

Supplementary Material for

Diet supplementation with fish-derived extracts suppresses diabetes and modulates intestinal microbiome in a murine model of high-fat induced obesity

Konstantinos Axarlis^{1,2}, Maria G. Daskalaki^{1,2}, Sofia Michailidou³, Nikolais Androulaki¹, Antiopi Tsourekis³, Evangelia Mouchtaropoulou³, Ourania Kolliniati^{1,2}, Ioanna Lapi^{1,2}, Eirini Dermitzaki^{1,2}, Maria Venihaki¹, Katerina Kousoulaki⁴, Anagnostis Argiriou^{3,5}, Zouhir El Marsni^{6,*} and Christos Tsatsanis^{2,*}

¹ Laboratory of Clinical Chemistry, Medical School, University of Crete, Heraklion 70013, Greece; mol-grad392@edu.biology.uoc.gr (KA); m.daskalaki@med.uoc.gr (MGD); nikolandroulaki@gmail.com (NA); raliakolliniatis21@gmail.com (OK); iwanna_lapi@hotmail.com (IL); renaderm@med.uoc.gr (ED); venihaki@med.uoc.gr (MV)

² Institute of Molecular Biology and Biotechnology, FORTH, 71100 Heraklion, Greece;

³ Institute of Applied Biosciences (INAB), CERTH, Thessaloniki GR-57001, Greece; sofia_micha28@certh.gr (SM), adatsourekis@certh.gr (AT); eva.mouchtaropoulou@certh.gr (EM), argiriou@certh.gr (AA)

⁴ Department of Nutrition and Feed Technology, Nofima AS, 5141 Bergen, Norway; katerina.kousoulaki@nofima.no (KK)

⁵ Department of Food Science and Nutrition, University of the Aegean, Myrina, 81400, Lemnos, Greece;

⁶ Seagarden AS, 4262 Avaldsnes, Norway;

* Correspondence: tsatsani@med.uoc.gr, Tel.: +30-2810394833 (CT); zouhir.el.marsni@seagarden.no, Tel.: +4752859482 (ZEM)

