SUPPLEMENTARY MATERIAL

Flores et al. ‘Intact polar lipids in the hadal seabed of the Atacama Trench point to lateral sediment transport and in situ production as key sources of labile organic matter’

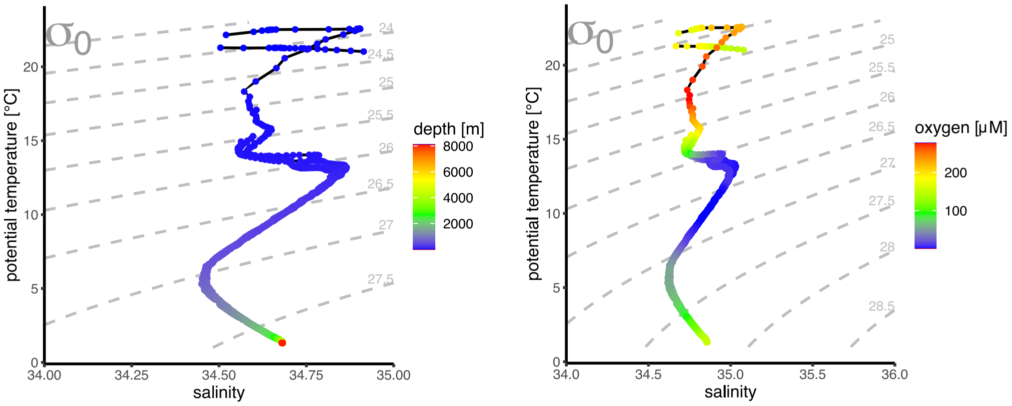
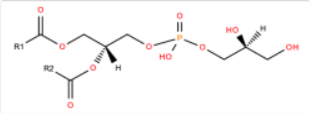
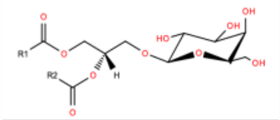


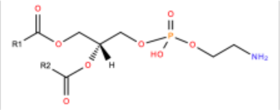
Figure S1. The potential temperature–salinity (θ–s) diagrams from CTD data coupled to an AUV (autonomous underwater vehicle). The color scale is related to depth (m) and oxygen concentration (μM).



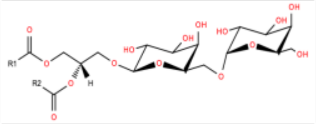
Phosphatidylglycerol Head group (PG)



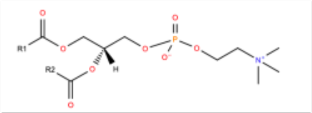
Monogalactosyl diacylglycerol Head group (MGDG)



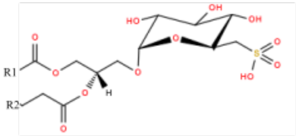
Phosphatidylethanolamine Head group (PE)



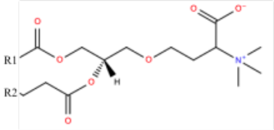
Digalactosyl diacylglycerol Head group (DGDG)



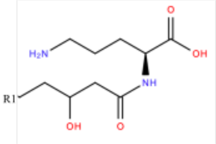
Phosphatidylcholine Head group (PC)



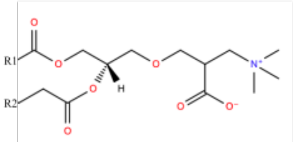
Sulfoquinovosyl diacylglycerol Head group (SQDG)



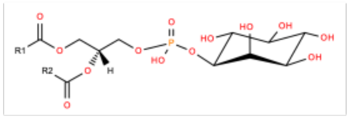
Diacylglyceryltrimethylhomoserine
Head group (DGTS)



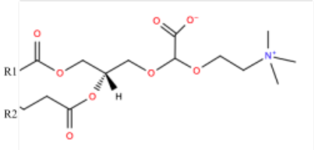
Ornithine lipid Head group (OL)



Diacylglyceryl-hydroxymethyltrimethyl-β-alanine
Head group (DGTA)



Phosphatidylinositol Head group (PI)



Diacylglyceryl carboxyhydroxymethylcholine
Head group (DGCC)

Figure S2. Chemical structure classes of IPL. R1 and R2 represent acyl groups, the charges are those expected at seawater pH. The structures were taken from public compound databases of LIPID MAPS (Sud et al., 2007).

