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## Supplementary data

Table S1 Fatty acid compositions (%) of the fish oil from Coregonus peled

Fatty acid	Peak area (%)
14:0	8.57
14:1,n-5	1.23
15:0	3.25
16:0	14.63
16:1,n-7	18.47
16:2,n-4,7	3.25
16:3,n-4,7,10	0.93
17:1,n-7	0.81
18:0	2.31
18:1,n-7	0.43
18:1,n-9	20.48
18:1,n-10	5.31
18:2,n-6,9	2.34
18:4,n-3,6,9,12	1.99
20:1,n-9	0.64
20:4,n-3,6,9,12	0.61
20:4,n-6,9,12,15	0.66
20:5,n-3,6,9,12,15	8.11
22:5,n-3,6,9,12,15	1.23
22:6,n-3,6,9,12,15,18	4.75
SFA	28.76
UFA	71.34
EPA+DHA	12.86

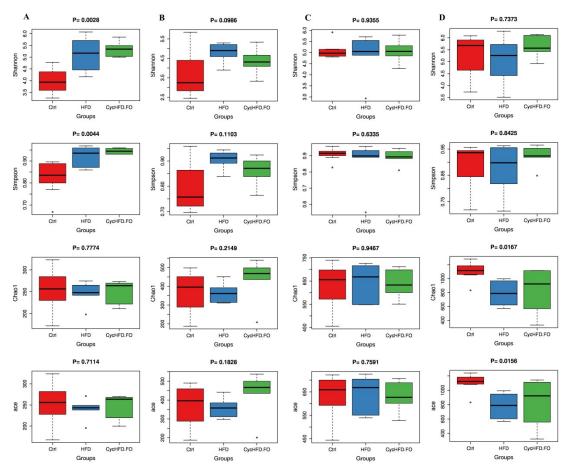


Fig. S1 Comparison of  $\alpha$ -diversity of gut microbiota during obesity (A), after obesity (B), during second obesity (C), and after second obesity (D).

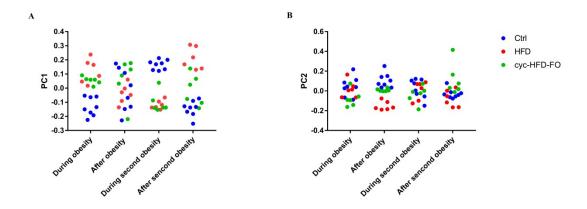


Fig. S2 Principal coordinate analyses (PCoA) of unweighted UniFrac distances of microbiota composition during obesity, after obesity, during second obesity, and after second obesity.

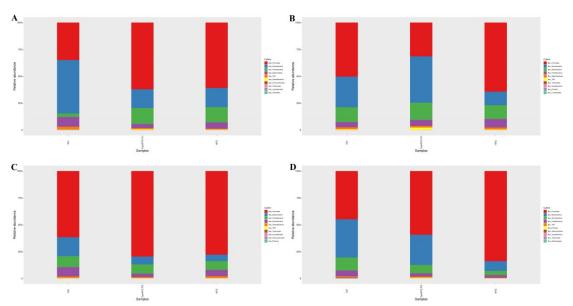


Fig. S3 Comparison of phylum taxonomic level during obesity (A), after obesity (B), during second obesity (C), and after second obesity (D).

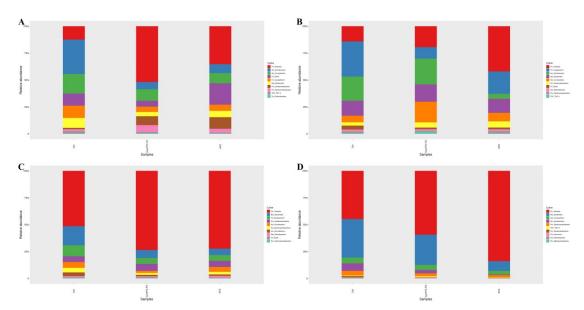


Fig. S4 Comparison of classes taxonomic level during obesity (A), after obesity (B), during second obesity (C), and after second obesity (D).

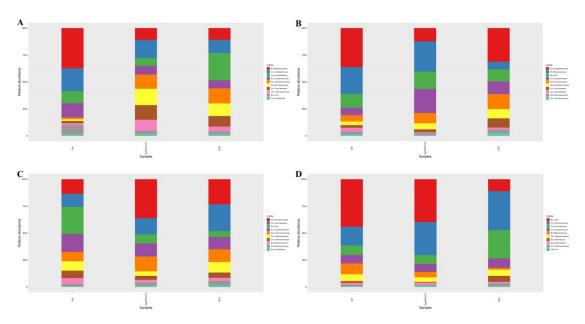


Fig. S5 Comparison of families taxonomic level during obesity (A), after obesity (B), during second obesity (C), and after second obesity (D).

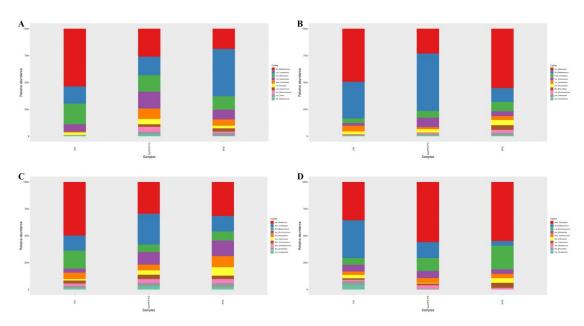


Fig. S6 Comparison of genus taxonomic level during obesity (A), after obesity (B), during second obesity (C), and after second obesity (D).