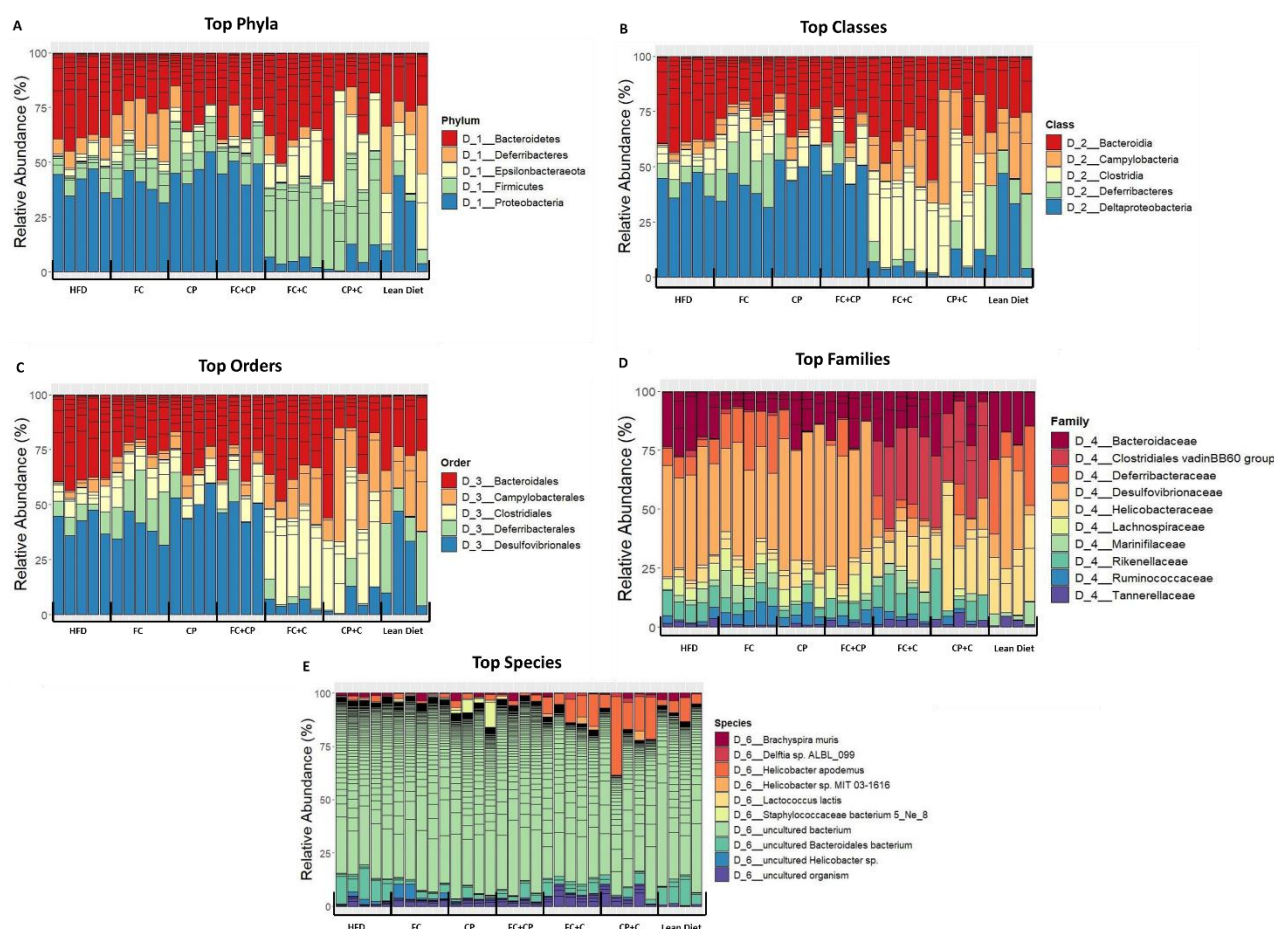


Figure S1. The effect of fish-derived dietary supplements on the intestinal microbiome composition of top A. phyla, B. classes, C. orders, D. families and E. species. Top genera are depicted in the main paper.

Table S1. Nutritional composition of supplemented diets given to each diet group.

Chemical composition	Unit (per 100g of supplemented food)	Diet Groups						
		S (ND)	S (HFD)	FC	CP	FC+CP	FC+C	CP+C
Energy	<i>Kcal</i>	272.4	537.8	538.0	534.0	536.0	538.1	536.1
	<i>KJ</i>	1138.8	2253.3	2254.8	2237.5	2246.1	2255.1	2246.5
Carbohydrates	<i>g</i>	44.0	24.6	24.6	24.6	24.6	24.6	24.6
Protein	<i>g</i>	22.3	35.2	34.8	33.8	34.3	35.0	34.5
Fat	<i>g</i>	2.9	33.2	33.4	33.4	33.4	33.3	33.3

Table S2. Summary of top genera found in the intestinal microbiome of high-fat induced obese mice and their role in inflammation and obesity.

Phylum	Genus	Role	Reference
Bacteroidetes	<i>Bacteroides</i>	Decreased during IBD, protect against pathogenic microorganism intestinal colonization	[1-3]
	<i>Alistipes</i>	Found in healthy individuals, protection against colitis	[4]
	<i>Odoribacter</i>	Short-chain fatty acid (SCFAs) producers	[5]
Firmicutes	<i>Lachnospiraceae NK4A136 group</i>	Butyrate producers, SCFAs	[6,7]
	<i>Ruminiclostridium 9</i>	Butyrate producers, SCFAs	[8]
	<i>Ruminiclostridium</i>	Acetate producers, SCFAs	[9]
Deferribacteres	<i>Mucispirillum</i>	Increased during intestinal inflammation	[10]
Proteobacteria	<i>Helicobacter</i>	Induction of inflammation mainly by <i>H.pylori</i>	[11,12]

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