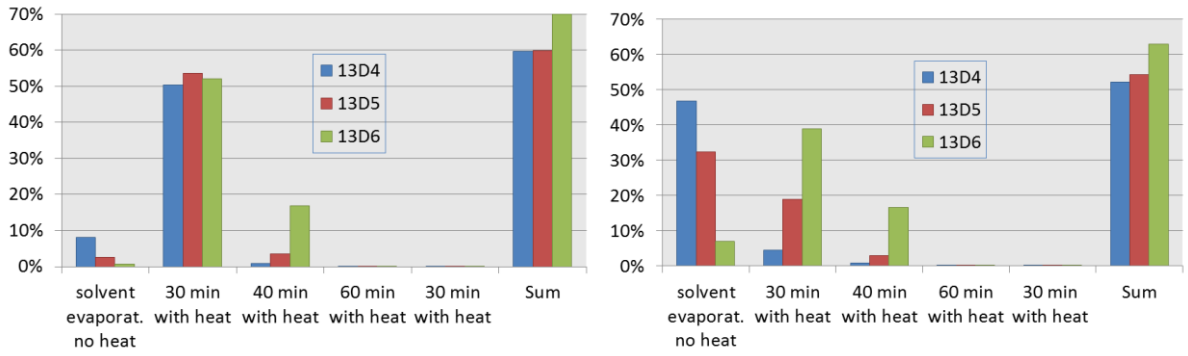

Figure S2. Recovery of the surrogate standards from 2 smelt samples for which 5 sorbent cartridges were deployed sequentially during the purge and trap clean-up

The second test of the extraction efficiency was to re-extract 8 biota samples. The same extraction method was applied, and a second batch of surrogate standard was added to the solvent used for re-extraction. The results showed that the second extract contained of the order of 10-20 % of quantity of D5 present in the initial extract (Table S5, the results for D4 and D6 are not shown due to the low levels present in the second extract). A zooplankton sample showed higher values (37%), and was attributed to the high water content of the sample, and it was thus decided to extract all zooplankton and mysis samples twice. The extraction efficiency of 80-90% for the other samples was judged sufficient. Note that the percent underestimation of the concentrations due to incomplete extraction is likely to be lower than suggested by the extraction efficiencies estimated here because the extraction efficiency of the surrogate standard was also incomplete, e.g. due to residual solvent in the extracted matrix. If the extraction efficiency of the surrogate standard and the native compound were the same, then there would be no error in the measured concentration.

Table S5. Quotient of D5 in the second and first extracts.

Sample	Extract 2/Extract 1 (D5, in %)
Zooplankton epilimnion	37
Mysis	18
Smelt	10

Recovery. The recovery of the ^{13}C labelled D4, D5, and D6 surrogate standards was determined for each sample. High and consistent recoveries were observed for all analytes in almost all matrices (Table S6). The recoveries were higher in the zooplankton and Mysis samples than in the fish samples, which could be due to the fact that the former were extracted twice while the fish samples were extracted once.

Table S6. Recovery of cVMS surrogate standards from the analysed samples (mean ± std dev in %).

Matrix	*N*	^{13}CD4	^{13}CD5	^{13}CD6
Zooplankton/Mysis	19	81±8	81±7	86±14
Fish	85	72±13	71±13	74±13

Repeatability. The repeatability of the method was assessed using the matrix control samples analysed during each round of extractions. The relative standard deviation (RSD) was between 8% and 11% for D5 and D6 (Table S7). This is a good result, particularly in light of

the low D5 and D6 concentrations in these samples. The RSD was higher for D4, which can be attributed to the very low levels in the matrix control samples (a factor of 2 above the LOQ for herring).

Table S7. Results of the analyses of the matrix control samples.

	D4	D5	D6
Herring (ng/g ww)			
N	13	14	14
Mean	0.9	6.8	2.3
standard deviation	0.3	0.7	0.2
RSD	32%	10%	11%

Accuracy. Due to the absence of a certified standard reference material for trace analysis of cVMS, the accuracy was evaluated by comparing the method with existing methods for which accuracy information is available. The method of Kierkegaard et al.[11] for analysing cVMS in biota was shown to perform successfully in an inter-laboratory comparison. This method had also been used to analyse the herring homogenate matrix control sample used in this study. The means concentrations for D5 (6.0 ng/g ww, n=18) and D6 (1.7 ng/g ww, n=18) obtained with this method during the year prior to the development of the new method are in reasonable agreement with the values of 6.8 ng/g ww and 2.3 ng/g ww obtained with the new method (Table S8). The somewhat higher mean concentrations measured with the new method as well as the better repeatability (10 versus 23% and 11 versus 31% for D5 and D6, respectively) may be a reflection of better and more repeatable extraction with the new method.

Table S8. Limit of quantification (LOQ) based on mean procedural blanks + 10 x standards deviation (SD).

