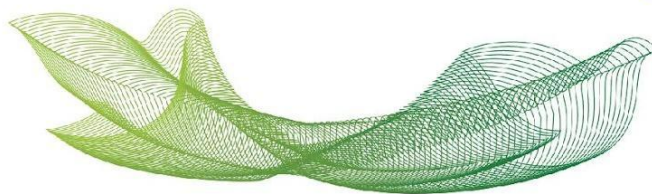


Tipo	Periódico
Título	Large Scale Genome-Centric Metagenomic Data from the Gut Microbiome of Food-Producing Animals and Humans
Autores	Leandro Nascimento Lemos, Fabíola Marques de Carvalho, Fernanda Fernandes Santos, Tiago Barcelos Valiatti, Dandara Cassu Corsi, Alessandro Conrado de Oliveira Silveira, Alexandra Gerber, Ana Paula C. Guimarães, Cintya de Oliveira Souza, Danielle Murici Brasiense, Débora de Souza Collares Maia Castelo-Branco, Elaine Kuroki Anzai, Francisco Ozório Bessa-Neto, Gláucia Morgana de Melo, Gleyce Hellen de Souza, Lúcio Fábio Caldas Ferraz, Márcia de Nazaré Miranda Bahia, Márcia Soares Mattos, Ramon Giovani Brandão da Silva, Ruanita Veiga, Simone Simionatto, Walter Aparecido Pimentel Monteiro, William Alencar de Oliveira Lima, Carlos Roberto Veiga Kiffer, Rodrigo Cayô, Ana Cristina Gales e Ana Tereza Ribeiro de Vasconcelos.
Autor (es) USF	Lúcio Fábio Caldas Ferraz e Walter Aparecido Pimentel Monteiro
Autores Internacionais	
Programa/Curso (s)	Programa de Pós-Graduação Stricto Sensu em Ciências da Saúde
DOI	https://doi.org/10.1038/s41597-022-01465-5
Assunto (palavras chaves)	One Health, Metagenomic Data, Gut Microbiome, Food-Producing Animals
Idioma	Inglês
Fonte	Título do periódico: Scientific Data ISSN (online): 2052-4463 Volume/Número/Paginação/Ano: v. 9, artigo número 366, p. 1-7, 2022
Data da publicação	25 de junho de 2022.
Formato da produção	Impressa ou digital
Resumo	The One Health concept is a global strategy to study the relationship between human and animal health and the transfer of pathogenic and non-pathogenic species between these systems. However, to the best of our knowledge, no data based on One Health genome-centric metagenomics are available in public repositories. Here, we present a dataset based on a pilot-study of 2,915 metagenome-assembled genomes (MAGs) of 107 samples from the human (N = 34), cattle (N = 28), swine (N = 15) and poultry (N = 30) gut microbiomes. Samples were collected from the five Brazilian geographical regions. Of the draft genomes, 1,273 were high-quality drafts (≥90% of completeness and ≤5% of contamination), and 1,642 were medium-quality drafts (≥50% of completeness and ≤10% of contamination). Taxonomic predictions were based on the alignment and concatenation of single-marker genes, and the most representative phyla were Bacteroidota, Firmicutes, and Proteobacteria. Many of these species represent potential pathogens that have already been described or potential new



	families, genera, and species with potential biotechnological applications. Analyses of this dataset will highlight discoveries about the ecology and functional role of pathogens and uncultivated Archaea and Bacteria from food-producing animals and humans. Furthermore, it also represents an opportunity to describe new species from underrepresented taxonomic groups.
Fomento	CAPES e CNPq