# Additional Files

# Addditional File 1. Table of metagenomic assembly statistics.

Additional descriptive information for these samples is provided in [58]. Abbreviations: nt, nucleotides; MBp megabase pairs; ctg, contig: cds, coding sequences.

# Additional File 2. Table of BLASTP matches for fish gut rpoB genes.

Top database matches for fish gut metagenome rpoB genes of 900 amino acids or longer. Matches to terrestrial ruminants were translated from assembled MAG nucleotide sequences downloaded from NCBI Genbank [57].

# Additional File 3. Relative abundances of eukaryotic 18S rRNA gene sequences in assembled metagenomic contigs.

Predicted 18S rRNA genes > 530 nt were pooled from all assembled contigs and given taxonomic assignments based on closest SILVA database match . Relative abundances were calculated based on assembly coverage depth multiplied by assembled 18S rRNA gene length. Additional details provided in Additional File 4.

# Additional File 4. Table of 18S rRNA gene matches to assembled metagenomic contigs.

Top SILVA Database (v138.1) matches to assembled metagenomic contigs were filtered for alignment lengths covering at least 30% of the database reference sequence (> 530 nt). Kmer coverage values (relative sequence abundance in DNA sample) were obtained from MetaSpades assembly program output.

# Additional File 5. Relative abundance calculations for predicted protein annotation keywords in fish gut and ruminant MAG samples.

# Abundance calculations were normalized according to total numbers of predicted proteins obtained in each assembled sample (Additional Files 6-10). Results have been sorted in order of compartmental differences, from highest relative abundance in hindgut to highest relative abundance in foregut.

# Additional File 6. Fish 5 annotations.

Predicted protein coordinates and functional annotations (prokka, CAZy, and SulfAtlas, and SignalP) from Fish 5.

# Additional File 7. Fish 6 annotations.

Predicted protein coordinates and functional annotations (prokka, CAZy, and SulfAtlas, and SignalP) from Fish 6.

# Additional File 8. Fish 7 annotations.

Predicted protein coordinates and functional annotations (prokka, CAZy, and SulfAtlas, and SignalP) from Fish 7.

# Additional File 9. Fish 8 annotations.

Predicted protein coordinates and functional annotations (prokka, CAZy, and SulfAtlas, and SignalP) from Fish 8.

# Additional File 10. 391 Ruminant MAG annotations

Predicted protein coordinates and functional annotations (prokka, CAZy, and SulfAtlas, and SignalP) from 391 ruminant MAGs [57].

# Additional File 11. Compartmental distribution of algal degradative enzyme keywords.

Prokka annotation keywords for assembled contigs have been normalized for total number of predicted proteins in each fish sample. Full data and significance calculations are provided in Additional File 5.

# Additional File 12. Comparative abundance calculations for carbohydrate hydrolysis and sulfatase enzyme classes.

Class abundances and statistical calculations have been normalized for total number of predicted proteins in each sample set. Full metagenomic annotations are provided in Additional Files 10-14.

# Additional File 13. Glucanase-containing CAZy classes.

Relative abundances of CAZy classes that include β-1,3- and/or β-1,4- glucanase activities were analyzed in kyphosid fish gut and terrestrial ruminant metagenomes. Abbreviations: avg norm, group average normalized per 1 million predicted proteins; F567, adult kyphosid fish; rum, terrestrial ruminant MAGs; HG, hindgut. Full data and significance calculations are provided in Additional File 12.

# Additional file 14. Separation distances for CAZy and SulfAtlas class pairs.

A) fish metagenomes. B) Terrestrial ruminant metagenomes. Complete data is presented in Additional File 15.

# Additional File 15. Co-localized CAZy and SulfAltlas classified genes and separation distances in fish gut and terrestrial ruminant microbiomes.

This file includes separation distances for all co-localized CAZy and SulfAtlas classified gene pairs occurring on the same contig, with separate tabs for with frequencies for all pairs occurring within an intervening distance of 25 genes or less, suitable as input for creating network diagrams using Cytoscape.

# Additional File 16. Co-localization network diagrams for individual ruminant enzyme classes.

Numbers in parentheses indicate relative gene frequencies per 1 million proteins in 391 ruminant metagenomes. Maximum intervening distance between nodes is 25 genes. CAZy and SulfAtlas classes lacking ruminant MAG co-localizations within the 25 gene limit have been omitted, but remaining classes are presented in the same order as main Figures 7 and 8,

# Additional File 17. Fasta format protein sequences from assembled fish gut metagenomes predicted using PROKKA.

File is accessible under Zenodo DOI 10.5281/zenodo.6635023

# Additional File 18. Fasta format protein sequences from 391 terrestrial MAGs [57] predicted using PROKKA.

File is accessible under Zenodo DOI 10.5281/zenodo.6635166