	D4			**D5**			**D6**[a]		
LOQ	mean ng	SD	LOQ, ng	mean ng	SD	LOQ, ng	mean ng	SD	LOQ, ng
Procedural blanks 1-4							4.9	0.8	**13**
Procedural blanks 5-20							1.0	0.4	**5.2**
Procedural blanks 1-20	0.50	0.41	**4.6**	0.42	0.22	**2.6**			

[a]*For D6 two LOQ were applied (the 4 first extraction rounds were contaminated from a source that was later identified)*

POP chemical analysis

Extraction Biological samples

The biota samples were homogenized and the internal standards PCB 30, 53, and 204 (Ultra Scientific) and PBDE 30, 119, and 181 (Cambridge isotope laboratories) were added. The samples were extracted twice with isopropanol:cyclohexane (50:50) followed by removal of isopropanol by addition of water. Solvents extracts were combined and water was added to yield an organic cyclohexane phase. The organic phase was separated from the aqueous phase

and the cyclohexane was evaporated under a gentle stream of nitrogen to obtain the total amount of fat extracted.

The proportion of fat or lipid in the samples was measured gravimetrically, with quantification results within the Quasimeme test programme (Table S9). The lipid was dried, weighed, transferred to smaller glassware where cyclohexane was added. Sulphuric acid (H_2SO_4) was added to digest excess fat. The acid was removed and replaced by fresh H_2SO_4. This procedure was repeated until the cyclohexane was remained colourless. Finally, the cyclohexane extract was evaporated under nitrogen and transferred to GC-vial for analysis. Extracts were split into different fractions for PCB/OC analysis and for PBDE analysis. The PBDEs fractions were further treated with an acetonitrile clean-up step prior to analysis.

PCB Quantification
Extracts were analysed on an Agilent 7890A gas chromatograph (GC) coupled to an Agilent 5975C mass spectrometer (Agilent JW Scientific, Santa Clara, USA). The instrument was operated in single ion monitoring (SIM) mode using electron impact ionization (69.9 eV). The GC was equipped with a 30 m Agilent DB-5 column (0.25 mm i.d. and 0.25 µm film thickness). Helium was used as the mobile phase and kept at constant flow of 1.2 ml/min. The GC-oven was kept at 60 °C for 2 min, raised to 250 °C at a rate of 7 °C/min and finally raised to 310 °C at a rate of 15 °C/min, where it remained for 2 min. Sample injection was 1 µl pulsed splitless injection at 20 psi for 1.2 min and the injector temperature was set to 300 °C. The transfer line, ion source and quadrupole were kept at 280, 230 and 150 °C, respectively. Quantification of individual compounds was done using the relative response of surrogate internal standard and comparing that to a calibration curve.

PBDE analysis
Determination of PBDEs was performed with a Hewlett Packard 6890Plus GC linked to a Hewlett Packard 5973 MS detector operated in negative chemical ionisation (with methane) and SIM mode. A 4 µL pulsed splitless injection (injector temperature of 280 °C and a pulse pressure of 50 psi held for 2 min) allowed transfer of analytes onto a DB-5MS column (Agilent Technologies Inc., 15 m, 0.25 mm i.d., 0.1 µm film thickness). The oven temperature was set to 120 °C. It was held for 2 min before being increased to 345 °C at 25 °C/min, and then held for 5 min. The carrier gas (He) flow was set to 1 mL min^{-1} for the first 13 min and increased to 1.4 mL min^{-1} at a rate of 0.1 mL min^{-1}. Ion source, quadrupole and transfer line temperatures were 250, 150 and 325 °C, respectively. Ion fragments m/z 79 and 81 were used for qualifying and quantifying PBDEs.

The analytical uncertainty was comparable to values for fish muscle reference material (Table S10).

Table S9. Lipid quantification results in the Quasimeme test programme. A Z-score ≤ |2| is acceptable.

Year	Sample	Assigned value	NIVA	Lipid
		% lipid	% lipid	Z-score
2007	R50: 92	14.044	17	0
	93	2.643	3	0.9
2008	R52: 94	57.49	58.1	0.1
	95	2.629	3.17	1.4
2010	R62:104	17.36	20	1.2
	105	2.705	3.1	1
2011	R64:106	11.82	10	-1.2
	107	3.22	3.2	0
2011	R66:108	57	49.7	-1
	109	4.079	3.9	-0.3
2012	R68:110	2.391	2.4	0
	111	3.19	3.2	0
2012	R70:112	2.08	2.14	0.2
	113	3.938	3.89	-0.1

Table S10. Analytical undertainty for fish muscle reference material HSD8.

	Average %	This study
HCB	40	<40
PCB 52	30	<30
PCB 101	26	<26
p,p-DDE	26	<26
PCB 118	26	<26
PCB 153	26	<26
PCB 105	26	<26
PCB 138	26	<26
PCB 156	26	<26
PCB 180	26	30
PCB 209	40	<40

S4. Results

Table S11. Percentage (%) of the samples in the pelagic food web of Mjøsa and Randsfjorden that were quantified below the limit of quantification (LOQ) for cyclic volatile methylsiloxanes (D4, D5, D6), or limit of detection (LOD) for PCBs, *p,p'*-DDE and PBDEs.

	Mjøsa	Randsfjorden (excluding/including whitefish)
D4	52	82 / 81
D5	0	0 /0
D6	13	61 / 54
PCB-153	0	0 /0
PCB-180	19	53 / 50
p,p'-DDE	0	0 /0
PBDE-47	0	N/A
PBDE-99	3	N/A

cVMS concentrations

Table S12. cVMS measured in A) Lake Mjøsa B) Lake Randsfjorden and C) Lake Femunden and their respective field blanks or reference material.

