

Supplementary Materials

Table S1. LefSe analysis results showing differentially abundant (log transformed LDA score > 2.5, $p < 0.05$) metabolic pathways (inferred by PICRUST2) in intestinal content ($n = 4$) and intestinal wall ($n = 4$). p -values were not adjusted.

Pathway	Type	LDA_score_log10	p-value
adenine_and_adenosine_salvage_III	Intestinal_content	−3.251	0.043
purine_ribonucleosides_degradation	Intestinal_content	−3.223	0.021
superpathway_of_purine_deoxyribonucleosides_degradation	Intestinal_content	−3.193	0.021
acetylene_degradation	Intestinal_content	−3.135	0.021
superpathway_of_N-acetylneuraminate_degradation	Intestinal_content	−3.085	0.021
superpathway_of_pyrimidine_deoxyribonucleosides_degradation	Intestinal_content	−3.056	0.021
superpathway_of_N-acetylglucosamine,_N-acetylmannosamine_and_N-acetylneuraminate_degradation	Intestinal_content	−3.040	0.021
superpathway_of_adenosine_nucleotides_de_novo_biosynthesis_I	Intestinal_content	−3.006	0.021
pyrimidine_deoxyribonucleosides_salvage	Intestinal_content	−2.938	0.043
chitin_derivatives_degradation	Intestinal_content	−2.920	0.021
starch_degradation_V	Intestinal_content	−2.908	0.043
thiazole_biosynthesis_II_(Bacillus)	Intestinal_content	−2.827	0.043
6-hydroxymethyl-dihydropterin_diphosphate_biosynthesis_III_(Chlamydia)	Intestinal_content	−2.818	0.021
adenosine_ribonucleotides_de_novo_biosynthesis	Intestinal_content	−2.720	0.021
superpathway_of_polyamine_biosynthesis_III	Intestinal_content	−2.650	0.043
superpathway_of_L-tyrosine_biosynthesis	Intestinal_content	−2.578	0.021
D-fructuronate_degradation	Intestinal_content	−2.557	0.021
flavin_biosynthesis_I_(bacteria_and_plants)	Intestinal_content	−2.553	0.021
methylphosphonate_degradation_I	Intestinal_wall	2.527	0.021
TCA_cycle_VII_(acetate-producers)	Intestinal_wall	2.542	0.043
L-histidine_degradation_II	Intestinal_wall	2.552	0.021
superpathway_of_polyamine_biosynthesis_II	Intestinal_wall	2.608	0.021
allantoin_degradation_to_glyoxylate_III	Intestinal_wall	2.615	0.021
superpathway_of_arginine_and_polyamine_biosynthesis	Intestinal_wall	2.620	0.021
superpathway_of_menaquinol-9_biosynthesis	Intestinal_wall	2.627	0.021
superpathway_of_menaquinol-10_biosynthesis	Intestinal_wall	2.628	0.021
enterobactin_biosynthesis	Intestinal_wall	2.636	0.021
superpathway_of_hexuronide_and_hexuronate_degradation	Intestinal_wall	2.639	0.021
superpathway_of_menaquinol-6_biosynthesis_I	Intestinal_wall	2.640	0.021
toluene_degradation_II_(aerobic)_(via_4-methylcatechol)	Intestinal_wall	2.675	0.021
toluene_degradation_I_(aerobic)_(via_o-cresol)	Intestinal_wall	2.684	0.021
superpathway_of_chorismate_metabolism	Intestinal_wall	2.760	0.021
glucose_degradation_(oxidative)	Intestinal_wall	2.761	0.021
superpathway_of_L-tryptophan_biosynthesis	Intestinal_wall	2.779	0.021
D-galacturonate_degradation_I	Intestinal_wall	2.786	0.021
peptidoglycan_biosynthesis_IV_(Enterococcus_faecium)	Intestinal_wall	2.794	0.043
2-methylcitrate_cycle_I	Intestinal_wall	2.794	0.021
NAD_salvage_pathway_II	Intestinal_wall	2.813	0.021
2-methylcitrate_cycle_II	Intestinal_wall	2.815	0.021
superpathway_of_heme_biosynthesis_from_glycine	Intestinal_wall	2.843	0.021