Figure S3. Pie chart representation of the relative abundances of distinctive IPL of Chlorophyll maximum proposed in Cantarero et al. 2020 shown in red and Non-distinctive IPLs of Chlorophyll maximum [Total IPL analyzed - distinctive IPL of Chlorophyll maximum] shown in turquoise in all sample types.

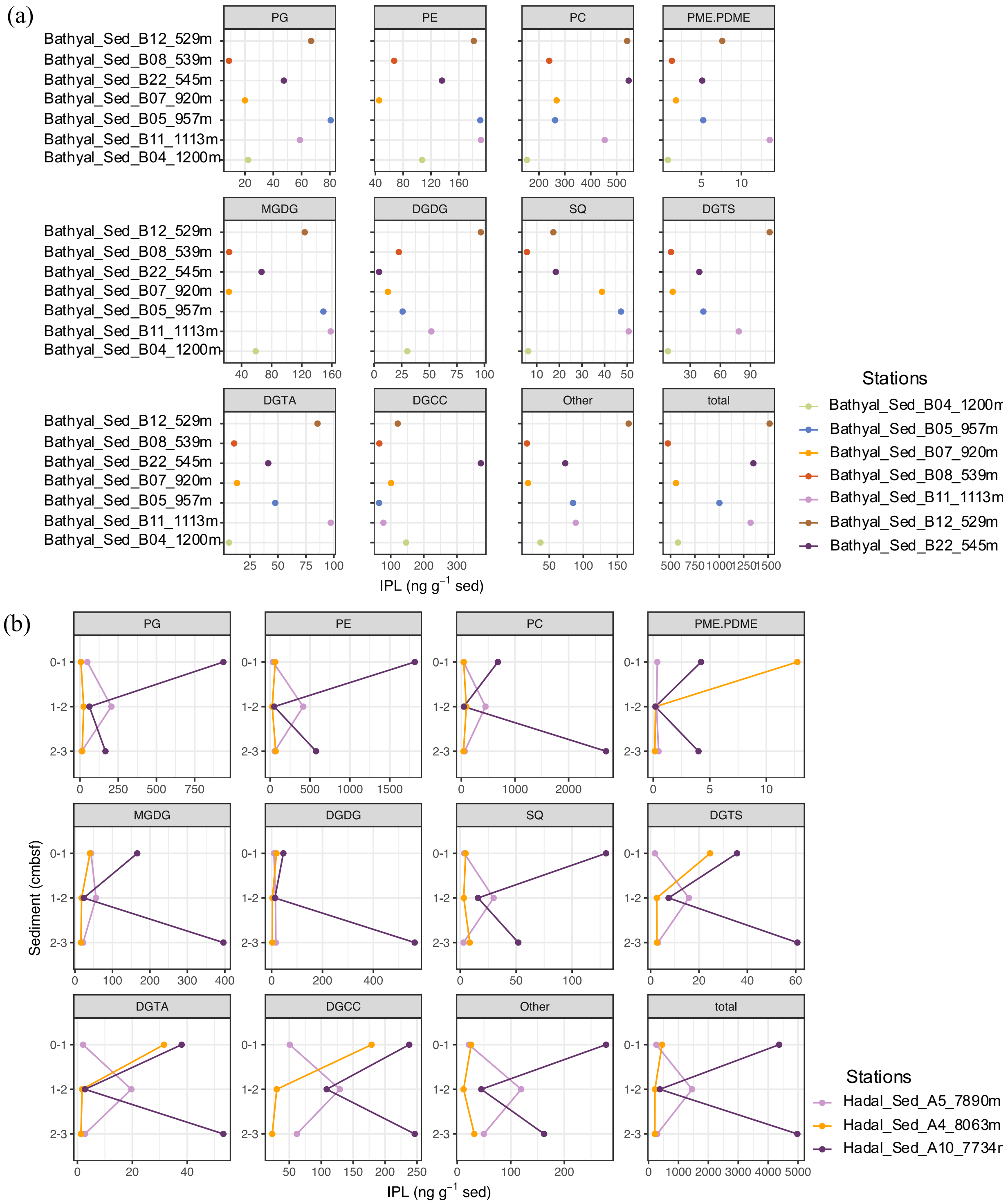


Figure S4. Total concentration of IPL by class, in (a) bathyal and (b) hadal sediments samples.