A) MJØSA

FIELD BLANKS (FB)	Identification	D4	D5	D6
		ng D4	**ng D5**	**ng D6**
Zooplankton FB-23	M-8a	0.4	0.6	0.1
Mysis FB-25	M-4a	2.7	1.8	0.8
Fish FB-18	MS-5. Gill net surface	3.2	2.5	1.2
Unexposed FBs(*mean of 3*)	FB28. 29. 5	1.6	1.1	1.2

Species	**Sample**	**ng D4**	**D4 ng/g ww**	**ng D5**	**D5 ng/g ww**	**ng D6**	**D6 ng/g ww**
Zooplankton epi	S9 + S10	< 1.8	< 0.2	17	2.3	< 2.5	< 0.3
Zooplankton epi	S11 + S12	< 1.9	< 0.2	20	2.4	< 3.0	< 0.4
Mysis	S1 + S2	6.1	1.8	49	14	< 4.9	< 1.4
Mysis	M-14	< 2.1	< 0.4	52	9.6	< 5.1	< 0.9
Zooplankton hypo	S4 + S5	< 3.2	< 0.5	89	15	< 4.0	< 0.7
Zooplankton hypo	S6 + S7	< 3.0	< 0.5	85	15	< 3.8	< 0.7
Zooplankton epi	B-5	12	0.5	55	2.4	7.9	0.3
Mysis	B-1	31	2.0	441	29	20	1.3
Mysis	B-3	10	1.1	491	50	16	1.6

Zooplankton hypo	B-2	35	2.4	2019	139	38	2.6
Zooplankton hypo	B-4	29	2	1953	156	35	2.8
Vendace	L-2	9.8	0.9	2083	196	119	11
Vendace	L-1	8.7	1.1	906	120	62	8.1
Vendace	L-3	7.5	1.0	2451	311	118	15
Vendace	L-4	6.8	1.1	830	134	46	7.4
Vendace	L-6	6.3	0.9	832	120	30	4.4
Vendace	L-7	6.1	0.8	1301	176	60	8.1
Vendace	L-8	< 4.5	< 0.6	593	76	55	7.0
Smelt. homogenate 6 ind.	K-1	< 2.1	< 0.2	394	36	16	1.5
Smelt. homogenate 6 ind.	K-2	< 2.3	< 0.2	373	34	19	1.7
Smelt. homogenate 6 ind.	K-3	< 2.1	< 0.2	331	32	16	1.6
Smelt. homogenate 6 ind.	K-4	< 3.6	< 0.3	457	39	24	2.1
Smelt. homogenate 6 ind.	K-5	< 3.1	< 0.3	374	39	23	2.4
Smelt	K-7	< 0.7	< 0.1	383	62	22	3.5
Smelt	K-8	< 0.4	< 0.1	243	38	13	2.0
Smelt	K-9	< 1.6	< 0.4	528	126	27	6.4
Smelt	K-10	< 1.1	< 0.2	313	59	25	4.7
Smelt	K-11	< 1.5	< 0.3	238	41	17	3.0
Brown trout	MT-1	5.3	0.8	1146	166	60	8.6
Brown trout	MT-2	6.1	0.8	1716	235	93	12.7
Brown trout	MT-3	< 4.3	< 0.6	1548	203	69	9.1
Brown trout	MT-4	< 2.7	< 0.4	804	131	38	6.1
Brown trout	MT-5	4.9	0.6	421	52	25	3.1

B) LAKE RANDSFJORDEN

FIELD BLANKS (FBs)	**SAMPLE**	**ng D4**	**ng D5**	**ng D6**
Zooplankton epi FB-20	R2	1.5	0.9	0.9
Fish whole procedure FB-21	R10	1.3	3.4	0.6
Smelt- sample preparation. FB-26	R13	2.1	3.9	1.9
Unexposed FBs(*mean of 3*)	FB28. 29. 5	1.6	1.1	1.2

SPECIES	**SAMPLE**	**ng D4**	**D4 ng/g ww**	**ng D5**	**D5ng/g ww**	**ng D6**	**D6 ng/g ww**
zooplankton epilimnion	R1	9.5	0.4	48	1.9	8.3	0.3

zooplankton epilimnion	R3	< 2.5	< 0.1	36	1.7	< 4.2	< 0.2
zooplankton epilimnion	R4	< 2.6	< 0.3	21	2.1	< 4.0	< 0.4
zooplankton epilimnion	R5	< 3.7	< 0.2	34	1.6	< 4.8	< 0.2
zooplankton hypolimnion	R6	< 2.3	< 0.4	83	16	< 2.7	< 0.5
zooplankton hypolimnion	R7	12	0.9	566	43	9.4	0.7
zooplankton hypolimnion	R8	< 1.4	< 0.1	40	3.0	< 1.9	< 0.1
zooplankton hypolimnion	R9	16	1.2	727	53	13	0.9
Whitefish	R17	< 2.4	< 0.2	16	1.2	< 3.2	< 0.2
Whitefish	R18	< 1.4	< 0.2	4.0	0.5	< 3.1	< 0.4
Whitefish	R19	< 2.3	< 0.2	37	3.3	< 4.5	< 0.4
Whitefish	R20	< 1.3	< 0.1	4.7	0.4	< 2.3	< 0.2
Whitefish	R21	< 0.8	< 0.1	2.8	0.2	< 1.9	< 0.2
Whitefish	R22	< 2.6	< 0.2	11	0.9	< 3.1	< 0.3
Whitefish	R23	< 1.3	< 0.1	6.5	0.6	< 2.4	< 0.2
Whitefish	R24	7.7	0.5	41	2.8	5.4	0.4
Whitefish	R25	< 2.8	< 0.3	13	1.3	< 3.6	< 0.4
Smelt	R11	< 1.8	< 0.2	131	15	8.7	1.0
Smelt	R12	< 2.4	< 0.3	169	20	10	1.2
Smelt	R14	< 1.8	< 0.2	129	16	11	1.4
Smelt	R15	< 1.4	< 0.1	324	25	10	0.8
Smelt	R16	< 1.9	< 0.2	201	18	11	1.0
Brown trout	R36	< 3.0	< 0.3	492	56	25	2.9
Brown trout	R37	< 0.7	< 0.1	81	9.9	< 8.5	< 1.1
Brown trout	R38	< 0.7	< 0.1	99	12	< 8.8	< 1.1
Brown trout	R39	9.6	0.9	1161	115	31	3.0
Brown trout	R40	< 2.0	< 0.2	422	41	17	1.6