L-methionine_biosynthesis_III	Intestinal_wall	2.867	0.021
protocatechuate_degradation_II_(ortho-cleavage_pathway)	Intestinal_wall	2.879	0.021
L-tyrosine_degradation_I	Intestinal_wall	2.881	0.021
ectoine_biosynthesis	Intestinal_wall	2.882	0.021
cob(II)yrinate_a,c-	Intestinal_wall	2.889	0.021
diamide_biosynthesis_II_(late_cobalt_incorporation)	Intestinal_wall	2.889	0.043
guanosine_nucleotides_degradation_III	Intestinal_wall	2.929	0.021
superpathway_of_glucose_and_xylose_degradation	Intestinal_wall	2.958	0.021
octane_oxidation	Intestinal_wall	2.958	0.021
L-leucine_degradation_I	Intestinal_wall	3.012	0.021
4-aminobutanoate_degradation_V	Intestinal_wall	3.033	0.021
purine_nucleotides_degradation_II_(aerobic)	Intestinal_wall	3.107	0.021
L-arginine_biosynthesis_III_(via_N-acetyl-L-citrulline)	Intestinal_wall	3.125	0.021
fatty_acid_salvage	Intestinal_wall	3.169	0.021
TCA_cycle_VIII_(helicobacter)	Intestinal_wall	3.204	0.021
adenosine_nucleotides_degradation_II	Intestinal_wall	3.311	0.021



Figure S1. A photo of defrosted mackerel icefish, *Champsocephalus gunnari*.