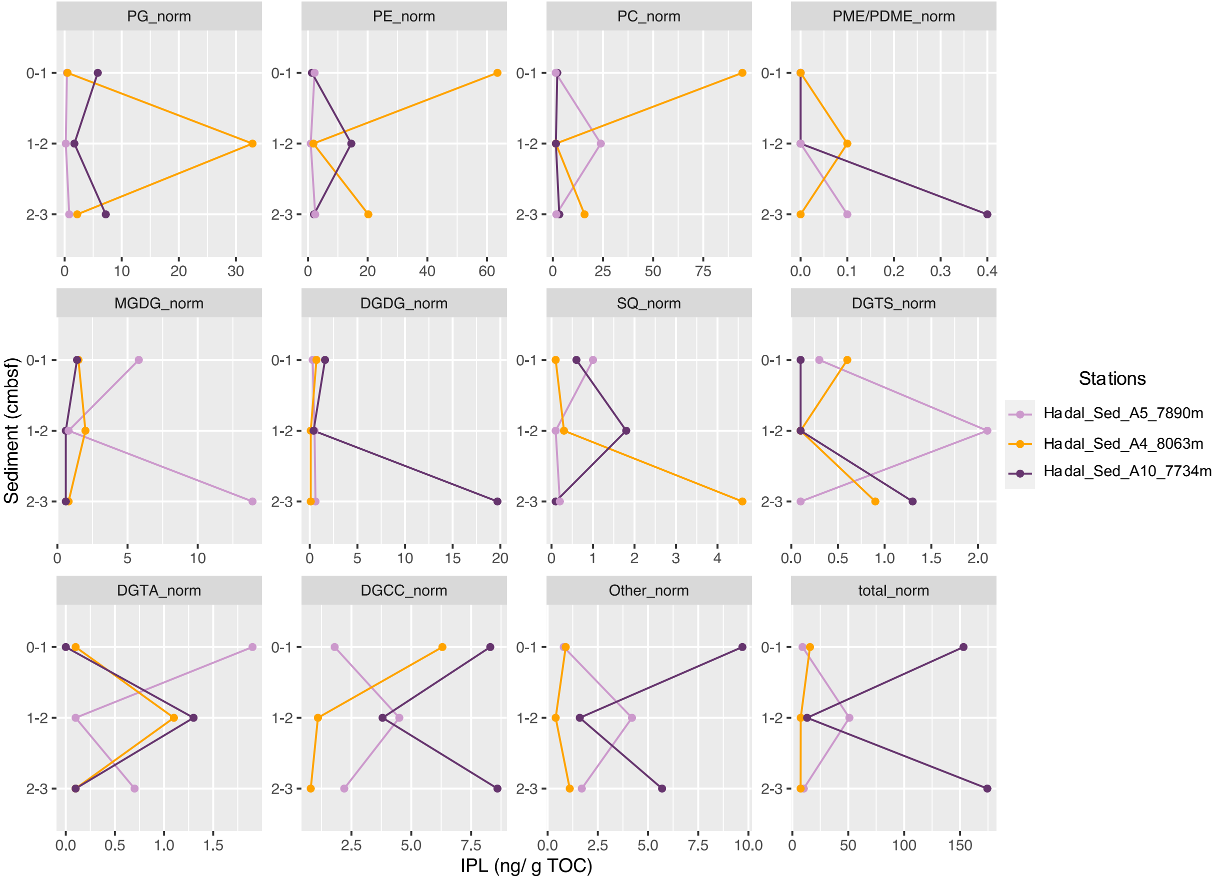


Figure S5. TOC-normalized IPL concentration (ng IPL/g TOC) in hadal sediments samples.