C) LAKE FEMUNDEN

FIELD BLANK (FB) SAMPLE		ng D4	ng D5	ng D6
Fish FB-10	F18	1.7	1.3	1.0
Unexposed FBs (*mean of 3*)	FB28. 29. 5	1.6	1.1	1.2

SPECIES	**SAMPLE**	**ng D4**	**D4 ng/g ww**	**ng D5**	**D5 ng/g ww**	**ng D6**	**D6 ng/g ww**
Char	F19	< 0.9	< 0.1	< 2.3	< 0.2	< 4.7	< 0.4
Brown trout	F26	< 4.4	< 0.5	3.3	0.4	< 8.0	< 0.9
Brown trout	F27	< 3.4	< 0.3	2.9	0.3	< 4.2	< 0.4
Brown trout	F28	< 3.3	< 0.3	2.9	0.3	< 4.1	< 0.4
Brown trout	F29	< 1.7	< 0.1	< 1.4	< 0.1	< 5.9	< 0.5
Brown trout	F30	< 1.6	< 0.2	4.3	0.4	< 3.6	< 0.4
Brown trout	F31	< 2.7	< 0.2	4.0	0.4	< 4.0	< 0.4

Table S13. Trophic descriptors (stable isotopes of nitrogen $\delta^{15}N$ and carbon $\delta^{13}C$ (‰), lipid content and legacy POPs (ng/g lipid weight) in species from pelagic food webs of Norwegian Lakes in 2012 [a].

Species	Biometry	Length (cm)			Weight (g)			SI	$\delta^{13}C$[b]			$\delta^{15}N$			Trophic level		
	N	Mean		SE	Mean		SE	N	Mean		SE	Mean		SE	Mean		SE
MJØSA																	
Zooplankton Epilimnetic								4	-27.5	±	0.3	7.7	±	0.0	2.0	±	0.0
Zooplankton Hypolimnetic								5	-27.8	±	0.5	9.7	±	0.6	2.6	±	0.2
Mysis								5	-27.0	±	0.1	10.5	±	0.3	2.8	±	0.1
Vendace	7	22.0	±	0.2	68	±	2	7	-26.7	±	0.2	13.9	±	0.1	3.9	±	0.0
Smelt. Small	35	10.8	±	0.1	5.9	±	0.1	5	-26.1	±	0.1	13.5	±	0.2	3.8	±	0.1
Smelt. Large	5	20.5	±	1.1	49	±	9	5	-24.8	±	0.2	15.8	±	0.1	4.4	±	0.0
Brown trout	5	56.4	±	2.3	2050	±	310	5	-25.0	±	0.3	15.6	±	0.1	4.4	±	0.0
RANDSFJORDEN																	
Zooplankton Epilimnetic								4	-28.5	±	0.0	6.3	±	0.0	2.0	±	0.0
Zooplankton Hypolimnetic								3	-29.1	±	0.3	9.5	±	0.9	3.0	±	0.3
Whitefish	10	24.6	±	2.3	160	±	30	9	-25.7	±	1.1	10.4	±	0.2	3.2	±	0.1
Smelt	25	12.5	±	0.1	10.3	±	0.2	5	-27.7	±	0.0	11.3	±	0.2	3.5	±	0.1
Brown trout	5	40.8	±	2.5	860	±	180	5	-25.8	±	0.4	12.2	±	0.3	3.8	±	0.1
FEMUNDEN																	
Arctic char	1	32.2	±		320			1	-23.4			6.9					
Brown trout	6	38.1	±	2.0	550	±	90	6	-20.4	±	0.4	9.3	±	0.5			

