

SEAFOOD-ASSOCIATED

Dataset	Source	Sample collection	n	16S region
Aquaculture perch	Bartelme, R. P., McLellan, S. L., & Newton, R. J. (2017). Freshwater recirculating aquaculture system operations drive biofilter bacterial community shifts around a stable nitrifying consortium of ammonia-oxidizing archaea and comammox Nitrospira. <i>Frontiers in microbiology</i> , 8, 101.	<ul style="list-style-type: none"> UWM Great Lakes Aquaculture Facility recirculating aquaculture biofilter collected during the final 2 months of one Yellow perch rearing cycle, and then immediately before the initiation of a new rearing cycle samples were collected approximately every week through the first half of the new rearing cycle 	14	V4V5 [1]
Wild nase	Guivier, E., Pech, N., Chappaz, R., & Gilles, A. (2020). Microbiota associated with the skin, gills, and gut of the fish <i>Parachondrostoma toxostoma</i> from the Rhône	<ul style="list-style-type: none"> two rivers from the Rhône basin (France) specimens were trapped, euthanised, and sampled mucosal tissues: skin (caudal fin), gills, and gut 	648	V4 [2]
Wild and hatchery salmon	Webster, T. M. U., Consuegra, S., Hitchings, M., & de Leaniz, C. G. (2018). Interpopulation variation in the Atlantic salmon microbiome reflects environmental and genetic diversity. <i>Applied and environmental microbiology</i> , 84(16).	<ul style="list-style-type: none"> Atlantic salmon fry (8 to 9 months posthatch) were sampled from four wild populations and three hatcheries Scotland, Wales, England, and France specifically selected geographically and geologically distinct sites to include environmental and genetic variation in this study skin mucus was sampled from each fish by swabbing the left-hand side of the body along the entire length of the lateral line 5 times in both directions. gut samples were obtained by sterile dissection of the whole intestine to include both intestinal contents and epithelium-associated microbial communities 	175	V4 [2]
Wild and farmed tench	Dulski, T., Kozłowski, K., & Ciesielski, S. (2020). Habitat and seasonality shape the structure of tench (<i>Tinca tinca</i> L.) gut microbiome. <i>Scientific reports</i> , 10(1), 1-11.	<ul style="list-style-type: none"> wild fish – Kortowskie Lake (Poland) farmed fish: fry of the following species were co-cultured: tench, common crucian, carp and grass carp entire gastrointestinal tract and its contents were aseptically removed from each individual fish. The gut content was obtained by squeezing it into sterile tubes 	32	V4 [2]
Wild trout	Vasemägi, A., Visse, M., & Kisand, V. (2017). Effect of environmental factors and an emerging parasitic disease on gut microbiome of wild salmonid fish. <i>MSphere</i> , 2(6).	<ul style="list-style-type: none"> rivers that drain into the Baltic Sea juvenile trout were collected from 10 genetically distinct but geographically close populations, as the primary aim of our study was to evaluate the effects of parasite and disease severity on the GIT microbiota whole mid and distal intestine (from the anus to the pyloric cecum) was dissected 	152	V3-V4 [3]

ENVIRONMENTAL

Dataset	Source	Sample collection	n	16S region
Treated wastewater	Beattie, R. E., Skwor, T., & Hristova, K. R. (2020). Survivor microbial populations in post-chlorinated wastewater are strongly associated with untreated hospital sewage and include ceftazidime and meropenem resistant populations. <i>Science of The Total Environment</i> , 740, 140186.	<ul style="list-style-type: none"> wastewater treatment plant post-chlorinated effluent 	10	V4V5 [1]
Beach water	Cloutier, D. D., Alm, E. W., & McLellan, S. L. (2015). Influence of land use, nutrients, and geography on microbial communities and fecal indicator abundance at Lake Michigan beaches. <i>Applied and environmental microbiology</i> , 81(15), 4904-4913.	<ul style="list-style-type: none"> along the eastern and western coastlines of Lake Michigan at four Wisconsin beaches and four Michigan beaches submerged sand was defined as sand located beneath the surface of the water 1 m from the shoreline. berm or wash zone was defined as the lakeward portion of the beach within the range of wave action. backshore was defined as the generally dry portion of the beach between the vegetation line and the berm crest that is wetted from intermittent wave action 	87	V4V5 [1]
River water	McClary-Gutierrez, J. S., Driscoll, Z., Nenn, C., & Newton, R. J. (2021). Human Fecal Contamination Corresponds to Changes in the Freshwater Bacterial Communities of a Large River Basin. <i>Microbiology spectrum</i> , 9(2), e01200-21.	<ul style="list-style-type: none"> urban & rural rivers around milwaukee sample sites were selected to represent both southern (urban) and northern (rural) areas of the watershed, as well as streams with historically impacted or unimpacted quality sites were designated as impacted based on atypical dissolved oxygen (DO) concentrations in a long-term-monitoring data set 	81	V4 [4]

[1] <https://vamps2.mbl.edu/resources/primers>

[2] Kozich, J. J., Westcott, S. L., Baxter, N. T., Highlander, S. K., & Schloss, P. D. (2013). Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq Illumina sequencing platform. *Applied and environmental microbiology*, 79(17), 5112-5120.

[3] Klindworth, A., Pruesse, E., Schweer, T., Peplies, J., Quast, C., Horn, M., & Glöckner, F. O. (2013). Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. *Nucleic acids research*, 41(1), e1-e1.

[4] Caporaso, J. G., Lauber, C. L., Walters, W. A., Berg-lyons, D., Lozupone, C. A., Turnbaugh, P. J., ... & Knight, R. (2011). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proceedings of the national academy of sciences*, 108(Supplement 1), 4516-4522.