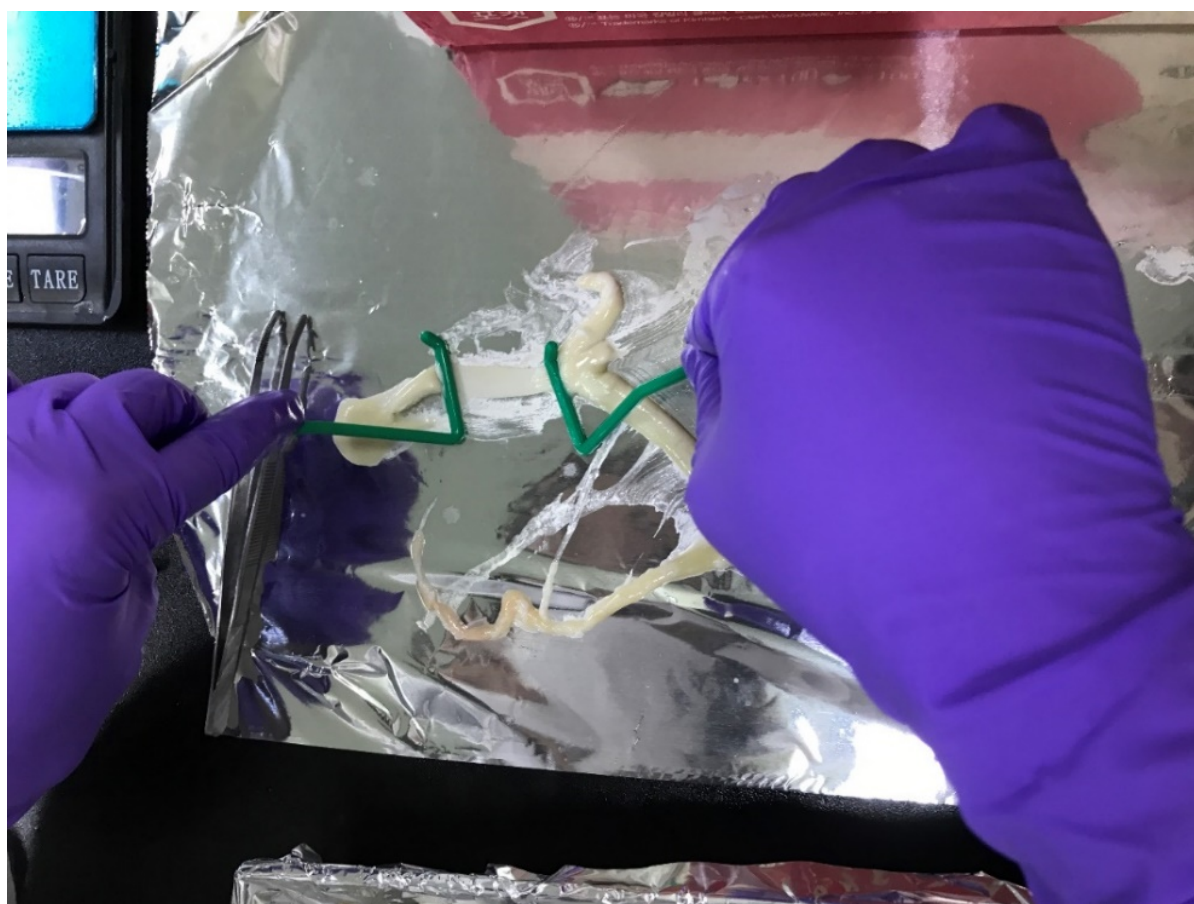


Figure S2. The use of spreaders for squeezing out the intestinal contents from the wall.

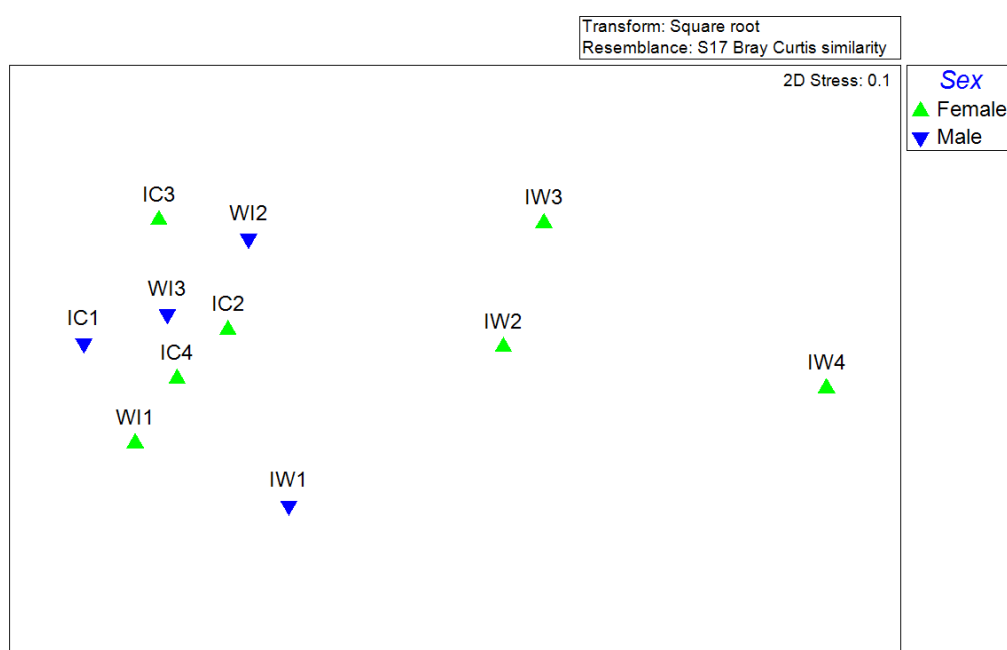


Figure S3. Non-metric multidimensional plot based on the Bray-Curtis dissimilarity between samples. Samples are grouped by sex. WI: whole intestine; IW: intestinal wall; IC: intestinal content.