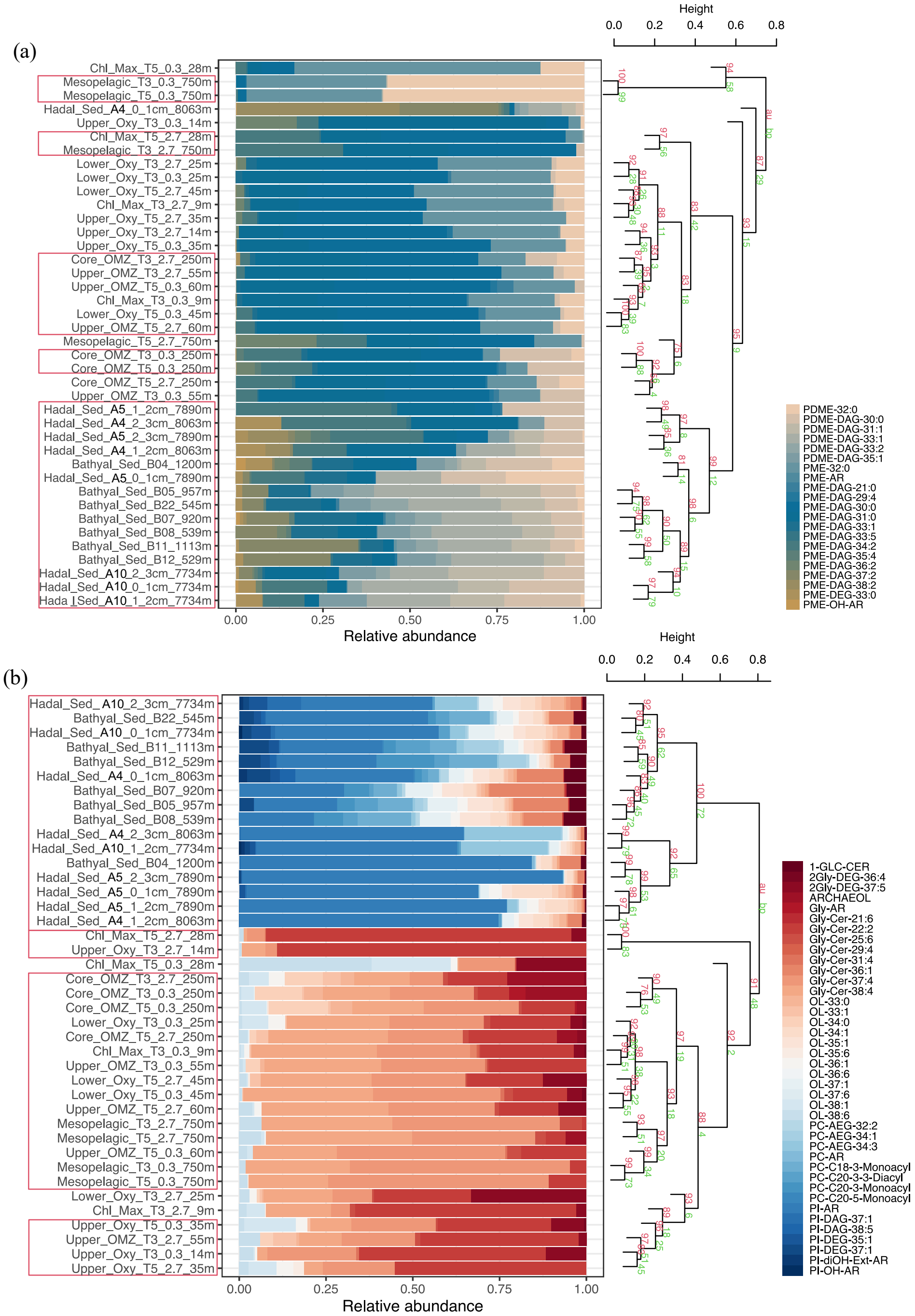


Figure S6. Cumulative bar chart of IPLs fractional abundances in all sample types. a) PDME, PME; b) Other lipids. The number of carbon atoms and unsaturation in core fatty acids follow the order shown in the legend. The right panel depicts a cluster analysis with approximately unbiased (AU) and bootstrap probability (BP) shown in red and green, respectively, and p-values shown at branching points. The number of bootstrap replicates is 10000. Clusters with AU ≥ 95% confidence are highlighted in red boxes on the left-hand side.