Table S 13 Cont.	Lipid			Lipid %	POPs	PCB-153			PCB-180			*p,p*'-DDE			PBDE-47			PBDE-99		
	N	Mean		SE	N	Mean		SE	Mean		SE	Mean		SE	Mean		SE	Mean		SE
MJØSA																				
Zooplankton Epilimnetic	4	0.72	±	0.04	2 (1)	10	±	0	<8			38	±	1	(11)			(1)		
Zooplankton Hypolimnetic	5	3.5	±	1.4	3	20	±	1	5	±	1	67	±	2	35	±	5	8	±	1
Mysis	5	2.5	±	0.6	4	25	±	6	<4			82	±	17	34	±	6	10	±	2
Vendace	7	1.2	±	0.1	7	330	±	70	69	±	15	890	±	170	420	±	80	150	±	30
Smelt. Small	5	1.0	±	0.0	5	73	±	11	10	±	4	220	±	29	105	±	10	16	±	1
Smelt. Large	5	1.3	±	0.2	5	340	±	50	50	±	11	850	±	120	550	±	90	16	±	4
Brown trout	5	2.9	±	0.6	5	320	±	80	54	±	13	840	±	210	660	±	200	68	±	18
RANDSFJORDEN																				
Zooplankton Epilimnetic	4	0.73	±	0.03	4	8	±	0	<7			21	±	2						
Zooplankton Hypolimnetic	3	1.7	±	0.5	3	26	±	7	8	±	2	51	±	13						
Whitefish	9	1.2	±	0.2	9	27	±	5	7	±	1	47	±	6						
Smelt	5	2.0	±	0.2	5	9	±	1	<3			23	±	2						
Brown trout	5	2.1	±	1.1	5	60	±	4	14	±	1	120	±	8						
FEMUNDEN																				
Arctic char	1	1.00																		
Brown trout	6	0.74	±	0.16																

a Epilimnetic zooplankton Mjøsa - Cladocerans *Daphnia galeata, Bosmina longispina*. Hypolimnetic zooplankton Mjøsa - Copepods *Limnocalanus macrurus*. Epilimnetic zooplankton Randsfjorden -*D. galeata,* Copepods *Eudiaptomus gracilis*. Hypolimnetic zooplankton Randsfjorden - *D. galeata, L. macrurus, Heterocope appendiculata*. Mysis – *Mysis relicta*. Vendace – *Coregonus albula*. Smelt – *Osmerus eperlanus*. Brown trout – *Salma trutta*. Whitefish – *Coregonus lavaretus.* Arctic char - *Salvelinus alpinus*.

b The $\delta^{13}C$ was adjusted for the samples' C:N value according to Post et al.[12]

Food web considerations

The smelt diet shifts from being predominantly zooplankton for younger and smaller smelt, to an increasing degree of cannibalism once the fish are in their fourth year (3+) and longer than approximately 10 cm^3. In contrast to the 2010 study, the large smelt in the present study did not have high cVMS concentrations relative to its trophic position (Figure 2). The smelt in 2010 were generally larger (20.5-23.7 cm, 45.3-97.5 g)[8], and thus older, than the large smelt in the present study.

Mjøsa hypolimnic zooplankton samples collected on August 2nd 2012 had markedly lower $\delta^{15}N$ values than the samples collected on August 21st 2012 (Figure 1). Mysis showed some variation among samples due to different sampling dates, with higher $\delta^{15}N$ in one sample collected in early July, compared to those sampled in early August.

Table S14. Qualitative species composition of hypolimnetic zooplankton in net hauls (500 µm) from Randsfjorden, August 29th 2012. 1= few individuals, 2 = common, 3 = abundant/dominating.

	R6	**R7**
Copepoda:		
Limnocalanus macrurus	1-2	3
Heterocope appendiculata	2	1-2
Cladocera:		
Daphnia galeata	3	3
Bosmina longispina	1	

Table S15. Product-moment correlation coefficients (r: left triangular matrix) between trophic position (TL), and log-transformed concentrations of cVMS and selected legacy contaminants in the food web in Mjøsa and Randsfjorden.

MJØSA[a] n = 31 (30 for PBDEs)

Variable	TL	D5	D6	D4	PCB-153	PCB-180	*p,p'*-DDE	PBDE-47	PBDE-99
TL	**1.00**								
D5	0.76	**1.00**							
D6	0.71	0.91	**1.00**						
D4[c]	-0.39	0.13	0.21	**1.00**					
PCB-153	0.89	0.84	0.85	-0.15	**1.00**				
PCB-180	0.76	0.77	0.80	-0.09	0.92	**1.00**			
ppDDE	0.88	0.84	0.86	-0.14	1.00	0.92	**1.00**		
PBDE-47	0.90	0.79	0.80	-0.14	0.99	0.90	0.98	**1.00**	
PBDE-99	0.57	0.82	0.78	0.31	0.78	0.75	0.78	0.74	**1.00**

RANDSFJORDEN[b] Upper right diagonal without whitefish (n=17). Lower left diagonal with whitefish (n=26).

Variable	TL	D5	D6	D4	PCB-153	PCB-180	*p,p'*-DDE
TL	**1.00**	0.76	0.56	-0.54	0.62	0.05	0.62
D5	0.29	**1.00**	0.62	0.02	0.69	0.26	0.65
D6[c]	0.31	0.74	**1.00**	-0.12	0.56	0.39	0.54
D4[c]	-0.49	0.16	0.14	**1.00**	-0.03	0.31	-0.06
PCB-153	0.61	0.14	0.16	-0.13	**1.00**	0.76	0.99
PCB-180[c]	0.08	0.03	0.25	0.24	0.73	**1.00**	0.75
ppDDE	0.61	0.24	0.22	-0.13	0.96	0.70	**1.00**

a Mjøsa correlations included epi- and hypolimnetic zooplankton, *Mysis relicta*, vendace, smelt and trout.
b Randsfjorden correlations included epi- and hypolimnetic zooplankton, whitefish, smelt and trout.
c >50 % of values used in correlations were below the established limit of quantification (LOQ) for cVMS and LOD for PCB-180.
d Correlation coefficients threshold for nominal p-values (0.05 level, two-tailed, pairwise correlations) at different sample sizes: n = 31, r = 0.36; n = 26, r = 0.39; n = 17, r = 0.48.

