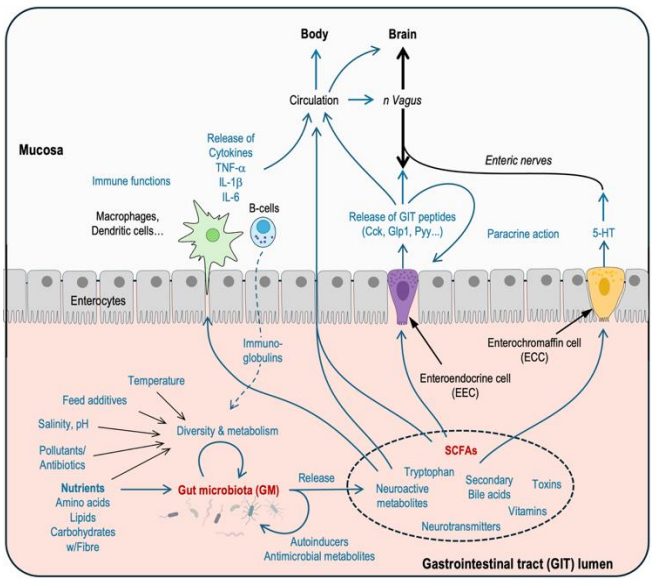
Mapping Atlantic salmon fatty acid receptor paralogs with potential roles in microbiota–gut–brain pathways

Ivar Rønnestad*, Virgine Gelebart, Ingvill Tolås
Department of Biological Sciences, University of Bergen, Bergen, Norway

Nutrient sensing regulates feed intake, digestion, metabolism, and growth through gut-derived endocrine and neural pathways. Beyond classical enteroendocrine cell signalling, the gut microbiota is increasingly recognized as a central component of the microbiota–gut–brain axis. **Microbial fermentation** produces short-chain fatty acids (SCFAs), which act both as metabolites and signalling ligands for fatty acid receptors.



In mammals, **SCFAs** activate intestinal fatty acid receptors, particularly in enteroendocrine cells, stimulating the release of appetite-regulating peptides and linking microbial activity to endocrine and neural pathways that converge on hypothalamic appetite networks. In fish, however, SCFA receptor function remains poorly defined.

Here, we **identified 11** Atlantic salmon **genes orthologous** to human **FFAR2** and **FFAR3**, likely reflecting expansion after the salmonid-specific whole-genome duplication, and profiled their expression in key tissues.

RT-qPCR revealed marked tissue-specific differences among paralogs. **ID8** (NCBI Gene ID: 123723724) showed the strongest gastrointestinal expression, particularly in the anterior and posterior hindgut. Although ID8 is among the more sequence-divergent paralogs, with lower similarity to human FFAR2/FFAR3 than several other candidates, its **strong hindgut enrichment** parallels mammalian FFAR2/3 localization. ID8 therefore emerges as a promising candidate for testing SCFA-responsive functions in Atlantic salmon.

Together, these findings provide a framework for investigating fatty acid receptor paralogs in microbiota–gut–brain axis signalling in Atlantic salmon.