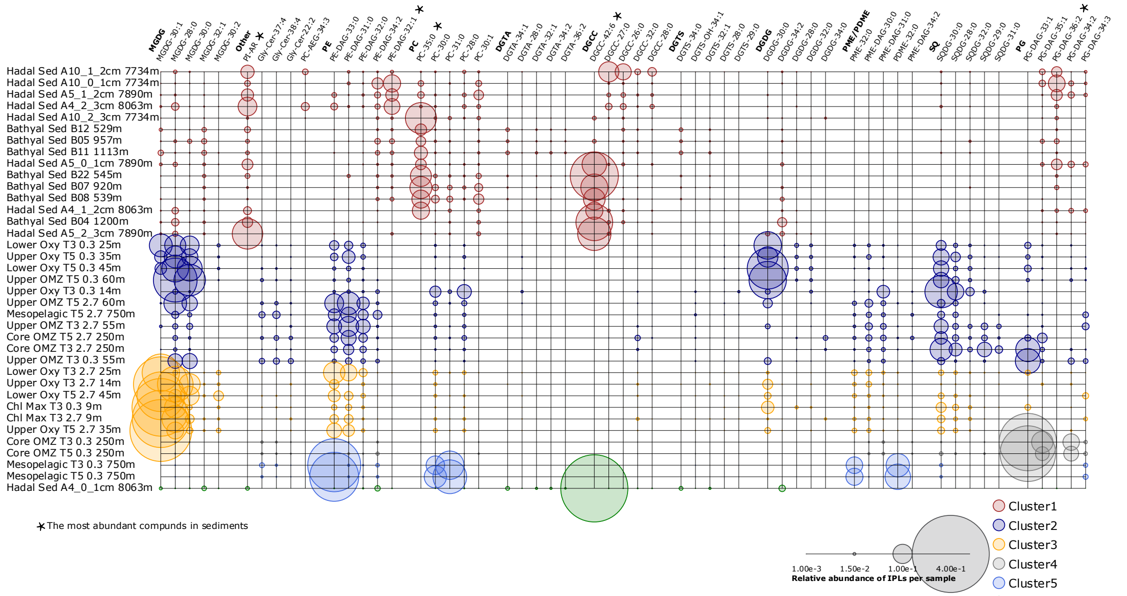


Figure S7. Relative abundance of the five most abundant IPL compounds per each class in the entire dataset used in this work. Circle ratios are proportional to the relative abundance of IPL compounds per sample. Samples are organized along the Y axis and shown in colors that match the hierarchical cluster analysis in Fig. 10. The scale for circumference size is shown in the legend.

Table S1. SIMPER (similarity percentage) analysis. Average abundance and contribution of IPLs that explained the main differences among the hierarchical clusters obtained previously (see Fig. 9) that include the water column and sediment sampling stations.

Groups Cluster 1 & Cluster 2
Average dissimilarity = 85.46

IPLs	Average Cluster 1	Average Cluster 2	Average dissimilarity	Dissimilarity/SD	Contribution (%)	Cumulative (%)
DGCC-42:6	0.07	0	3.74	0.9	4.37	4.37
SQDG-30:0	0	0.08	3.6	1.93	4.21	8.59
DGDG-30:0	0	0.07	3.52	0.95	4.12	12.71
MGDG-28:0	0.02	0.08	3.48	1.13	4.08	16.79
MGDG-30:0	0	0.07	3.06	1.23	3.58	20.37
PC-35:0	0.06	0	2.96	1.3	3.46	23.83
PE-DAG-31:0	0.01	0.06	2.64	1.59	3.09	26.92
PI-AR	0.05	0	2.32	1.2	2.72	29.64
PE-DAG-33:0	0.01	0.04	1.93	1.47	2.25	31.89
SQDG-28:0	0	0.04	1.89	1.81	2.21	34.1
PG-DAG-33:1	0	0.04	1.87	0.85	2.19	36.3
PE-DAG-32:0	0	0.03	1.5	1.42	1.76	38.05
PG-DAG-36:2	0.03	0	1.37	1.15	1.6	39.65
PE-DAG-32:1	0.03	0	1.31	0.95	1.53	41.19
MGDG-30:1	0.01	0.02	1.26	0.76	1.48	42.66
PC-30:2	0.02	0	1.24	0.62	1.45	44.11
PC-30:1	0.02	0	1.17	1.67	1.37	45.48
PE-DAG-29:0	0	0.03	1.15	1.06	1.35	46.83
PME-DAG-30:0	0	0.02	1.1	1.89	1.29	48.12
PME-DAG-31:0	0	0.02	1.09	1.32	1.28	49.39
PC-29:2	0.02	0	0.95	1.4	1.11	50.51