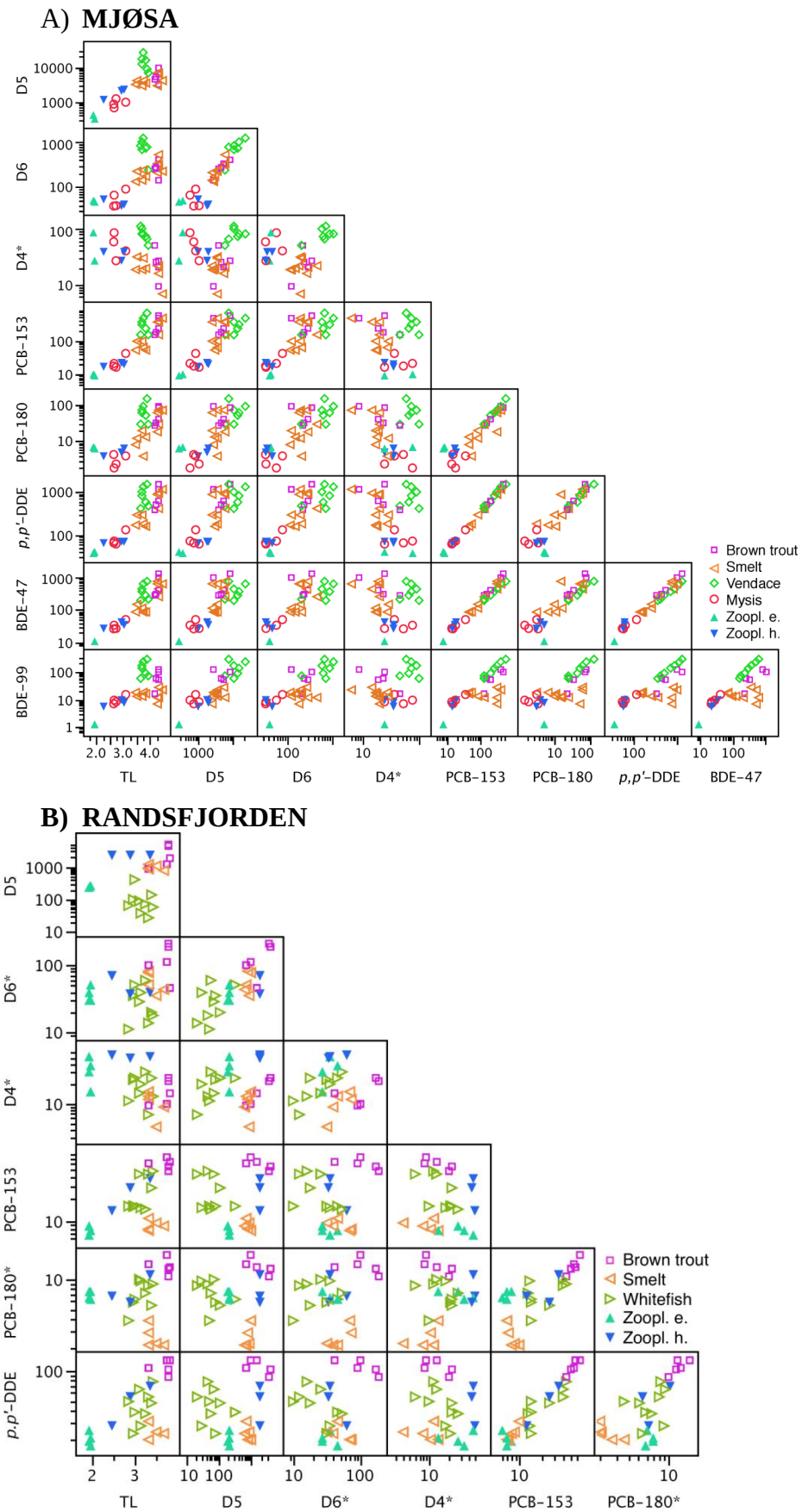

Figure S3. Scatter plot matrix for lipid normalized concentrations of cVMS and legacy POPs, and trophic level (TL) in A) Mjøsa and B) Randsfjorden. Zoopl e. and h. is zooplankton epilimnetic and hypolimnetic, respectively.

Table S16. Trophic magnification factor (TMF) statistics for cyclic volatile methylsiloxanes (D4, D5, D6) and selected legacy chlorinated and brominated contaminants in the Lakes Mjøsa [M] and Randsfjorden [R]. TMFs are based on the regression of lipid normalised concentrations onto trophic level (TL) estimated from stable isotopes of nitrogen.