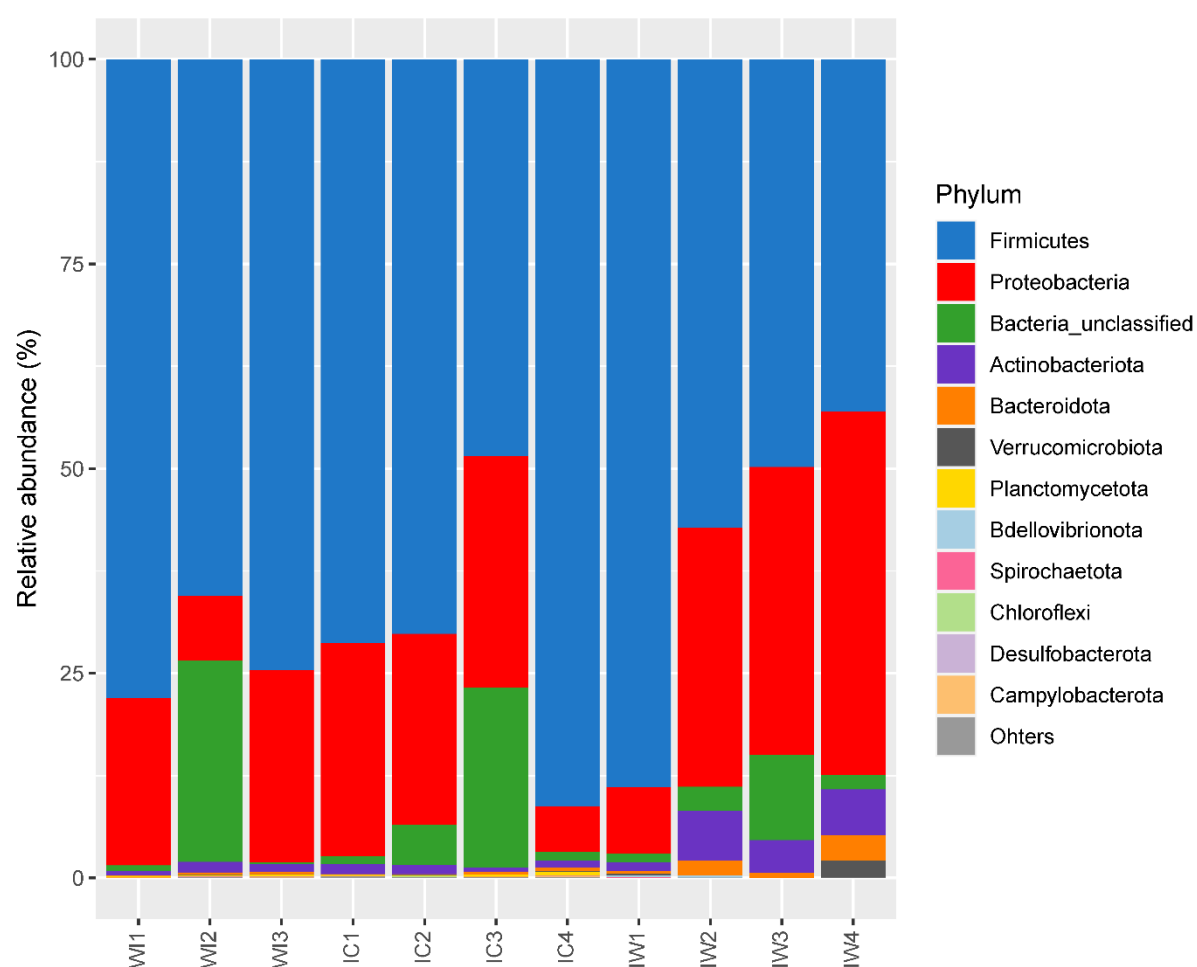


Figure S4. Phylum composition of the *C. gunnari* gut microbiome. WI: whole intestine; IW: intestinal wall; IC: intestinal content.