Groups Cluster 1 & Cluster 3
Average dissimilarity = 84.70

IPLs	Average Cluster 1	Average Cluster 3	Average dissimilarity	Dissimilarity/SD	Contribution (%)	Cumulative (%)
MGDG-30:1	0.01	0.27	13.24	6.19	15.63	15.63
MGDG-28:0	0.02	0.1	4.35	1.68	5.14	20.77
DGCC-42:6	0.07	0	3.74	0.9	4.41	25.19
PC-35:0	0.06	0	2.95	1.29	3.49	28.67
PE-DAG-33:0	0.01	0.06	2.83	2.01	3.34	32.01
MGDG-30:0	0	0.05	2.44	1.3	2.88	34.89
PI-AR	0.05	0	2.32	1.2	2.74	37.63
PE-DAG-31:0	0.01	0.05	2.07	1.73	2.44	40.07
DGDG-30:0	0	0.03	1.6	1.64	1.89	41.97
SQDG-30:0	0	0.03	1.45	2.05	1.72	43.68
PG-DAG-36:2	0.03	0	1.37	1.14	1.61	45.3
PE-DAG-32:1	0.03	0	1.29	0.94	1.53	46.82
PC-30:2	0.02	0	1.24	0.62	1.46	48.29
PC-30:1	0.02	0	1.15	1.63	1.36	49.64
MGDG-30:2	0	0.02	1.08	1.6	1.27	50.92

Groups Cluster 1 & Cluster 4
Average dissimilarity = 85.99

IPLs	Average Cluster 1	Average Cluster 4	Average dissimilarity	Dissimilarity/SD	Contribution (%)	Cumulative (%)
PG-DAG-33:1	0	0.29	14.63	66.25	17.02	17.02
PG-DAG-35:4	0	0.09	4.24	36.43	4.93	21.95
PG-DAG-35:1	0.01	0.09	4.05	3.59	4.71	26.67
DGCC-42:6	0.07	0	3.74	0.89	4.35	31.01
PG-DAG-34:2	0.01	0.08	3.63	5.35	4.22	35.23
PC-35:0	0.06	0	2.89	1.26	3.36	38.6
PI-AR	0.05	0	2.32	1.18	2.7	41.3
PG-DAG-36:1	0	0.04	1.8	6.37	2.09	43.39
PE-DAG-34:1	0.01	0.04	1.75	4.39	2.03	45.42
PG-DAG-36:2	0.03	0	1.37	1.13	1.59	47.01
PE-DAG-32:1	0.03	0	1.3	0.93	1.51	48.52
PC-30:2	0.02	0	1.24	0.61	1.44	49.96

Groups Cluster 1 & Cluster 5
Average dissimilarity = 89.03

IPLs	Average Cluster 1	Average Cluster 5	Average dissimilarity	Dissimilarity/SD	Contribution (%)	Cumulative (%)
PE-DAG-33:0	0.01	0.26	12.94	17.5	14.54	14.54
PC-31:0	0.01	0.16	7.47	9.31	8.39	22.93
PDME-32:0	0	0.13	6.33	22.82	7.11	30.03
PC-30:0	0.01	0.11	4.66	6.45	5.24	35.27
PME-32:0	0	0.09	4.37	68.49	4.91	40.18
DGCC-42:6	0.07	0	3.74	0.89	4.2	44.38
PC-35:0	0.06	0	2.96	1.28	3.33	47.71
PI-AR	0.05	0	2.32	1.18	2.61	50.31