Chemical	Whitefish [R]	Model term	Estimate	SE	t Ratio	p>|t|	Estimate CI Lower 95%	Estimate CI Upper 95%	TMF	TMF CI Lower 95%	TMF CI Upper 95%	R^2	N	Interactions (TLxLake) t-test	Interactions (TLxLake) p(t)	Comments
D5	Included	Intercept	3.60	0.70	5.12	0.0000	2.19	5.01								
D5	Included	Lake[M]	0.80	0.15	5.31	0.0000	0.50	1.11								
D5	Included	Lake[R]	-0.80	0.15	-5.31	0.0000	-1.11	-0.50								
D5	Included	TL	1.03	0.20	5.03	0.0000	0.62	1.43	2.79	1.86	4.20	0.57	59	0.86	0.4	
D5	Excluded	Intercept	3.80	0.44	8.72	0.0000	2.93	4.68								
D5	Excluded	Lake[M]	0.33	0.11	3.15	0.0029	0.12	0.54								
D5	Excluded	Lake[R]	-0.33	0.11	-3.15	0.0029	-0.54	-0.12								
D5	Excluded	TL	1.10	0.13	8.73	0.0000	0.85	1.36	3.01	2.33	3.88	0.66	50	0.47	0.64	
D4*	Included	Intercept	4.43	0.40	11.15	0.0000	3.63	5.22								
D4*	Included	Lake[M]	0.38	0.09	4.47	0.0000	0.21	0.55								
D4*	Included	Lake[R]	-0.38	0.09	-4.47	0.0000	-0.55	-0.21								
D4*	Included	TL	-0.36	0.12	-3.10	0.0031	-0.59	-0.13	0.70	0.56	0.88	0.16	59	1.08	0.28	
D4*	Excluded	Intercept	4.44	0.42	10.64	0.0000	3.60	5.28								
D4*	Excluded	Lake[M]	0.37	0.10	3.62	0.0007	0.16	0.57								
D4*	Excluded	Lake[R]	-0.37	0.10	-3.62	0.0007	-0.57	-0.16								
D4*	Excluded	TL	-0.36	0.12	-2.95	0.0050	-0.60	-0.11	0.70	0.55	0.89	0.12	50	1.05	0.3	
D6	Included	Intercept[M]	1.62	0.59	2.73	0.0103	0.41	2.82								
D6	Included	TL[M]	1.00	0.16	6.20	0.0000	0.67	1.33	2.72	1.96	3.77	0.55	33	2.15	0.04	Separate regression after significant test for interaction
D6*	Included	Intercept[R]	2.61	0.75	3.47	0.0020	1.06	4.16								
D6*	Included	TL[R]	0.38	0.23	1.62	0.1173	-0.10	0.86	1.46	0.90	2.36	0.10	26	2.15	0.04	Separate regression after significant test for interaction

D6*	Excluded	Intercept	1.80	0.44	4.06	0.0002	0.91	2.69							
D6*	Excluded	Lake[M]	0.36	0.11	3.37	0.0015	0.15	0.58							
D6*	Excluded	Lake[R]	-0.36	0.11	-3.37	0.0015	-0.58	-0.15							
D6*	Excluded	TL	0.85	0.13	6.63	0.0000	0.59	1.11	2.34	1.81	3.02	0.61	50	1.92	0.06	
PCB-153	Included	Intercept[M]	-1.30	0.56	-2.32	0.0279	-2.45	-0.15								
PCB-153	Included	TL[M]	1.62	0.15	10.78	0.0000	1.31	1.92	5.04	3.71	6.85	0.80	31	2.98	0.005	Separate regression after significant test for interaction
PCB-153	Included	Intercept[R]	0.35	0.70	0.50	0.6196	-1.10	1.81								
PCB-153	Included	TL[R]	0.83	0.22	3.79	0.0009	0.38	1.28	2.29	1.46	3.60	0.37	26	2.98	0.005	Separate regression after significant test for interaction
PCB-153	Excluded	Intercept[R]	0.42	0.83	0.51	0.6200	-1.35	2.19								
PCB-153	Excluded	TL[R]	0.78	0.26	3.04	0.0083	0.23	1.33	2.19	1.26	3.80	0.38	17	3.01	0.004	Separate regression after significant test for interaction
PCB-180	Included	Intercept[M]	-2.78	0.85	-3.29	0.0027	-4.50	-1.05								
PCB-180	Included	TL[M]	1.52	0.23	6.75	0.0000	1.06	1.98	4.58	2.89	7.26	0.61	31	3.91	0.003	Separate regression after significant test for interaction
PCB-180*	Included	Intercept[R]	1.63	0.65	2.50	0.0198	0.28	2.98								
PCB-180*	Included	TL[R]	0.08	0.20	0.41	0.6838	-0.34	0.50	1.09	0.72	1.65	0.00	26	3.91	0.0003	Separate regression after significant test for interaction
PCB-180*	Excluded	Intercept[R]	0.43	1.05	0.41	0.6849	-1.80	2.67								
PCB-180*	Excluded	TL[R]	0.34	0.33	1.04	0.3137	-0.36	1.04	1.41	0.70	2.82	0.07	19	3.01	0.004	Separate regression after significant test for interaction
ppDDE	Included	Intercept[M]	0.45	0.54	0.84	0.4068	-0.65	1.55								

ppDDE	Included	TL[M]	1.43	0.14	10.00	0.0000	1.14	1.73	4.19	3.12	5.61			3.24	0.002	Separate regression after significant test for interaction
ppDDE	Included	Intercept[R]	1.59	0.58	2.75	0.0110	0.40	2.79								
ppDDE	Included	TL[R]	0.67	0.18	3.76	0.0010	0.30	1.04	1.96	1.36	2.84	0.76	31	3.24	0.002	Separate regression after significant test for interaction
ppDDE	Excluded	Intercept[R]	1.62	0.69	2.35	0.0330	0.15	3.09								
ppDDE	Excluded	TL[R]	0.66	0.21	3.09	0.0075	0.21	1.12	1.94	1.23	3.07	0.37	17	3.05	0.004	Separate regression after significant test for interaction
PBDE-47	Not relevant	Intercept[M]	-1.37	0.59	-2.33	0.0275	-2.58	-0.16								PBDE only measured in [M]
PBDE-47	Not relevant	TL[M]	1.74	0.16	11.22	0.0000	1.42	2.06	5.72	4.16	7.86	0.81	30			PBDE only measured in [M]
PBDE-99	Not relevant	Intercept[M]	-0.83	1.10	-0.75	0.4601	-3.09	1.43								PBDE only measured in [M]
PBDE-99	Not relevant	TL[M]	1.08	0.29	3.71	0.0009	0.48	1.68	2.95	1.62	5.35	0.33	30			PBDE only measured in [M]

*more than 50% of data quantified below quality threshold (LOQ for cVMS, LOD for legacy POPs).

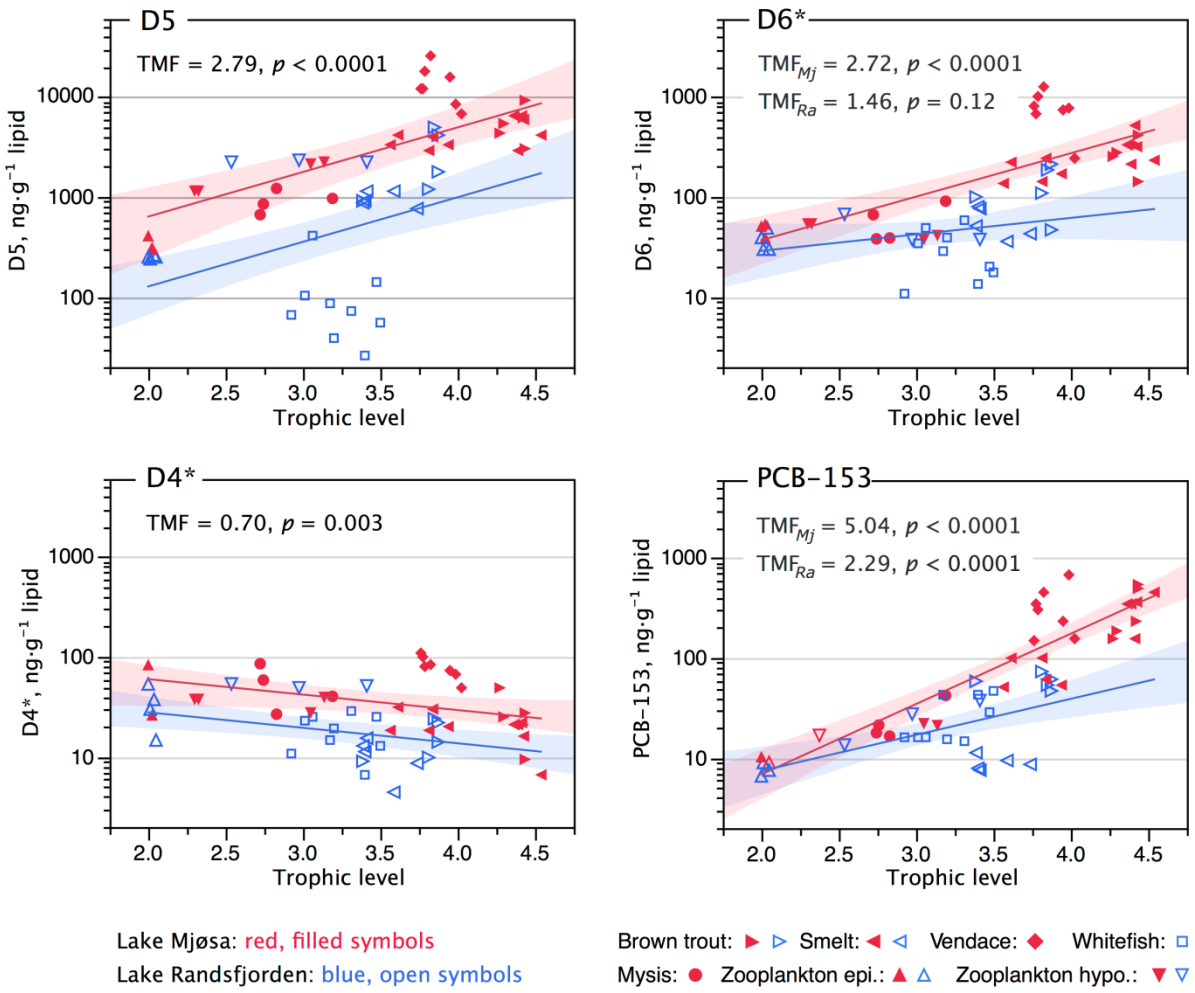

Figure S4. Relationship between lipid normalized concentrations of cVMS (D4, D5 D6) and PCB-153, and trophic level (TL) from Lake Mjøsa and Randsfjorden pelagic food webs, including whitefish from Randsfjorden. Chemicals marked with asterix (*) have >50% of data below LOQ in one or both of the lakes. Zooplankton epi and hypo are epi- and hypolimnetic zooplankton, respectively. Trophic magnification factor (TMF) estimated separately for Mjøsa (Mj) and Randsfjorden (Ra) when the interaction TLxLake was significant.

S4. References

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